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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted:
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ACCESSION AC096619
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ACCESSION AC124411
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ACCESSION: AC095214
ACCESSION: ALG69976
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ACCESSION: AC110100
ACCESSION: AC129113
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                                                                                      August 24, 2004, 13:46:45; Search time 11231 Seconds (without alignments) 3.981 Million cell updates/sec
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GenCore version 5.1.6
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Maximum Match 100%
Listing first 45 summaries
                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 0.5
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Mapping information for this clone was provided by Dr. Wes Warren, obstatment of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                               The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers en (http://www.chori.org) from male CS7BL/64 mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                            NEICHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
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                                                                                            restriction digest.
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Query Match 36.9%; Score 840.902; DB 1; Length 183326; Best Local Similarity 68.6%; Pred. No. 0.024;	TATCTT	354	OY 414 TGGTCAGATAGGACATAGAGTATTATTACAATTGTCTTTATCTGTCGAGACTTGCTTTG 473	QY 474 TITIGAAAIAIGIAFICAAFITIGGAGAGFITICATAGGGTGCTGACAGAAGGTACAGTC 533	Qy 534 TITGTGTTTTGGTGAAATAGTCTGTAAATATCTCTAGGTCCACTTGGTTTATGACATCAG 593  Db 41006 TITTGTGTTCAGAAATGTTCTACAAATATTTTAGGTCCATTGGTTTCTAATGTAAG 41065	Qy         594         TTAGCTCCAGCATTTCTCTCTTTTTTTTTGTTGACATGACTGTTGGAGAAAT         653           Db         41066         TTAGCTCCAGTACCTGTTTAGCTTTTGTCTGA-ACAACCTATTTATCGGCAAGAAT         41124	654 GGGGTATTGAAGTAGCCCACTATCTGTGTGAGG-TCAATATGTGATTTTAGCTGTAGC	41125 GGAGTATTGAAATCACCCACTAACACTGTGAGGGATCAATATGTGACTTTAGCTGTGGTGTGTGT	Db 41185 AGIGITICITITAIGAACIIGGACCIIGITITICGGIGCAGAGAIAAIAAGALAGGCA 41244  Qy 773 ATGICCICITGGIGGAITITCCTITGAIGCCTAIGIAGIATCTICCCAAICICAIC 829  Db 7136 ATGICCTICTICGAIGGAITITCCTITGAIGCCTAIGIAGIATTCTICCCAAICICAIC 829	830 IGCTIAGITITIGGGTTAAGTCIAT-TAGTCAGATATTAAAATGACTGTATCGGCTTG 1	887 CITCITAGGGCCATTIGCTTAGAATATC-TITTCCATCCTTTACTCTAAGGTGATGTCT 887 CITCITAGGGCCATTIGCTTAGAATATC-TITTCCATCCTTTAAGGTGATGTCTT 813.85 CTTCTTAGGGGCCATCTAGAATATGACTAGAATAGATAAGAATATGAATAGAATAAGAATATGAATAGAA	946 ATCCATGGTAGGTTGTCTTTTTTGGATGCAGCAGTAGGAT-CTTGTTTTCATA		TITIACIGGGLAACIAAGACLACIGALCII 4133 TIGIGGAIICTIGITAICIIGCACIIGIGAAGIGIGIG 1121	41537 AAAAAGTGTTAATGAGCAGTCTCTGTTGATTCCTGTCCTTTTTTCTCTTGTGTGTG	rcigigigicitationgreticidagigigigidagigigigigigigigigigigigigig	Db 41657 TGTGTCTGTCTCTGTCTCTCTCTCTCTCTGTGTGTGTGT	Db 41717 IGTCTGTCTCTCTCTCTCTCTCTCTCTGTGTGTGTGTGTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 287253;
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        212409: gap of unknown length
287253: contig of 74844 bp in length.
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Best Local Similarity 68.6%; Pred. No. 0.034;
Matches 1486; Conservative 0; Mismatches 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6636. ,13865 '-
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13966. ,22641
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Monte="assembly_name:Contigl31"
1585...3263
Mote="assembly_name:Contigl32"
                                                                                                                                                                                                                                                                                                                                                             364. 4684
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                                                                                                                                                                                                                                                                                                                                                                                                                    4785. .8535
/note="assembly_name:Contig144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32742. 50896
/note="assembly_name:Contig147"
50997. 137224
/note="assembly_name:Contig148"
137325. .212309
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/chromosome="UNK"
                                                             Location/Qualifiers
                                                                                                                                                                                                                          clone="RP23-111N9"
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AC147502 287253 bp DNA linear HTG 05-DEC-2003
Mus musculus chromosome UNX clone RP23-111N9, WORKING DRAFT
SEQUENCE, 10 uncrdered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (05-DEC-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (basel to 287253) Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
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unknown length
of 74985 bp in length
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 282424 bases at least Q40
Consensus quality: 286117 bases at least Q20
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of 1321 bp in length
unknown length
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unknown length
of 5230 bp in length
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1679 bp in length
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HTG; HTGS_PHASB1; HTGS_FULLTOP
MUS musculus (house mouse)
Mus musculus
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unknown length
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                   DEFINITION
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AUTHORS
TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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JOURNAL
                                                                                                                                                                                                                    RESULT 2
AC147502
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0y 1813TTATITIGACTTAACATTICTTGACCAAGGTATCCATTICTTCTATCTTGAC 202639 0y 1868 TICACTCCCGACATTCCTCTATCTTGACTAACATTTCTTGACTAACATTTCTTGACTAACATTCTTGATTGA	REBULT 3 AC114097 AC114097 AC114097 RATLES HORVEGICUS CLONE CH230-90E1, *** SEQUENCING IN PROGRESS ***. AC114097.5 GI:30580092 KEYNORDS AC114097.5 GI:30580092 KEYNORDS RATLUS HTGS PHASEZ; HTGS PART; HTGS_ENRICHED. AC114097.5 GI:30580092 KEYNORDS RATLUS HORVEGICUS (Norway rat) RATLUS NORVEGICUS (Norway rat) CORGANISM REATOR NEAZOR; Chordata; Craniata; Vertebrata; Euteleostomi; MAMMALIA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MAMMALIA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MATHORS MIZHY, D.MATHO, M. Matharanalke, D. Barber, M., Bannstead, M., Benahmed, F., Baldwin, D., Bandaranalke, D., Barber, M., Barnstead, M., Benahmed, F., BRYARL, N., Bular, J., Blankenburg, K. Blyth, P. Brown, M., BRYARL, N., Bular, J., Blankenburg, K. Blyth, P. Brown, E., Cardenas, V., Carter, K. Gavazos, I. Canderon, Didha, M. Cree, A., D'Souza, L., Cardenas, V., Carter, K., Cavazos, I. Canderon, Didha, N., Debard, C., Dederich, D., Deblgado, O., Chang, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Depper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Fanger, M., Ganza, M., Harlandez, M., Hanles, S., Hadun, S. L., Handun, C., Hamilton, C., Kraft, C.L., Lebow, H., Levan, J., Levan, J., Levan, J., Levan, J., L
	1307 TAGGRCTGCATTGAAGATATTTTTACATCTGATTTTATCTTAGAATTCTTTCT

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Lorensubwari, M. M. M. Y. Lorador R. T. Lorador R. T. Mangum, A. Mandahari, M. Mandahari, Mandahari, M. Wandahari, M. Wandahari,
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

REFERENCE AUTHORS TITLE JOURNAL

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116565 TTGCCTCAAAACTGTCTTTATTGTTTTTCCATGACTTTGGGCATGTTGTATTTTCATTTTC 116506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116277 rccarddacrgargagaaagrararrcrirrgagricaagrgaararrcrgraararc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       745 GTTTGGTGCATAGACATTAAGAATTGCAATGTCCTCTTGGTGGA---TTTTCCTTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116445 ATTTAGTGGTGAGTTGTTTTAGTTTTCATGAATTT-------TTTGTAATCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 GTTGTTGTTATCTAGATTTAAGCTGTGGTGGTCAGATAGGACATAGAGTATTATTTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  506 CATAGGGTGCTGACAAGAAGGTACAGTCTTTGTGTTTTGGTGAAATAGTCTGTAAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 TCTAGGTCCACTTGGTTTATGACATCAGTTAGCTCCAGCATTTCTCTGTTTCGTTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                802 CCTATGTAGTATTCTTCCCAATCTCATCTGCTTAGTTTTGGGTTTAAGTCTAT-TAGTCA
                                                                                                                                                                                                                                                                                                                                                                                               207 TTACCACTGCTCTCTCTCTCTTTCTCTAACACTTCTGGGCCAGGGTAGGGGCACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               686 AGG-TCAATATGTGATTTTAGCTGTAGCTGTGCTTGTTTTATGAACTTGGGTGACATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              861 GATATTAAAATGACTGT--ATCGGCTTGCTTCTTAGGGCCATTTGCTTAGAATATCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCTTTTATCTGTCGAGACTTGCTTTGTTTTGAAATATGTATTCAATTTTGGAGAGTTT
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 511; Indels 184; Gaps
are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 230813: contig of 230813 bp in length.
                                                                                                                                                                                                                                                                                                                   Length 230813;
                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                      1. .230813
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/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-9081"
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Pred. No. 0.06:
                                                                                                                                                                                                                                                                                                                34.2%;
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 68.5
Matches 1509; Conservative
                                                                                                                                                                                                                                                                                                                Query Match
Best Lócal Similarity
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115801 GCAGAAGGATGGATCCTCATTTACACATTCATCCTTAGGCTGCCTTTTTGTTGGGT 115744	1035 AATTAAGATCATTGAGTGATGATGAAGAATTATCAATGAGGAGTGTTTGTGGATTCT 1094	115743 AACTGAGACTACTGATCTTAAGAGTTGTCAATGGGCAGTATTTGTTGATTCC 115692	1095 IGTTATCTTGCACTTGTGAAGTGTGTGTGTGTGTGTGTGTG	115691 TGTTATTTTTTTTCTCTTGTGTGGGTCTCTGTGTGTGTCTTTTGTGTTTATATCTTT 115632	1155 G 1155 G 1155	115631 GIGICIGIGIAICIGCCIGCCIGCCICICICICICICICI	1156	1 CTCTCTCTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTG	1199 TCTGTGTTCTCTCCCCCCTTTTGATTTTTGGCCTGGAATATTATTATTATTTTTTTT	259		1317 TITGAAGATAGATATTCTITACATCTGATTITATCTIAGAATGTCTTTCTTTCTATCTAACT 1376	115395 TTTGTATATAGATGCTGCTTAAATTTGATTTTATCTTAAAATATCTTCCTCCGTCT 115340	1377 ATTGTGACA-GAAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGACATCTGTAGTCTCTTGG 1435	115339 ATTGTAATATTTTTTTTTTTTAGTAGTAGTGTGGCCTGACATCTGTGGCCTCTTAG 115280	1436 AGTCTGTAGCACATCTGTGCAGGGCCTTCTTACATTTTGAGTTTCTATTGGAAAGTCAG 1495	115279 AGTOTIGIGGACCATOTIGICTAGGCCOTTATGGCTTTTACAGTOTCCATT-GTGAATTOAG 115221	1496 GIGTAATICTAATACATCTGCCTTTATATGTTAATIGGTCTTTTTTCCCTTGCATCTTTT 1555	115220 didinadichacadgichdrithacatdinatcrcccccccdaaghir 115168	1556 AATATICITICITIGITCIATACTITITAGIGATITIGATIATAICACIGIGGGGAGI 1613	115167 AAAATICTITITTTTTTTTTTTAATGTGTTTGAGTTTTAAGTGCTCGGAGGACT 115108	1614 TICTITICCGGICCAARCTATITIGGIGITITIGIATICCTICTIGIACCTIGATAGGCARCT 1673	115107 icciricradcicre-icrairiddadircadiaiccircridiaccirdaraddcaici 115049	1674 CITICICAAGGITAGGAAATITITITITITITIGGITITICITGAAAATATITITCCTGCTIT 1733	115048 CTTICTGTTAGGGAAATTTTTTTTCTGATTTTGTAGAAATATTTTCTGTGCCTT 114991	1734 TGACCTGCCTTCTTCCCCTTCTATTCCTTTGGTTTTTGGATAGTGT 1782	90 IGACITGAGITICITICITCCICIATICCIATICCICICAAAIA1GACCITTGAGGIG 114	1783 CTCTGGCTTCCTGGATGTTT	1826 AACATTTTCTTTGACCAAGGTATCCATTTCTTCTATCTTGACTGCCTGAGATTCT 1885		1886 CICTICIATOTOTICIATIOTOTOAGIGAGGCTIGICAGGGTICCIG-ITGGGTICT 1944	114814 -TCTTCTATCTTTATAAT-TTTTGGTGAGGTTTGCCTCTGAGGTTCCAGTTTAAGTTCC 114757	1945 TAATTITICALTICCAGAITICCTICAGTITGGGITTIGITTATIAATICTATITCCAC 2004 
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ACTO2426.6 GI:3389990

MAG mascollus (house mouse)

Mus musculus charcheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

Birran, B., Nusbaum, C. and Lander, E., Ali, A., Allen, N.,

Mus musculus charcheria (house mouse)

Mus musculus charcheria (house mouse)

RS Birran, B., Musbaum, C., Lander, E., Ali, A., Allen, N.,

Bairran, S., Barta, N., Bastien, V., Boyuslavkiy, L., Boukhgalter, B.,

Brown, A., Camarata, J., Campopiano, A., Chararo, B.,

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Direct Submission

AL Subramanian, A. Arachchi, H. M., Barna, N., Barna, N., Bloom, T., Changer, D., Chang, J., Changer, J., Chang, J., Changer, J., Johnson, J., Hallen, N.,

Barna, J. S., Dodge, S., Dooley, K., Donnelleil, A., Allen, N., Hall, J., Horron, L., Hallen, N., Halen, N., Hallen, N., Hallen, 2178 AGGGTTTTAGCAGGGACAI--ATTGICCTGGTTGTTATTGICTGTGTTTTTGCTTTGGCA 2235 114638 AC102426 192016 bp DNA linear ROD 27-SEP-2003 Mus musculus chromosome 1, clone RP24-88A10, complete sequence. AC102426 AC102426.6 GI:33859950 RESULT 4
AC102426
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS g 엄 à 쉽 ò 8 ò 쉽 g

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complement(4*4', ...*29')

complement(2*69...263)

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complement(2702...2714)

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19864. 19886
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|668]. .16790
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12139...12195
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7587. .7606
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complement (7608. .120.
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complement(12196. .1
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. .17796
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5942. .5969
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Submitted (19-Aug-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

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B brren, B. Nusbaum, C., Lander E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Collymore, A., Cook, A., Cooke, P., Corum, B., Chang, J., Choepel, Y., Collymore, A., Cook, P., Cocum, E., DeAriano, K., FitzGerald, M., Gage, D., Galagan, J., Gradyna, S., Frizgerald, M., Gage, D., Galagan, J., Hagopian, D., Hagos, B., Kamat, A., Kartas, A., Kalls, C., Landers, T., Levine, R., Jones, C., Macdonald, P., Major, J., Mahning, J., Mathews, C., McCathy, M., Meldim, J., Meneus, L., Mihova, T., Mabbitt, R., Waclean, C., Micol, R., Mahova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peerson, K., Phukkang, P., Smith, C., Speneer, B., Schauge-Thomann, N., Stolanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V., S., Viel, R., Voll, R
Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meddim, J., Mended, Y., Murphy, T., Naylor, J., Mended, J., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Morbu, C., O'Connor, T., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Spencer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
                                                                                                                                                                                                                                                                                                                              Submitted (31-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 192016)
Birren, B., Nusbaum, C. and Lander, E.
Direct Submission
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Mus musculus clone RP24-467J24, WORKING DRAFT SEQUENCE, 4 unordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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On Apr 17, 2003 this sequence version replaced gi:17060796.
All repeats were identified using RepeatMasker:
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP24-467J24
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AC102686.2 GI:30018186
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Mus musculus (house mouse)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u> AGTTGTTTGGTTTTCCATAAGTTTGTAAGTTTTCTGTTTTCTGTTGTTGTTGTTGTTAT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156990 CTGGCTTTAATACATGGTAGTCAGATAGGATGAGCGATGTACTATTTTTGTTTTTCTTGTA
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                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                   1571: contig of 1571 bp in length
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7052: contig of 5381 bp in length
7152: gap of 100 bp
93807: contig of 86655 bp in length
93807: contig of 80655 bp in length
27550: contig of 133643 bp in length.
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156696 TOANDACCIONTITACATONG——COGNECIDATITACACACIOGACIACATOT 1466191 156616 TOANDACCIONATITACACACACACACACACACACACACACACACACACAC	1595 ATTATGCACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGGTGTTTTGTATGCTTCT 1654
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TCCTGGTTGTTATTGTCTGTGTTTTTGCT 2229 GTGAGGCTTGTCTCTGAGGTTCCTG-TTG 1938 AITTICCICCCGGTAITIACAITITCAIA 2058 CTTCCCCTTCCTCTATTCCTTTGGTT--- 1770 TAAGGATCTCTATCATACCATACAGGC 155215 CCAGGATGTTTTGTGTCAGAACTGTTTTA 155514 V., Lander, E., Ali, A., Allen, N.,
V., Boguslavkiy, L., Boukhgalter, B.,
no, A., Chang, J., Chazaro, B.,
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i., Marguls, M., Marguls, V., Marguls, V.,
i., O'Domnell, P., O'Neil, D.,
ing, P., Pierre, N., Pollara, V., CCAAGGACCTTTTATGAATTCATAAATG 2118 CCTGGATGTTTTATGCCTGGATTATTTTA 1820 TTTCTTCTATCTTGTCTTCACTGCCTGAG 1880 ATGTT-GCATTCTCAGGGCCTATTGTAAT 2177 DNA linear HTG 09-JUN-2003 RKING DRAFT SEQUENCE, 38 unordered niata; Vertebrata; Euteleostomi; urognathi; Muridae; Murinae; Mus. S\_FULLTOP.

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of 464 bp in length

100 bp

of 609 bp in length

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of 671 bp in length

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in 671 bp in length

in 100 bp

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Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stange, Thomann, N., Stoojanovic, N. Strauss, N., Subramannan, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 9, 2003 this sequence version replaced gi:22380823. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                           Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: Sequence_submissions@Senome.wi.mit.edu
Contact: Sequence_submissions@Senome.wi.mit.edu
Contact project Information
Center project name: 118952
Center clone name: 560_I 9
Center clone name: 560_I 9
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.56073
Consensus quality: 206419 bases at least Q40
Consensus quality: 212661 bases at least Q20
Insert size: 182000; agarose-fp.
Insert size: 183698; sum-of-contigs
Quality coverage: 10.3 in Q20 bases; sum-of-contigs
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COMMENT

100 bp of 1308 bp in length 100 bp of 1479 bp in length 100 bp 100 bp of 1051 bp in length 100 bp of 843 bp in length ap of 100 bp ontig of 58740 bp in length 100 bp of 32728 bp in length 100 bp of 24389 bp in length 44371 bp in length of 886 bp in length 100 bp of 931 bp in length 100 bp of 1324 bp in length 00 bp f 1962 bp in length 00 bp 100 bp of 3703 bp in length 00 bp f 1662 bp in length 00 bp 1489 bp in length 1402 bp in length 1736 bp in length 00 bp £ 978 bp in length

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/clone="RP24-56019"
/clone_lib="RPCI-24 Male Mouse
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25578, .26092 //note="assembly_fragment"
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Best Local Similarity 67.6%;
Matches 1349; Conservative
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	2068	QY 2128 GICCTIGCCTICAGCTAIGTIGCATICTCAGGCCTAITGTAAIAGGGTTTIAG 2187  Db 128450 GITTTIGCTTAIGCTTCAACCAIGTTGAAAIAI-TCAGIGICAGGTTGCTGGGCTAICA 128508  MA	2188 CAGGGACATATTGECTGGTTGTTATTGECTTTGGCATATAGACGGCTG 2247	128509 TGGAGACATATTGTCTT		Db 128569 GTTTTGGGTTTAGGGT 128584 Db	RESULT 7 OY	•	sequence.	z		ORGANISM mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			JOURNAL Submitted (17-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:	humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk COMMENT On Apr 18, 2003 this sequence version replaced gi:2504345.		from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.	Center: 1911 Come Trust Sanger Institute	Web site: http://www.sanger.ac.uk	Concact: numquery@sanger.ac.uk  Concact: numquery@sanger.ac.uk	Noting sequence assembly data is compared liber overlapping clones.  Where differences are found these are annotated as variations.  Do not the the	variation annotation may not be found in the sequence submission.	corresponding to the overlapping tions, as we submit sequences with only a small overlap as described above.  The sequences were finished as fallows unless otherwise noted; all	rolls sequence was finished as follows unless constructs are regions were either double-stranded or sequenced with an alternate	chemistry or covered by high quality data (1.6., pared quality >= 30); an attempt was made to resolve all sequencing problems, such	as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the companies and the companies and the companies of the companies of the companies of the companies.	assembly was confirmed by restriction digest, except on the lare occasion of the clone being a YAC.	The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:	Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEF; INLORMATION On the WORMPEP database can be found at	http://www.sanger.ac.uk/Projects/C_elegans/wormpep RF23-Z18A4 18 from the RPCI-23 Mouse BAC Library	constructed by the group of Fierer de Jong. For further details see http://www.chori.org/bacpac/home.htm	VECTOR: DEACES.6. Location/Qualifiers

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clone_lib="RPCI-23"
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Db 115970 CTAAGCACCTGGGATGGGAAGGTTGTAATTTTAGGTGCTGAT 116012	RESULT 8 AC102201 LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS AC102201 LOCUS LOCUS LOCUS LOCUS LOCUS ACCESSION AC102201		MacCarthy, M. McBwan, P., Margor, V., Margols, V., Margols, V., Marcarthy, M., McBwan, P., McKernan, K., McPheeters, R., Meldrim, J., Mihova, T., Minoya, V., Murphy, T., Naylor, J., Nauron, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stranss, N., Subramannan, A., Talamas, J., Testaye, S., Theodore, J., Tonham, K., Theodore, J., Tonham, K., Talamas, J., Testaye, S., Tala	Viel, R., Vo, A., Wilson, B., Wu, X., Wandan, D., Ye, W.J., Young, G., Vall, R., Vo, A., Wallson, B., Wu, X., Wandan, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  TITLE Direct Submission JOURNAL Submitted (13-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  REFERENCE 3 (Gases I to 158685) AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dehrellano, K., Cook, A., Cooke, P., Corum, B., Dehrellano, K.	Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferrahara, P., Ftragerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, M., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Mahning, J., Matchews, C., McCarthy, M., Maddrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., O'Neil, D., Oliver, J., Pecerson, K., Phunkhan, P., Pierre, N.	Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vol., Wilson, B., Wu, X., Wwman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. TITLE Direct Submission JOURNAL Submitted (04-MRA-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 4, 2003 this sequence version replaced gi:22381218.  All repeats wave identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
	1250 ATAITHTCITGADAGGGTAACAICHTAGAITGAAGTTTHTCICCTAGCCTTCTT 1307 114990 GTGTTHTCITGAGTAGGGTGCTCTTTAGGTTGGAGTTHTCTTCTTAGGATTTCTTTAGGATTGCTTCTGT 115049 1308 AGGTCTGCATTTGAAGATAGTTCTTTACATCTTTATCTTAGAATGTTTTTTTT	1488   AAGTCAGGTGAATTCTAATACATCTGCCTTTATATGTTAATTGCTTTTTTCCCTTG   1547	1666 - AGGCATCTTTCTCAAGGAATTTTTTTTTTTTTTTTTTTT	115525 CTTCTTAGGCTGACCCAGGGTCCCTGGATGCTTTGTGCCAGGAGTTTTTTAGATTTAACA 115584  1830 TTTTCTTTGACCAAGGTATCCATTCTTCTATCTTGTCTTCAGGATTTTTTAGATTTAACA 115584  115585 TTTTCTTTGACCAAGGTATCATTTCTTCTAACCTGCTGAGATTCTCTTT 115644  115585 TTTTCTTTGACTGATGATTTCTTCTTCTAACCTGTCTTCAGGATTCTTTT 115644  1890 TGTATTCTTTGATTCTTGAAGAGCTTGTCTCTGAGGTTCTTAATT 1949  115645 TTCATCTCTTGATTTTTTTTTTTTTTTTTTTTTTTTTTT	1950 TITCATITCCAGARTICCTGAGTITGGGTTTGTTATTAATTCTATTTCCACTTTCA 2009  115704 GITTICTGTTTGGGTTTTCTTTATTGATCCAGTTTTCA 115747  2010 GGTCCTGAAATGTTTTACTCAGTTTTCCTCCCAGTATTTAATCATCGTTTTTAA 2069  115748 GGTCTTGAATGTTTTACTCATTTTCTTCATAGATTTTATAAATGTTTCTTAA 115791  2070 TGGATTTATTCATTTGTTTGTTTATTAAAATGTAAAATGTAAAAGTTTCTTAA 115791	

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Best Local Similarity 68.6%;
Matches 1396; Conservative
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-------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBA
                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                        Center clone name: 556 J 13

Sequencing vector: Plasmid; via, 100% of reads Sequencing vector: Plasmid; via, 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
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Consensus quality: 155435 bases at least Q20
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Insert size: 143000; agarose-fp
Insert size: 156985; sum-of-contigs
Quality coverage: 10.9 in Q20 bases; sum-of-contigs
                                                   Web site: http://www.seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: sproject Information
Center project name: L18206
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Oy 1818 TIAGACTIAACATTITCTTIGACCAAGGTATCCATTICTTCTATCTIGTCTTCACC	1878	OY 1938 GGGTTCTTAATTTTTTCALTTCCAGATTTCCTTCAGTTTGGGTTTTGTTTATT  Db 74970 CAAGTTCCTAAGTTTTTTTGATTTCCACGTTTCCTCACTTTGGGGTTTCTTTATT	Qy 1995 CTATITCCACTITCAGGICCTGAAAIGITTTACTCATITITCCTCCCAGTATITI 	Qy 2053 TICAIAGGITICITIAAIGGAITIATICAITICCICITICAAGGACCITITAIGAA.	Qy 2113 AAAATGTAAGGTCCTTGCCTTGTGCTTCAGCTATGTGT-TGCA-TTCTCAGGGC	Qy 2172 IGTAATAGGGTTTTAGCAGGACATATTGTCTGGTTGTTGTTGTCTCTGTTATTGTCTCTGTTGTTGTTGTTGTTGTGTGTTGTTGTTGTTG	Qy 2224 TTTGCTTTGGCATATAGACGGCTGAGTTTGGGATGATTGTAATTCTAGGTGCTGAT 	AC102739 206312 bp DNA linear HTG	WORKING	HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP. Mus musculus (house mouse) NM mus musculus Eukarvota; Metazoa; Chordata; Craniata; Vertebrata;		JOURNAL Unpublished REFERENCE 2 (bases 1 to 206312) AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Aller Anderson, S., Barna, N., Bastien, V., Boqualavkiy, L., Boukhde	Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P. Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,	<pre>Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Illev,I., Johns Jones,C., Kamat,A., Karatas,A., Kalls,C., LaRoque,R., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,</pre>	MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldri Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Ng Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,P.	Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schup	nani s.M.	Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. TITLE Direct Submission
743 GICTITGGIGCALAGACALTAAGAALTGCAATGICCICTIGGIGGAL-TITCCITIGAIG 801	73894 GIGITIGGIGCATAGAAGITAAGAAITICAGIGICCICTIGGIGGAIGITICCITIGAIG 73953 802 CCIAIGIAGIAITICCCAAICICCATAGITIAGGITIAAGICIAT TAGICA 860	GATATTAAAATGACTGTATCGCTTCTTAGGCCATTTGCTTAGAATATC-TTTTC		GTAGGATGGATCTTGTTTTCATATCCATTCTGTTACCCAGTATCTTTTTTTT	1098		GIGIGIGIGIGIGIGIGICICIGIGICIIGIGICIIGIGIGICIGIGIICICICCCCCC	1219 ITGALTITIGGCCTGGAATTATTATTATTCATATTTTCTTGAATGTGGGTAACATCTTT 1278	1279 AGAITGAAGITITICICCIAGCCITCITIAGGICIGCAITIGAAGAIAGAIAGAITICITIAC 1338 14338 GAGITGAAGITCICIAGIT - CCITCICIGGGGAIGGAITIGAAGAIAGAIAGAITGCITAA 74395	1339 AICIGAITTIAICTIAGAAIGICTITICTICCAACTATIGIGACAGAAAGITTITCIA 1398 	1399 AGIGCAGIAGICTGGCCTGACATCTGTAGACTCTGTAGAGTCTGTAGCACATCTGTGCAGG 1458	1459 GCCTTCTTACATTTTGAGTTTCTATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCT 1518 	1519 ITATAIGITAATIGGICTITITICCCTIGGATCTITITAATATTCTTTGTTCTATAC 1578	1579 ITTTAGTGATTATTATGCACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGG 1638 -	1639 IGITITGIAIGCTICTIGIACCTIGATAGGCAICTCTTTCTCAAGGTIAGGAAATTTTTC 1698 	1699 TITITIGGITTICTIGAAAATATITICCCIGCTITIGACCI-GCCTICCTCCCCTCCTC 1757		74795 TACTCCTATTGTTTCTACATTTAGTATTCTCATAATGTTCCAGATTTCTTGGCTGTGCCT 74854
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AATTCAT 2112 ||||| TATTCAC 75149 ACTGCCT 1877 ||||| GATGCCT 74909 TCCTGTT 1937 |||||||| TCCTGTT 74969 GGCCTAT 2171 |||||| |GGCCTTC 75209 CTGTGTT 2223 ||||||| TTGTGTT 75269 ATTAATT 1994 |||| | | ATTGAGT 75029 TTGTGT 75089 20-AUG-2002 7 unordered TACATT 2052 s,C.,
drim,J.,
Nguyen,C.,
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ity 69.2%; Pred. No. 0.077;
servative 0; Mismatches 451; Indels 174; Gaps
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Qy         2122 GTPAAGGTCCTTGCCTTGAGCTATGTT-GCATTCTCAGGGCCTATTGTAATAGG 2180           Db         129905 TTTAAGGTCTTTGTGGCTCCAGCTCTGTTGGAATACTCAGGCCTGCTGTGTGTTTTTGTTTG	MERBILITION MAIN BABLES LANGE BABAT  ACCESSON MUNICATION MAIN BABLES LANGE DEART.  ACCESSON MAINTENN MAIN FINGS PRABEL; HTGS DEART.  SCHUNCES MAINTENN MAINT	Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nayren, C., Micoll, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
1061   TGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTATCTTGCACTTGTGAAGTGTGT   1120		2002 CACITICAGGICCIGAAAIGITITACICAITITCCICCAGIAITIACAITITCAIAGGI 2061

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GAGTATTGAAGCTTCCCACTGTCAGAATGTAAG-------TATCAATTAGTAC 75528
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Pred. No. 0.12;
0; Mismatches 456; Indels 140;
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                                   Ψu, X.,
                                                                                             Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X Wyman, D., Young, G., Zainoùn, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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| organism="Mus musculus"
| organism="Mus musculus"
| mol type="genomic DNA"
| db_xref="taxon:10090"
| clone="RP24-492C11"
| clone lib="RPCI-24 Male Mouse BAC"
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Topham, K., Travers, M., Travis, N., Trigilio, Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Zahnoun, U., Zembek, L., Zimmer, A. and Zody, M. Direct Submission (16.NOV-2001) Whitehead Institute	TITLE	1773 IGCAIAGIGICICIGGCTICCIGGAIGITITIAIGCCIGGAITAITIAGACITAACAIIT 1832 	8 8 8
Arynond, C., Retta, R., R. Raback, M., Riley, R., Roman, J., Rosetti, M., Roy, A., Santos, R., Scentan, S., Severy, P., Sponcer, B., Strauss, M., Subramanian, A., Talamas, J., Testans, M., Subramanian, A., Talamas, J., Testans		CIGCITITICACCI-GCCITCITCCCCI	B &
McCarthy, M. McCbwall, F., McKernan, K., McPhee Mcneus, L., Mihova, T., Mlenga, V., Murphy, T., Norbu, C., Norman, C.H., O'Connor, T., Obone Oliver, J., Peterson, K., Phunkhang, P., Paerr		GGCATCTTTTTCAAGGTTAGGAAATTTTTTTTTTTTTTT	S a
Junes, D. HeatCrd, A., Horton, L., Hulme, W., Jones, C., Kamat, A., Karatas, A., Kells, C., Lamazares, R., Landers, T., Lehoczky, J., Levi Mandanal D., Majora T., Mandanal D.		1607 GGGGAGTITCTTITCCGGTCCAAICTATITGGTGITTTGTATGCTTCTIGTACCTIGATA 1666 	8 G
Choepely., Colangelo, W., Collins, S., Colly, Cooke, P., Colangelo, W., Collins, S., Colly, Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S. Ferreira, P., FitzHugh, W., Gage, D., Galagan, Girde, Cord C., Calagan, Cinde		1547 GCATCTTTAATATTCTTTCTTTGTTCTATACTTTTAGTGATTTGATTATTATGCACTGT 1606 	දු පු
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	REFERENCE AUTHORS TITLE	1427 GTCTCTTGGAGTCTGTAGCACATCTGTGCAGGCCTTCTTACATTTTGAGTTTCTATTGG 1486 	දු දු
Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus Bukaryota, Metazoa; Chordata; Craniata; Ver Manmalia, Entharia, Ecdontia; Coinvoquetti	SOURCE ORGANISM	1367 TICTCCAACTATIGTGACAGAAAGITTICIAAGIGCAGIAGICTGGCCTGACATCTGIA 1426 	දු පු
	ACCESSION VERSION	1307 TAGGTCTGCAITTGAAGATAGGTATTCTTTACAICTGAITTTAICTTAGAATGTCTTTCT 1366 	දි දි
AC099619 236604 bp DNA	RESULT 11 AC099619 LOCUS	1249 CATATTITCTIGAATGIGGGTAACAICTITAGAITGAAGTITTICICCTAGCCITCIT 1306 	S 8
2238 TAGACGGCTGAGTTTGGGATGATTGTAATTCTAGGTGCTGA 74040 TAGGCATCTGGGTTTGGAAAGTTTGTAATTCTAAGTGCTG	Oy 22 Db 740	1189 GICTIGICIGICITCTCTCCCCCTCTTTGATTTTTGGCCTGGAATTATTATTAT 1248 	P 9
		1129 GIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGI	g g
CITGCCTTGTGCTTCAGCTATGTTG-CATTCT 	,	1069 AICAAIGAGCAGIGITIGIGGAIICTIGITAICTIGCACTIGIGAAGIGIGIGIGIGI 1128 	දු දු
	•	1009 TGTTACCCAGTATCTTTTCTAGAGAAATTAAGATCATTGAGTCATTGAGTGTTGAGAATT 1068 	85 A2
	,	950 -AIGGIAGGIIGICFITITIGGAIGCAGCAGIAGGAIGCAICTIGITICAIAICCAIIC 1008 	8 8
	,	893 AGGGCCATTTGCTTAGAATAICTTTTC-CATCCTTTTACTCTAAGGTGATGTCTATCC 949 	g 8
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J.S., Dodge,S., Faro,S.,
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Tr., Naylor,J., Naylor,J.,
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J., Woll, Young,G.,
J., Young,G., CCTGT-TGGGTTCTTAATTTT 1951 ATTTCATAGGTTTCTTTAAT 2070 | ||| |||||| TGCTGTGGTAGGGTTGCTGGG 74101 CATAAAATGTATGTTAAGGTC 2130 TATTGTAATAGGGTT---- 2183 CTGTGTTTTTGCTTTGGCATA 2237 linear HTG 24-JAN-2003 RAFT SEQUENCE, 25 ertebrata; Euteleostomi; i; Muridae; Murinae; Mus. te/MIT Center for Genome MA 02141, USA | | GTT 73999 GAT 2279 <u>.</u>

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Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washingcon.edu/RM/Repeatmasker.html
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Insert size: 24204; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; sum-of-contigs
Quality coverage: 10.6 in Q20 bases; sum-of-contigs
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.larity 67.2%; Pred. No. 0.088;
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VERSION KEYWORDS

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SOURCE INFORMATION:
The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
Mapping information for this clone was provided by Dr. Wes Warren, obsertment of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
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This sequence is the entire insert of the clone.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                              'organism="Mus musculus'
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1207. 1634
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|5218. .15612
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10601. .10con
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/rpt_family="B4"
1482<u>3</u>. .15002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391. .509 /
/rpt_family="L1"
646. .828
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9013. .9297
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1927. .12038
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                                                      75425 AGGGATGTTGGGCTCTAGTGAGGGCATTTTGTTCCAGCTTTTATTGACTGTGTTTTAATT 75484
                                                                                                                                                                                                                                                                  AC124411 177414 bp DNA linear ROD 13-NOV-2003
Mus musculus BAC clone RP24-267C20 from chromosome 13, complete
       2170 ATTGTAATAGGGTTTTAGCAGGGACATATTGTCCTGGTTGTTATTGTCTGTGTTTTTGCT 2229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Mar 19, 2003 this sequence version replaced gi:28261652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
3 (Dases I to 177414)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
4 (Dases I to 177414)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse,)
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 177414)
VanBrunt,A. Bielicki,L., Van Brunt,A. and Kozlowicz,A.
The sequence of Mus musculus BAC clone RP24-267C20
Unpublished (2001)

2 (bases 1 to 177414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (06-FEB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 177414)
MCPharson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 6 (bases 1 to 177414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                            75485 CTGATGTCTAGGCATCTGGGTTTGGGATGATTGTAGTTCTAGATGCTGAT 75534
                                                                                                   2230 TIGGCATATAGACGCTGAGTTTGGGATGATTGTAATTCTAGGTGCTGAT 2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: M_BB0267C20
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AC124411.5
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rpt\_family="MaLR" 5613. 16707 rpt\_family="MaLR" 6708. 17102

repeat\_region repeat\_region repeat\_region

restriction digest.

AAGTITGTAAGTITTCTGTTGTTCTGTTGTTGTTGTTATCTAGATTTAAGCTGTGG

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TICTIAGATAGGATGCAGGTACCATTTCAGTTTTCTTGTATCAATTGAGACTTGCTTTG

TGGTCAGATAGGACATAGAGTATTATTCAATTGTCTTTTATCTGTCGAGACTTGCTTTG

533

473

151921 TGTCCAAGTATGTGGGTTAATTTTGGAGAAGTTCAATGAGGC----AGTAAGTATATTC 151975

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152215

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654 GGGGTATTGAAGTAGCCCACTATCTGTGTGAGGTCAATATGTGATTTTAGCTGTAGCT

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833

6 6 6 6 6

TAGGGCCATITGCTTAGAATATCTTTTCCATCTTTTACTCTA-----AGGTGATGTCT

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77031. 37074
77031. 37074
77074. 37078
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frpt family="ERV1"
77925. 39008
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17579. .17951
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Query Match

33.0%; Score 752.002; DB 1; Length 177414;

Best Local Similarity 66.6%; Pred. No. 0.071;

Matches 1340; Conservative 0; Mismatches 515; Indels 158; Gaps 20;

294 TATITCITGATTTCIAGCTCATITITAACTCAGIAGTGATTGGTTTCGT 353

151747 TCTTTCTAAAATATCTTGACTCAATATTTTCAGTATTGAGTTGTTTCAT 151806

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REFERENCE 1 (bases 1 to 18474)  AUTHORS Leongamornlert, D.  AUTHORS Direct Submission  JOURNAL Submitted (11-SEP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CEB10 1834, UK. B-mail enquiries:  COMMENT COMPANT COO this sequence version replaced gi:22265406.  COMMENT CENTER: Wellcome Trust Sanger Institute  Center code: SC  Web site: http://www.sanger.ac.uk  Contact: humquery@sanger.ac.uk  Contact: humquery@sanger.ac.uk  During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  This sequence was finished as follows unless otherwise noted: all	regions were aither double-stranded or sequenced with an alternate chemistry or covered by high quality duality brind attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone cr more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr., TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at the properties of bound at the plant of the properties of the group of Pieter de Jong.  FEATURES  Location/Qualifiers  Location/Qualifiers	Query Match         32.0%;         Score 729.201;         DB 1;         Length 184474;           Best Local Similarity 68.7%;         Pred. No. 0.097;         Indels 82;         Caps 22;           Matches 1295;         Conservative 0;         Mismatches 508;         Indels 82;         Caps 22;           Qy         432 ATTTGAATTTCTTTCATCTGTAGAGATTGCTTTGTATTGAATAGGTCA 178280           Qy         492 ATTTGGAG-AGTTTCATAGGGTGCTGACAGAGGAGAATATTGGTGAA 549           Internal ATTTGGAGAAGATTCCATGAGGTGCTAAATAGAGAGAATTTGGTGAA 549           Db         178281           ATTTGGAGAAATTCCATGAGGTGCTAAATAGAGAGAATTTTATAGTTGGTGGGG 178339           Qy         550 ATAGTCTGTAAATTCATCAGGTGCTAAATAGAGAGAATTTGGAGATTTGGTGGCGTTTGGTGGGGTGGGGATTTTATAGATTAGAGTCCAGGATTT 608           Db         178340 ATGTTCTGTAAATATCTGTTAAAATATCAGTTAAATAATCAGTTAAATACCGAGATTT 178399	Oy 609 CTCTGTTTCGTTTTTGTTGAGATGACCTAACTGTTGGAGAATGGGATATTGAAGTAG 668  Db 178400 TTCTGTTTTTGTTTTTGTCAACTCAACTGTTGACTAGAGTAGGGTATTGAAGTTT 178458  Oy 669 CCCACTATCGTGTGTGAGGTCAATATGTGATTTTAGCTGTGCTTGTTTTATGA 728  Db 178459 CCCACTATCAGTGTGAGGTCAATATGTGATTTTAGCTGTAGTTTTTATAGA 728  Oy 729 ACTTGGGTGACATTGTGTTTGGTGCAATAGTGTAAAGATTGTTATTAAA 178518  Db 178519 ACTTGGGTGACATTGGTTTGGTGCAATAGAATTGTAAAATTGTTTTTTAAA 178578  Oy 789 TT-TTCCTTTGATTGGTGCAATAGTGTTAAAAATTGTAAAATTCTTTGGGG 843
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Birren, B., Nubbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nubbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, W., Bloom, T., Boquslavkiy, L., Boukhgalter, B., Cankardta, J., Chang, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., DaArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Frizderald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Grahm, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jindblad-Toh, K., Liu, G., MacLean, C., MacOndald, P., Major, J., Mathews, C., Nacarthy, M., Meldrim, U., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Roereson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Roerey, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Roy, A., Milson, B., Standon, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wilson,
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Quality coverage: 13.4 in Q20 bases; sum-of-contigs
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                                                                                                                                                         82; Gaps
                                                                                                         Length 204031;
                                                                                                                                                         Indels
                                                                                                         DB 1;
                                                                                                                                                         508;
                                                                                                      Score 729.201;
Pred. No. 0.1;
0; Mismatches
/note="assembly_fragment
                            clone_end:T7
vector_side:right"
                                                                                                         32.0%;
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                                                                                                                                                               Conservative
                                                                                                                                     Similarity
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musmanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musmanalia; Euteleostomi; Direct Submission  1. Submitted (10-100, Vol.2002) Wellcome Trust Sanger Institute Cambridgeshire; CBio 18, UK. E-mail enquiries: humquer/@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov. 3, 2002 this sequence version replaced gi:2337500.	/clone_Ibb="RP23-554A20" /clone_Libb="RP23-554A20"  31.8%; Score 725.001; DB 1; Length 211131; Best Local Similarity 68.1%; Pred. No. 0.11;  290 CTCTATTCTCATTCTATCTTGCTCTTGCCCATTTTAACTCAGAGTGATTGTTGCTTTGGCTCATTTTAACTCAGAGTGAGT
ORGANISM REFERENCE AUTHORS JOURNAL COMMENT	Query Match Best Local 1 Matches 140: Qy 290 Db 164255 Qy 406 Db 164265 Qy 466 Db 164268 Qy 524 Db 164088 Qy 524 Oy 582
α U . μ	8 8 8 8 8 8 8 8 8
17826	Db 178917 TATTCA-TTTCCTTCATATTTCTTCATAGATTTCTTTCAGGATTTTTTTT

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclome; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSERCT; Tr:, TREMBL; Wp:, WORWERP; Information the WORWERP database can be found at http://www.snaper.ac.uk/Projects/C_elegans/wormpep RP23-479N10 is from the RPCI-23 Mouse BAC Library.

FOR further details see http://www.chori.org/bacpac/home.htm
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Pred. No. 0.086;
0; Mismatches 612; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="2"
/clone="RP23-479N10"
/clone_lib="RPCI-23"
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illarity 65.9%;
Conservative 0
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Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
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This sequence will be replaced by the family be replaced by the family be reserved.

1173: contig of 1173 bp in length 1273: gap of 100 bp 1174 4401: contig of 100 bp 1174 4501: gap of 100 bp 1174 4501: gap of 100 bp 1175: contig of 100 bp 1175: contig of 100 bp 1175: contig of 100 bp 1177: contig of 26800 bp in length 1177: gap of 100 bp 1177: contig of 26800 bp in length 1177: gap of 100 bp 1177: gap of 100 bp 1177: contig of 26800 bp in length 1177: gap of 100 bp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Center project name: L24684
Center clone name: L24684
Center clone name: 270 L8
Center clone name: 270 L8
Center clone name: D150 L8
Center clone name: Asamisty Byenomery Statistics
Sequencing vector Plasmid, n/a, 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 141631 bases at least Q40
Consensus quality: 141631 bases at least Q20
Consensus quality: 141937 bases at least Q20
Insert size: 145000; agarose-fp
Insert size: 142029; sum-of-contigs
Quality coverage: 9.5 in Q20 bases; sum-of-contigs
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5 140254: gap of 100 bp
5 142529: contig of 2275 bp in length.
Location/Qualifiers
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/organism="Mus musculus
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/db xref="taxon:10090'
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                                      .8076 TGTCTTTAACACGTCAGATTCTTTCTTCCATATCGTGTATTCTGTTGGTGATGCTGTAT 18135
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2161 TCAGGGCC-----TATTGTAATAGGGTTTTAGCAGGACATATTGTCCTGGTTGTT 2211
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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AC115852.4 GI:24182195
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130917 TIGCTITGIGACCAIGIGI------AIGIGGIGAATITIGGAGGAGGAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130805 Argangiridariccarratirciargiriag-arrengicarangaecrar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATAAGITIGIAAGITITCIGITGITICTGITGITGITG----TIAICTAGATITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGCTITICITITICAAATATGTATTTCAATTTTGGAGAGTTTCATAGGGTGCTGACAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 612; Indels
                  lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                           31.6%; Score 719.803; I
larity 65.9%; Pred. No. 0.089;
Conservative 0; Mismatches 63
                                                                                                                                    4502. .99416
/note="assembly_fragment"
/note="assembly_fragment"
|113.75. .140154
|note="assembly_fragment"
|103.75. .140154
|note="assembly_fragment"
|140.55. .142.59
|note="assembly_fragment"
             /clone_lib="RPCI-24 Male
1. 1173
/note="assembly_fragment"
                                                                                         1274. .4401
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                             vector_side:right"
                                                                                                                                                                                                                                                                                                                                                    clone end:T7
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Best Local Similarity
Matches 1350; Conserv
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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                             The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the entire insert of the clone. This clone is overlapped by AC122018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 153772
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                       NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="MER1_type"
483. .3586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP24-462H23"
/clone=lib="RPCI-24"
326. .45mily="Alu"
546. .747
/rpt_family="MIR"
1790. .1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,886. .8253
/rpt_family="MalR"
8533. .8916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d533. .8916
/rpt_family="MaLR"
9222. .9364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/rpt_family="Alu"
6958. .7144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="Malk"
971. .2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2044. 2685
/rpt_family="84"
2782. 2964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="ERVK"
5772. .6818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="ERVK"
6862. .6953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'rpt_family="ERV1"
'886. .8253
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1666. .9692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="MIR"
648. .3768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="L1"
9365. .9665
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844. .2685
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rpt_family="L1"
.0086. .10673
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6425. .6643
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.0041. .10071
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11040. .11175
                                                                                                                                             MAPPING INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  AC129304 153772 bp DNA linear ROD 27-NOV-2003
Mus musculus BAC clone RP24-462H23 from chromosome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (28-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Barkway, St. Louis, MO 63108, USA
(Dases 1 to 15372)
MCPherson J.D. and Waterston, R.H.
Burkway, Dr. Louis, MO 63108, USA
Parkway, St. Louis, MO 63108, USA
Robberson, J.D. and Waterston, R.H.
McPherson, J.D. and Waterston, R.H.
McPherson, J.D. and Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 153772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 153772)
Shah, N. and Meyer, R. The sequence of Mus musculus BAC clone RP24-462H23
Unpublished (2001)
         129264 TATCACCTTCATAAGGITGGTTTTAAGGTTATTACTTGTGTTTCAGCTGTGTGTAGAATG
                                                                               2161 TCAGGGCC-----TATTGTAATAGGGTTTTAGCAGGGACATATTGTCCTGGTTGTT
                                                                                                                          129204 rccacanctrocreraciacearactraacirccccrearaccarcracaaccrarr
                                                                                                                                                                       2212 ATTGICTGTGTTTTTGCTTTGGCATATAGACGGCTGAGTTTGGGATGATTGTAATTCTAG
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Center: Washington University Genome Sequencing Center Center Genter WUGSC
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3 (bases 1 to 153772)
McPherson, J.D. and Waterston, R.H.
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Mus musculus
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HTG.

VERSION KEYWORDS SOURCE ORGANISM

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Que: Best Matc	Query Match Best Local Similarity 68.1%; Pred. No. 0.1; Matches 1272; Conservative 0; Mismatches 490; Indels 106; Gaps 21;
ò	270 TICCCICTCCAAACACTICTATTICTTGATTICTATCTTGGCTC-ATTITTAACT 328
QQ	20081 TITATICAATCCTAGGAAGTCTTTTTTTTTTTTTTTTTTT
ò :	329 CAGTAGTGAGTTGTTTGGTTTCCATAAGTTTGTAAGTTTTCTGTTGTTGTTGTTGTT 388
d d	41 GAGTAGAGAGTTGTTCAGTGTCTACACTTTCTGTTGTTTCTATT 20
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අ	20245 CTIGTATCTGCTGAGACTTGCTTTGTGTCTGAATATGTGATCAGTTTTGGAGACAATTCC 20304
ò	507 ATAGGGGGCGAGAAGAAGGTACAGTC-TITGGGTTTTGGTGAAATAGTCTGTAAATATC 565
qq	20305 ATGAGGTGCTGAGAAGGTATATTCTTTTGTGTTTGGGTGGAATGTTTTGTAGATATC 20364
λ	566 T-CTAGGICCACTTGGITTATGACATCAGTTAGCTCCAGCATTTCTCTGTTTCGTTTTT 624
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ò	625 GTTGAGANGACCTAACTGTIGGAGAGAATGGGGTATTGAAGTAGCCCACTATCT 678
qq .	TTTTCTGGTTGCCCTGTCTATTGGCAAGAGTAGGGTATTGAAGTCTCCCACTGT
ò	679 GIGNGTG-AGGICAATATGTGATITTAGCTGTAGCTGTGCTTGTTTTATGAACTTGGGTG 737
qq	20485 CIGIGIGAAAGICAAIGCAIGAITIAAGCIAACAIAGIAICIGCITIAIGAACIIGGGIA 20544
ò	738 ACATTGTGTTTGGTGCATAGACATTAAGAATTGCAATGTCCTCTTGGTGGAT-TTTCCTT 796
Ор	20545 CTCTTGTGTTTGGGGCATAGGTGTTAAGAATCAAAACGCCATGTTGGTGGATCTTTCCTT 20604
ò	797 IGAIGCCTAIGTAGIATICTICCCAAICTCATCIGCTIAGTITIGGGTIAAGICTA 855
ΩÞ	GICTGAAATACCCTGCCTGTCTTCTGGTTAGGTTTTGGGTTGATGTGGATT
ò	856 AGTCAGATATTAAAATGACTGTATCGGCTTGCTTCTTAGGGCCATTTGCTTAGAATATCT 915
qq	20665 TGTCAGACAGCAAAATGGCAACACCAGATTGCTTAGGACTATCTGCGTAGAATACCT 20724
ò	916 T-FICCATCTITIACICIAAGGIGAIGICIAICCAIGGIAGGIAGCTIGICITITIGGAIGC 974
qq	20725 TCTIGCAACCCTTIATCCTTAGGTAATGGCTACCCTTGATGTTGAAGTATGGTTTTTGGA 20784
ò	975 AGCAGTAGGATGTTTTTTTTTTTTTTTTTTTTTTTTTTT
QQ	20785 récadeahdaarccronrinacarccrincrenadacronarcrininardeger 20844
ò	1035 AATTAAGAICATIGAGCATICA GAIGTIGAGAATTATCAATGAGCAGTGTTIGTGGATICT 1094
qq	20845 AATTGAGACCATTGAGAGATATCAATGAGAAATGAGATTTTTGATTT 20896
ò	1095 TGTTATCTTGCACTTGTGAAGTGTGTGTGTGTGTGTGTGT
qq	20897 IGIGATITIGGIGGIGALGGGGGTGGGGGGGGGGGGGGGG
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ò	1215 TCTTTTGATTTTTGGCCTGGAATTATTTATTATTCATATTTTCTTGAATGTGGGTAACAT 1274
qq	sggariatitarrcccagirrgirgiritrriricacci
ò	1275 CTTTAGATTGAAGTTTTTCTCCTAGCCTTCTTTAGGTCTGCAT-TTGAAGATAGATA 1330

AUTHORS MCPherson, J.D. and Waterston, R.H.  TITLE JOURNAL Upublished AUTHORS L (bases 1 to 271609) AUTHORS MCPherson, J.D. and Waterston, R.H. AUTHORS L (bases 1 to 271609) AUTHORS L (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park REFERENCE AUTHORS 3 (bases 1 to 271609) AUTHORS 3 (bases 1 to 271609) AUTHORS	Center: Mashington University Genome Sequencing Center Code: WAGSC  Web site-thirtp://Dec. tenthrp://dec. within Consect: submissionacheston.wasti.edu/geo/index.shtml  Consect: submissionacheston.wasti.edu  Consect: submissionacheston.wasti.edu  Consect: submissionacheston.wasti.edu  Submissionacheston.wasti.edu/geo/index.shtml  Consect: submissionacheston.wasti.edu  Consecusis quality: 26736 bases at least Q30  Consecusis quality: 26736 base	18882: gap or distingui
	1511 AFCTGCCTTTALATCTALATTTCCCTACACCTTTTALATCTTTCTT	

143645 143886 TGATGCGTCTGAAATACCCTGCCCTGTCTTCTTGGTTAGTTTTGGGTTGATGTGGTTTT 143945 144006 TCTTGCAACCCTTTATCCTTAGGTAATGGCTACCCTTGATGTTGAAGTATGGTTTTGGA 144065 143465 143525 143705 143706 TTTTTTTTTCTGGTTGCCCTGTCTATTGGCAAGAGTAGGGTATTGAAGTCTCCCACTGTCA 143765 143766 CTGTGTGAAAGTCAATGCATGATTTAAGCTAACATAGTATCTGCTTTATGAACTTGGGTA 143825 143885 144005 144177 14342 1034 1214 21; 624 855 448 737 328 143422 GAGTAGAGAGTTGTTCAGT------GTCTACACTTTCTATT 143826 CTCTTGTGTTTTGGGGCGTAGGTGTTAAGAATCAAAACGCCATGTTGGTGGTGGTCTTTCCTT 143946 rercadacadaarrecaacaccadarrecrierradeacrarreceararacer 975 AGCAGTAGGATGGATCTTTTTTTTCATATCCATTCTGTTACCCAGTATCTTTTTTTAGAGA 144066 TGCAGCAGAATGAATCCTGTTTTTACATCCTTTCTGTTAGACTGTATCTTTTTTATTGGT 1035 AATTAAGATCATTGAGTCATTGAGTGTTATCAATGAGCAGTGTTTGTGGATTCT 1275 CITTAGATIGAAGTITTTCICCTA---GCCTTCTTTAGGTCTGCAT-TTGAAGATAGATA 143466 ATTGATATCCAGCTTTAATCCATGGTGGTCTGATAGGGTGCAGGGAGTTATTTCAACTTT 143586 ATGAGGTGCTGAGAAGGTATATTCTTTTGTGTTTGGGGTGGATGTTTTGTAGATATC 143646 TOTTGGGTTCATCTGGTTTATAACATCAGTTAGCTCCAGCATTTCTCTACTTAGTTTTTT 619 GIGTGIG-AGGICAATATGIGATTTTAGCTGTAGCTGTGCTTGTTTTATGAACTTGGGTG 738 ACATTGTGTTGGTGCATAGACATTAAGAATTGCAATGTCCTCTTGGTGGAT-TTTCCTT TGATGCCTATGTAGTATTCTTCCCAATCTCATCTGCTTAGTTTTGGGTTTAAGTCTA-TT 916 T-TICCATCCTTTTACTCTAAGGTGATGTCTATCCATGGTAGGTTGTCTTTTTGGATGC 270 TTCCCTCTCTTCCAAACACTTCTATTTCTTGATTTCTATCTTGGCTC-ATTTTTAACT 329 CAGTAGTGAGTTGTTTTGCGTTTTCCATAAGTTTTGTAAGTTTTTCTGTTGTTGTTGTTGTTGTT 389 GITGITATCTAGATTTAAGCTGTGGTGGTCAGATAGGACATAGAGTATTTTCAATTGT CTTTTATCTGTCGAGACTTGCTTTGTAAATATGTATTCAATTTTGGAG--AGTTTC 507 ATAGGGTGCTGACAAGAAGGTACAGTC-TTTGTGTTTTGGTGAAATAGTCTGTAAATATC 566 T-CTAGGICCACTIGGITTATGACAICAGITAGCICCAGCAITTCTCTGITTTGTTTTT 625 GTT-----GAGATGACCTAACTGTTGGAGAGAATGGGGTATTGAAGTAGCCCACTATCT 856 AGTCAGATATTAAAATGACTGTATCGGCTTGCTTAGGGGCCATTTGCTTAGAATATCT 144126 AATTGAGA-----CCATTGATGTTGAGAGATATCAATGAGAAAGGTTTTTGATTCT 0; Mismatches 490; Indels 106; Gaps 144238 GIGTGTGTGTGTGTGTGTGTGTGTTTTCCCCTTTTTATTTGCTGG--------Matches 1272; Conservative 449 197 1095 1215 1155 ò 원 셤 g g à d g ద ò 엄 à ద g à 셤 à d à 요 à 셤 à 셤 à ò à ò ò à à

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144401 TIGCTIACATITIGCTITIATCATAAAATGTCTTGTTTTTCTTCATCTATTGTGAATG 144460
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                                                                       ririgciaggialaaragigiaggciggcarcigiigicicriilaaricigiaggcacarr 144520
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Rattus norvegicus clone CH230-50H7, WORKING DRAFT SEQUENCE.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,

AC126868.4 GI:30521522 HTG: HTGS PHASE2; HTGS DRAFT; HTGS\_FULLTOP. Rattus norvegicus (Norway rat) Rattus norvegicus

ACCESSION VERSION KEYWORDS SOURCE ORGANISM Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

(bases 1 to 247119)

Rattus

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Anyalebechi, W. Acyagia, D. Modelin, M. Baca, B. Baden, H.,
Biswalia, Y. Balari, J. Bindehburg, Y. Biyth, B. Baca, B. Bach, H.,
Biswalia, Y. Buhay, C. Burch, P. Burrell, K. Caldecon, B. Groom, M. Biswalia, Y. Charler, Y. Carace, J. Cadecon, S. Gardenna, V. Carter, K. Caldecon, B. Cardenna, V. Carter, M. Carter, M. Carter, M. Carter, J. Carden, J. Carden, J. Carden, J. Charler, J. Charler

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                                 GAAAAGAAGGTATATTCTTTGTGTTTGGGTGAAACGTTCTGTAAATATTCTGTTAGTTCCA
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                                                                                                 TGTTGAGATGAC
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  GACAAGAAGGTACAGTCTTTGTGTTTTGGTGAAATAGTCTGTAAATATCT-CTAGGTCCA
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                                                                                                                                                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length

(see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 247119: contig of 247119 by in length.
                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bom.tmc.edu

Contact: hgsc-help@bom.tmc.edu

Conter project name: GFDW

Center clone name: CH230-50H7

Center clone name: CH230-50H7

Conter clone name: CH230-50H7

Consensus quality: 235042 bases at least Q40

Consensus quality: 237296 bases at least Q30

Consensus quality: 238799 bases at least Q30
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               Center: Baylor College of Medicine
Center code: BCM
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/mol_type="genomic DNA"
/b xref="taxon:10116"
/clone="CH230-50H7"
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clone_end:T7"
2169._.2761
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Best Local Similarity
Matches 1379; Conserv
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38060 38120 38059 igiticalciagaacciicigiaggecigaririgiagacagarariatiaaaririgec 38000 37944 1465 37884 37766 1287 TITITCICCTAG -- CCTTCTTTAGGICTGCATTTGAAGATAGATATTCTTTTACATCTGAT 1345 1585 GGCCTGGAATTATTTATTCATATTTCTTGAATGTGGGTAACATCTTTAGATTGAAG 38119 GTTCTCAAACTATTTGTTTCCTGTGTTTTCATGGGTATAGTCAACCTCCTTAGGTGAAG 37999 TTTATCATAGAATAAATC---TTCTCCATCTATGGTGATTGAATGTTTC-CTGAGTAGAG TITATCTTAGAATGTCTTTCTTCTCCAACTATTGTGACAGAAAGTTTTTCTAAGTGCAG 1466 TACATITITGAGITICIALIGGAAAAGICAGGIGIAATICIAAIACATCTGCCTITIAIAIG 37883 GGCTATTAGAGTCCCCACT-GAGAGTCATTTGTAATTTTAGTAGGTCTGCCTTTATATG Tractride-cectricectridecaectritaararicitriciericierararitagi 1406 TAGICTGGCCTGACATCTGTAGTCTTTGGAGTCTGTAGCACATCTGTGCAGGGCCTTCT

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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Charder, C., Chen, S., Chan, Y., Charder, D., Charder, G., Chen, R., Chen, Y., Charder, D., Deberich, D., Deberich, D., Deberich, D., Deby, R., Devisa, M.L., Davis, C., Derson, S., Pinley, M., Flags, N., Porbes, L., Foster, M., Foster, M., Garta, R., Garta, R., Garta, R., Garta, M., Hanlon, S.L., Handluch, C., Hamilton, C., Hamilton, C., Karta, R., Karta, M., Karta, M., Kovat, C., Kowito, S., Kally, S., Manden, E., Monden, E., Morta, M., Martin, M., Martin, R., Martin, R., Martin, S., 
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Submitted (199-007-2002) Human Genome Sequencing Center, Department
Submitted (199-007-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 23, 2002 this sequence version replaced gi:21903232.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequening reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence
contigs will be indicated in the feature table.
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Direct Submission
Submitted (28-ARR-2002) Human Genome Sequencing Center, Department Submitted (28-ARR-2002) Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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Center clone name: CH230-11409
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3 (bases 1 to 259629)
Rat Genome Sequencing Consortium.
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TITLE
JOURNAL
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                              1586 GATTIGATTATTATGCACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGGTGTTTTG 1645
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AC119553.4 GI:23269701
HTG, HTGS_PHASE1, HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tuc.edu/docs/Genbank draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
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               Assembly program: Phrap, version 0.990329
Consensus quality: 217607 bases at least Q40
Consensus quality: 220515 bases at least Q30
Consensus quality: 222444 bases at least Q20
Estimated insert size: 234666; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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Pred. No. 0.15;
0; Mismatches 537; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in length
                                                                                                                                                                                                                                                                                                                                                                                                                        1 5391: contig of 5391 bp in length
2 5491: gap of unknown length
2 39105: contig of 33614 bp in length
3 3205: gap of unknown length
6 259629: contig of 220424 bp in length
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
Summary Statistics
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db xref="taxon:10116"
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122888 122948 123210 GITCICAAACIAITIGITICCIGIGITITICAIGGGIAIAGICAACCICCITAGGITGAAG 123270 123446 123057 123177 123505 123564 123684 ATTCTGTTGAAAATATTTTTTTTTGGGTTTCTTCTCCTTCTATCCTTTTGTTTCT 123743 123683 123854 1047 1345 1645 1167 1227 1405 1465 1819 987 872 rcirrccrarcic -----rcirrigarir gaagicierir reinageraaane GCTACACCTGGCTTCTTAGGGTCATTATCTGAAATATCTTTCCAATACTCTTTAC ATCCTATTTCCACGGCCATCCTGTTAGTCTATTGTTT------AATTGGGTAATA GAGTCATTGATGTTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCAC TITITICICCIAG - - CCTICITIAGGICIGCATITIGAAGATAGATATICITITACATCTGAT ---ATGGTAGGTTGTCTTTTTGGATGCAGCAGTAGGATGG TCTTCCCAATCTCATCTGCTTAGTTTTGGGTTTAAGTCT-ATTAGTCAGATATTAAAATG ACTGTATCGGCTTCCTTAGGGCCATTTGCTTAGAATATCTTTCCA--TCCTTTTAC TITATCTTAGAATGICTTTCTTTCTACCAACTATTGIGACAGAAAGTTTTTCTAAGTGCAG 123447 GGCTATTAGAGTCCCCACT-GAGAAGTCATTTGTAATTTTAGTAGGTCTGCCTTTATATG TOTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTCTCTCCCCCTCTTTGATTTTT ----TTCCCTTTTGATTTGCT GGCCTGGAATTATTATTATTCATATTTTCTTGAATGTGGGTAACATCTTTAGATTGAAG 123387 TAGICTCGGTTGGCAACTGTGGTTTCTTGGTATCTGATGAACATCTGCTCAGGTCTCTCT 1466 TACATTTTGAGTTTCTATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATG TTAATIGGICITITITICCTIGCAICTITIAATAITCTITCTITGITCTATACTITIAGI GATITIGATITATITATGCACTGTGGGGAGTITICTTTTCCGGTCCAATCTATTTGGTGTTTTG 123565 GTTTTGATTATTATGTTTGAGGAGTCTTTTCTTTTCTGGTCTCATCTATTTTGTGTTCTG 123625 TATGCTTCTTAGACCTTGACAAGTATCTCCTTTTTTAAG-TAGGGAAATTTTCTTCTATA TAGTOTGGCCTGACATCTGTAGTCTTGGAGTCTGTAGCACATCTGTGCAGGGCCTTCT GITTICITGAAATAITTICCCTGCTTTIG-----ACCTGCCTTCTTCCCCTTCCTCTA 1760 TICCITIGGITITIGCATAGIGICTCTGGCTICCTGGATGTTTTATGCCTGGATTATTTT TAGATTTGGTCTTTTCATAGGATTGCAGATTTCCTCCATGTTTTGTGTTTGAAATTCTTT 1820 AGACTTAACATTTTCTTTGACCAAGGTATCCATTTCTTCTATCTTGTCTTCACTGCCTGA 123804 AGATTTAACAATTTCTTTGCCCCATGTATTAATTTCTTCTATTGTAT------CTGA TATGTATGTATGTGT------

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Rat Genome Sequencing Consortium.

B rat Genome Sequencing Consortium.

B intect Submission

Submitted (04-5EP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

EB (ED Sequencing Consortium.

Direct Submission

AL Submitted (20-0002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

ON Nov 20, 2002 this sequence version replaced gi:23683160.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold' individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequence in the feature table.
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M.P., McNeill, T.Z., Menen, E.,
Milosavijevic, A., Miner, G., Minja, E., Montemayor, J., More, S.,
Milosavijevic, A., Miner, G., Minja, E., Montemayor, J., Morris, S.,
Nwackelemen, O., Okwunou, G., Olarnpunsagon, M., Pal, S., Parks, K.,
Pagternak, S., Paul, H., Perez, M., Pégankoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Rives, C., Rodkey, T., Rachlin, E., Revers, K., Redgier, M.A., Reigh, R.,
Railly, B., Reilly, M., Rachlin, E., Rose, M., Rose, R., Riggs, F.,
Rives, C., Rodkey, T., Rojan, A., Rose, M., Rose, R., Raiz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shataman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
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Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warker, B., Wang, J.,
Willsan, R., Wallson, R., Walczyk, R., Woden, H., Worley, K.,
Wight, D., Wright, R., Wul, Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Wight, D., Wright, R., Wul, Yakub, S., Yen, Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
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Center: Cade: BCM
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: ngsc-help@bcm.tmc.edu
Contact: project name: GQXS
Center project name: CH230-31M10
Center clone name: CH230-31M10
Center clone name: Phasp: yearistics
Assembly program: Phasp: yersion 0.990329
Consensus quality: 198575 bases at least Q40
Consensus quality: 198346 bases at least Q20
Consensus quality: 198346 bases at least Q20
Consensus quality: 195346 bases at least Q20
Estimated insert size: 192812; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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NOTE: This is a "working draft' sequence It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
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Allen, C., Allen, H., Alabrocks, S., Amin, A., Anguano, D.,

Anyalebechi V. Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

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Bayant, M., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Chacko, J., Charvez, D., Chen, G., Chen, R., Chen, Y., Chen, Y., Chen, Y.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

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Davila, M. L., Davis, C., Davy-Carroll, R., Doraper, H., Duyan-Rocha, S., Durn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Flaggy, N., Forster, M., Foster, M.,

Fraser, C.M., Gabisi, A., Gane, R., Falls, T., Fan, G.,

Harvey, Y., Havlak, P., Hawes, S., Haddus, S.L., Haddes, W., Hernandez, J.,

Hennandez, R., Hines, S., Hladun, S.L., Honderson, N., Hernandez, J.,

Jackson, L., Jacob, L., Jalay, R., Chan, C., Liu, S., Liu, J.,

Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Xovar, C.,

Karpathy, S., Kelly, S., Kelly, S., Klan, L., La, Z., Liu, J.,

Liu, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorensuhewa, L., Loulseged, H., Mahnoud, M., Malloy, K., Mangum, A.,

Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG, HTGS PHASE1, HTGS DRAFT, HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * 1 229513: contig of 229513 bp in length * 229514 229613: gap of unknown length * 221651 231050: contig of 1437 bp in length * 231151 233002: contig of 1852 bp in length * 231151 233002: contig of 1852 bp in length * 231151 233002: contig of 1852 bp in length * 231151 233002: contig of 2094 bp in length * 231151 233003 133102: gap of unknown length * 233103 2331196: contig of 2094 bp in length. FEATURES * Location/Qualifiers * 1.235196 * Accession number will * 231150 1235196 * Location/Qualifiers * Location/Qualifiers * 1.235196 * Accession number will * 231150 1235196 * Location/Qualifiers	116"   100 C   100 C	Query Match 31.3%; Score 713.403; DB 1; Length 235196; Best Local Similarity 68.8%; Pred. No. 0.14; Matches 1349; Conservative 0; Mismatches 491; Indels 122; Gaps 28; Qy 295 ATTICTIGATITCTACTIGGCTCATITITAACTCAGAAGTGAGTTGCTTAGATTCCATA 354 Db Actor	355 AGTITGIAAGITITCTGIIGTTGITGITGIIGTGIIGTAGAAAGIIGIIGAAGIIGAGAAGIIGAAGIIGAAGIIGAAGIIGAAGIIGAAGIIGAAGAA	475 TITGAAATATGTATTCAATTITGAGAGTITCATAGGGTGCTGACAGAAGGTACAGT 532  40763 GTACAAGTATGTGTCAATTITGAGAAAAGGTTCTATGAGGTGCAGAGAGGTGCTATT 408 533 C-TITGTGTTTTGGTGAAATAGTCTGTAAATATCT-CTAGGTCCACTTGGTTTATGACA 590	591 CAGTTAGCTCCAGCAITTCTCCTGTTTTTTTTTTTTTTGTAGATGACCTAACTGTTGAGAG  40883 CTGTTAGCCCAGTATTCTCTGTTTTTGTTGAGATGACCTAACTGTTGAGAG  551 AATGGGGTATTGAGTAGCCCACTATTGTAGAGTCAATATGTGATTTAACTGTA  651 AATGGGGTATTGAGTAGCCCACTATTGTGTGAGTCAATATGTGATTTTAACTGTA  40942 AGTGAACTATTGAAGTCTCCCACAATATGTGAATTTTAACTGTA	711 GCTGTGCTTGTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACTTAGG 41002 GTGGTCTTTTTCCAAATTTGGGTGGTACCCTTGTGTTTGGGAATACAGATGTTAAGA 767 ATTGCAATGTCTCTTTGGTGGATTTTCCTTTGATGCCTATGTAGTATTCTTCCCAATC 767 ATTGCAATGTCCTCTTGGTGGATTTTCCTTTGATGCCTATGTAGTATTCTTCCCCAATC 767 ATTGCAATGTCTGTGGATTTTCCTTTGATGCCTATGTAGTATTCTTCCCAATC	825 TCATCTGCTTAGTTTTGGGTTTAAGTCTA-TTAGTCAGATATTAAAATGCTGTATCGGG 883  41121 TCTTTGATTGGTTTGGGTTTAAGTCTA-TTAGTCAGATATTAAAATGGCTACGGG 883  41121 TCTTTTGATTGGTTTGGTTTGATTGTTTGTTTGTTAGGCTAGCTA

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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                             42438 AGTIGGIICICCITGIGCIICAGCIAIGIIGGAGIAITCAGG 42479
                                                                                                                                                                                                                                                                                                                                                                2165 GGCCTATTGTAATAGGGTTTTAGCAGGGACATATTGTCCTGG 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS PHASEL; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 23
AC128004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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Direct Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Nov 20, 2002 this sequence version replaced gi:23665065.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Arlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Arlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the enack of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (19-UIL-2002) Human Genome Sequencing Center, Department Submitted (19-UIL-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 247726)
Rat Genome Sequencing Consortium.
Direct Submission
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Yon Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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Center: Baylor College of Medicine
Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: http://www.hgsc.bcm.tmc.edu/
Center project Information
Center project Information
Center clone name: CH230-262L8
Center clone name: CH230-262L8
Conter source: Program: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 198410 bases at least Q40
Consensus quality: 19867 bases at least Q20
Consensus quality: 201676 bases at least Q20
Consensus quality: 201676 bases at least Q20
Consensus quality: 100070 bases at least Q20
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9 245448; gap of unknown length
9 246588; contig of 1110 bp in length
9 246588; qap of unknown length
9 247724; contig of 1068 bp in length.
Location/Qualifiers
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/organism="Rattus norvegicus"
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Worley, K.C.
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1174 168510 1234 168549	1294 TCTIAG-CCTTTTTAGGCTAGATTGTTAGATTGTTTAGATTGTTAGATTGTTAGATTGTTAGATTGTTAGATTGTTAGATTGTTAGATTGTTAGATTGTTAGATTGTTAGATTGTTAGATTTTTGTTAGATTTTTT	QY         1412 GGCTGACATCTGTGGGGTCTGTAGGACATCTGTGGAGGGCTTCTTACATT 14/1           Db         168712 GGCTGGCATCTGTGGTCTCTTAGAGTCTGCAAGACATCTGCCCATGCCTTTCTGGATTT 168771           QY         1472 TTGAGGTTTCTATTGGAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATGTTAATT 1531           Db         168772 TAGAGTCTCTATT-GAGAAGTTTGGTGAATTCTAATAGATCTGCCTCTATATGTTCTT 168830           QY         1532 GGTCTTTTTTCCCTTGCATCTTTTAATATTCTTTTGTTCTATACTTATAGTGATTTG 1591	168831   GGTCTTT-TTCCATTGCAGCTATTAATATTCTTTCTTTGTTGTTTGTT	1710 TCTTGAAATATTTTCCCTGCTTTTGACCT-GCCTTCCTCCCTTCCTCTATTCC 159010 IGTCAAAATATTTCTGGGTTTTTTGAGCTGGGATTCTACTCCTTCTTCTATTCCTATTATTCTATTAT	0y 1813 TTATTTTAGACTTAACATTTTCTTTGACCATGGTATCCATTTCTTCTTGTCT 1868  169130 ACTTTTAGATTTAATATTCTTTTAACAGGTATCCATTTTT-TATTATTATCT 169188  0y 1869 TCACTGCCTGAGATTCTCTTCTTTTTTTTTTTTTTTTTT	Db 169247THGAGCTCTTAATTTTCTTCTAGAATTTTCTCAGTTTG 169296  Qy 1989 TTAATTCTCACTTTCAGGTCCTGAAATGTTTTACTCATTTTCCTCCAGTA 2044  Db 169297 TTGCTTCTTTCAGTCTTGAAATGTTTTATTCTATCCACTGTTTGT 169356  Qy 2045 TTGCTTCTATTCCATTTTCAGGTCTTGAATGTTTTATTCTTTATTCATTTTTATT 2104  Db 169357 TTTCTATTTCTTTAATGGATTTATTCATTTCCTTCAAGGACCTTTAT 2104  Db 169357 TTTCTATTTCTTTAATGGATTTACTAATTTTGCCCAATTGTTTAT 169414	
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FEATURES
                                                                                                                             COMMENT
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                                 ACU95157 245174 bp DNA linear HTG 09-MAY-2003 Rattus norvegicus clone CH230-8N16, WORKING DRAFT SEQUENCE, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 245174)
                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebzata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                  AC095157.6 GI:30467202
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
Rattus norvegicus
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Direct Submission
                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
RESULT 24
AC095157/c
LOCUS
                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
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TITLE
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Direct Submission

Submitted (19-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24817806.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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69.3%; Pred. No. 0.15;
ive 0; Mismatches 479; Indels
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Center code: BCM
Center code: BCM
Context code: Attp://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-8N16
----- Summary Statistics
Assembly program: Atlas;
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clone_end:T7"
         Genome Sequencing Consortium.
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239487. .241599
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clone_end:T7_
site:EcoRI
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Best Local Similarity 69.3
Matches 1307; Conservative
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\	435 ATTATTICAATIGICITITATCIGICGAGACTIGCITIGIATITGAATATGTATTCAATT 494	495 TTGGAGAGTTTCATAGGGTGCTGACAAGAAGGTACAGTC-TTTGTGTTTTGGTGAAAT 551	AGICTGTAAATATCTCTAGGTCCACTTGGTTTATGACATCAGGTTAGCTCCAGCATTT	CTCTGTTTCGTTTTGTTGAGATGACCTAACTGTTGGAGAAATGGGGTATTGAAGTAG 	669 CCCACTATCTGTGTGTG-AGGTCAATATGTGATTTTAGCTGTAGCTGTGCTTGTTTTATG 727	728 AACTTGGGGACATTGTGTTTTGCATAGACATTAAGAATTGCAATGTCCTCTTGGTGG 787	788 A-TITICCITICALGCCTATGTAGTATICITCCCAAICTCACTTAGTITIGGGTT 846	847 AAGICIATIAGICAGATATIAAAAIGACIGIATCGGCIIGCIICCITAGGGCCAITIGCIT 906 	907 AGAATATCTTTTCCATCCTTTTACTCTAAGGTGAIGTCTÀTCCATGGTAGGTTGTCT	TITITGGAIGCAGCAGTAGGAIGCAICTTTTCATATCCATTCTTTACCCAGTACCT	TITICIAGABAATIAAGATCATIGAGTCATIGATGATGATGATCAATGAGGAGTGT 1083	1084 TIGIGGATICTIGITATICTICCACTIGITAGGGGGGGGGG	1144 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1204 GTTCTCCCCCTCTTTGATTTTGGCTGGAATTATTT-ATTCATATTTTGA 	1262 AIGTGGGTAACATCTITAGATTGAAGTTTTTCTCCTAGCCTTCTTTAGGTCTGCATT 1318	1319 IGAAGATATTCTTTACATCTGATTTTATCTTAGAATGTCTTTCTCCCAACTAT 1378 	1379 TGTGACAGAAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGACATCTGTAGTCTCTTGGAGT 1438	1439 CIGTAGCACATCTGTGCAGGCCTTCTTACATTTTGAGTTTCTATTGGAAAAGTCAGGTG	1499 TAATTCTAATACATCTGCCTTTATATGGTCTTTTTTTCCCTTGCATCTTTTAAT 1558
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AAAATATTTCCCTGCTTTTGAC 1737 ATTCTCTTCTATCTTGTAT 1903 IGTTAAGGTCCTTGCCTTGTGCT 2143 TGTAATAGGGTTTTAGCAGGGAC 2194 ||| | || || || || |||||||| || trencecrigeageririnaar 62448 --TACCTITCTAGGCATCTCCTT 62334 ATTAIGCACTGTGGGGAGTTICT 1617 Gracciigaragecarcrerr 1677 FICTIPATITITICATITICAGA 1963 SGCATATAGACGCTGAGTTTGG 2254 linear HTG 21-OCT-2002 DRAFT SEQUENCE, 9 ordered TOP.

Vertebrata; Euteleostomi; thi; Muridae; Murinae; Mus.

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71989 rcagiririagaaagrciriraaririchiraririchgririrgacacaririri--rrcagrag 72046
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                         is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                          This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

10573 10572: contig of 10572 bp in length 10673 12088: contig of 1416 bp in length 12089 12189 gap of 100 bp 12089 contig of 1174 bp in length 13189 13362: contig of 1174 bp in length 13362: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28091: gap of 100 bp
40867: contig of 1276 bp in length
40967: gap of 100 bp
52499: contig of 11512 bp in length
52599: gap of 100 bp
154378: contig of 101779 bp in length
154478: gap of 100 bp
167223: contig of 12745 bp in length.
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1: contig of 9279 bp in length
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1: contig of 5150 bp in length
1: gap of 100 bp
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1. .10572
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28092. :40867
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40968. :52499
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'note="assembly_fragment
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vector_side:left"
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              Anderson, S., Barna, W., Bastlein, V., Bogualawkiy, L., Boukhgalter, B., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Groepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Debrellano, K., Debarrik, S., Collymore, A., Cook, A., Cooke, P., Debrellano, K., Debarrik, S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gorde, S., Govette, M., Graham, L., Grand-Pierre, N., Hagos, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Lakocque, K., Lamazares, R., Lahockky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Madonal, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Madonal, P., Mardis, M., Major, J., Marquis, N., Matthews, C., McCarthy, M., Menga, V., Murphy, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Pollara, V., Raymond, C., Rosetti, M., Sohnor, R., Schauer, S., Scholmovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Severy, P., Spencer, B., Stange-Thoman, S., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Connon, Wilson, M., Williams, J., Ve, W.J., Young, G., Connon, Williams, J., Ye, W.J., Young, G., Connon, W., Minch, J., Ve, W.J., Young, G., Connon, W., Minch, J., Ve, W.J., Young, G., Connon, W., Minch, J., Ve, W.J., Young, G., Connon, W., Williams, J., Ye, W.J., Young, G., Connon, W., Williams, J., And Zody, M., Williams, J., Zimmer, A., and Zody, M., A
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Direct Submission

Bubmitted (101-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (bases 1 to 167223)

Sarrah, N. Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazarc, B., Cheepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGarald, M., Gage, D., Galagan, J., Radath, R., Karatas, A., Karatas, A., Kaham, L., Grand-Pierre, N., Hafez, N., Hages, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Indblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matherws, C., McCarthy, M., Maldraim, J., Mayen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tackayer, S., Theodocale, J., Tophan, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Travers, M., Vole, I., Simmer, A. and Zody, M. Direct Submission

Numan, C. 21, 2002 this sequence version replaced gi:21326539.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 166423; sum-of-contigs
Quality coverage: 11.3 in Q20 bases; agarose-fp
Quality coverage: 11.5 in Q20 bases; sum-of-contigs
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QY 1567 TITGITCE           Db 73240 TITGITCTC	1627	Db 73300 CAATCTACT		Qy 1741 -CCTTCTT	73420	Oy 1787 GGCTTCCTO       Db 73480 AATTTCCTO	Qy 1847 ATCCATT	Db 73535 ATTTATTT	QY 1907 GTCAGTGAV        Db 73595 ATAGGTGA	1964	73655	Qy 2024 TIACTCAT	7	Qy 2084 ICCICITC	Db 73774 TCCTCTTT	Qy 2144 TCAGCTAT	Db 73834 TCAGCTAT	2201	73894	0y	RESULT 26	ACITATION AC110100 DEFINITION RATEUS DOF		VERSION AC110100.6 KEYWORDS HTG; HTGS	M	Mammalia;	RATTUS. REFERENCE 1 (bases AUTHORS Muzny, D.Ma	Allen, C., . Anyalebech Baldwin, D.	Biswalo,K. Bryant,N.,
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රු අ	1567	TITGIICIAIACITIIAGIGAITIGAITAIAIGACACIGIGGGGAGIITICITIICGGIC 1626 
& 8 8	1627	CAATCTATITGGTGTTTTGTATGCTTCTTGTACCTTGATAGGCATCTCTTTCTCAAGGTT 1686
yo da	1687	AGGAAATITITCTITITIGGITITCTIGAAAATATTTCCCTGCTTTTGACCTG 1740 
% qa	1741	-ccrtcrrccccrrccrratrcc
à a	1787	7 GGCTTCCTGGATGTTTTAGCTGGATTATTTAGACTTAACATTTTCTTGACCAAGGT 1846
SP GS	184	7 AICCALITICITCIAICTIGICITCACCIGCCIGAGAITCICICTICTATCITIGIAITCT 1906
QY DP	1907	7 GICAGIGAGGCIIGICTICIGAGGIICCIGIIGGGIICITAAITITITGAITICAGA 1963 
γ <sub>0</sub>	1964	4 TITCCTICAGTITIGGGTITIGTITATTAATICTATTICCACTITICAGGTCCTGAAATGTI 2023
රු යි	202	4 TIACTCATTITCCTCCCGGTATITACATTITCATAGGTITCTTTAATGGATTTATTCATT 2083
රු අ	208	4 TCCTCTTCAAGGACCTTTTATGAATTCATAAAATGTAGTTAAGGTCCTTGCCTTGTGCT 2143
λ δ	214	TCAGCTATGTTGCATTCTCAGGCCTATTGTAATAGGGTTTTAGCAGGGACATATTG 2200
ó f	0 0	E (
8 6 8	226 395	TGTAATICTAGGT 2273
RESULT 26 AC110100 LOCATION DEFINITION ACCESSION VERSION VERSION VERYWORDS SOURCE ORGANIC REFERENCE AUTHORE	NO P SE	AC110100  Rattus norvegicus clone CH230-212E13, WORKING DRAFT SEQUENCE, 2 unordered pieces. AC110100.6 G1:25139572 HTG; HTGS PHASE1; HTGS_DBAFT; HTGS_FULITOP. Rattus norvegicus (Norway rat) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases I to 250188) Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baras, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, B., Baca, E., Baden, H., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

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Cardense W. Carters. C. Divosao, D. Changers, J. Cessar Ln. Y. Charlon, C. Cockrells. C. Cockrells. C. Cockrells. C. Cockrells. Cox. Cockrells. C. David. C.
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REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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49175 AIGTAT-TITGICAGACAACAAAAGGCTATACCAGCTIACTTATTATACCCATITGCTI 49233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48760 AATTITICAATCTICTIGIAICTGCTAAGACITGCITIGIGICTGAATATGIGATCAATT 48819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49115 ATTITICCITIGACAAGTATAAAGTATTCTTCCTGTCTCTTCTGGTTAGTTTTGGTTTG 49174
                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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                                                                                           Assembly program: Phrap, version 0.990329
Consensus quality: 227481 bases at least 040
Consensus quality: 232076 bases at least 030
Consensus quality: 232076 bases at least 030
Consensus quality: 232076 bases at least 030
Estimated insert size: 239268; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 TTGGAG--AGTTTCATAGGGTGCTGACAAGAAGGTACAGTC-TTTGTGTTTTTGGTGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             669 CCCACTATCTGTGTGTG-AGGTCAATATGTGATTTTTAGCTGTAGCTGTGCTTTTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48995 cccacrercadgardreaaadrcaardrerdrahrraadcraaadragrerreard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19055 AACTICAGIACCCTIGIGITITIGGGCCATAGATGITAAAAATCAAAATGICATCTIGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 ATTATTTCAATTGTCTTTTATCTGTCGAGACTTGCTTTGTTTTTGAAATATGTATTCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 AGICTGTABATATCTCTAGGTCCACT - - TGGTTTATGACATCAGTTAGCTCCAGCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48880 Gricigiacaiaicheridearicaiciereiaiaiaeacaireariaechraecairí
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 250188;
                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33012 33011: contig of 33011 bp in length
33012 33111: gap of unknown length
33102 250188: contig of 217077 bp in length.
Location/Qualifiers
1. 250188
//organism="Rattus norvegicus"
//mol_type="genomic DNA"
//db xref="taxon:10116"
//clone="CR230-212E13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 706.902; DB 1; Length
Pred. No. 0.16;
0; Mismatches 481; Indels
                                           Center project name: GOFV
Center clone name: CH230-212E13
Contact: hgsc-help@bcm.tmc.edu
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/note="wgs_contig"
33112. .35207
/note="wgs_contig"
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Best Local Similarity 69.2'
Matches 1305; Conservative
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Db 50265 TITCCCTCAGGTTTCCTTATATACATT  Oy 2024 TTACTCATTTCCTCCCAGGTATTTACACTT  Db 50383 TCCTCTTTAACAATCTTCACAGGTTTCTTATACAATCTTCACAGGTTTCTTATACAATCTTCACAGGTTTCTTATACAATCTTCACAGGTTTCTTATACAATCTTCACAGGTTTCTTATACAATCTTCACAGGTTTCTTATACAATCTTCACAGGTTTCTTCACAGGTTTCTTATACAATCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTCTTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTTCTTCACAGGTTCTTTTCACAGGTTTCTTTC
997 AGMANACTICACO
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50265 TITCCCTCAGTTIGGGTTICCTTATIAGTTTTATTTCTACATTCAGATCTTGAACTGCT 50	2024 TTACTCATTTTCCTCCCAGTATTTACATTTTCATAGGTTTCTTTAATGGATTTATTCATT 20 1	2084 TCCTCTTCAAGGACCTTTTATGAATTCATAAAATGTATGT		2195 ATATTGTCCTGGTTGTTATTGTCTGTGTTTTTGCTTTGGCATATAGACGGCTGAGTTTGG 22	2255 GATGATIGTAATICTAGGIGCTGAT 2279 	r 27	AC129113 168169 bp DNA linear HTG 19-NOV- Rattus norvegicus clone CH230-342J7, WORKING DRAFT SEQUENCE.	AC1291 AC1291 HTG; F Rattus	<pre>ACANISM Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Battus</pre>	THORS Muzny, D. Marzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranalke, D., Barber, M., Barnstead, M., Benahmed, F.,	BISWALO,K., BLAIT,J., BIAIXEDDUIG,K., BIYCH,F., BIOWU,M.,  Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,  Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,  Charko, I. Charez, D., Chan, G., Chen, W., Chen, Y., Chen, Y.,	Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cayle, M.L., Davils, C., Davy-Carroll, L., De Anda, C., Dedrich, D., Davila, M.L., Davils, C., Davy-Carroll, L., De Anda, C., Divise to Davila, M. D., Davils, C.,	Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., C., Draper,H., Dugan-Rocha,S., Dunh,A., Durbin,K., Duval,B., Eggan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,	Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster, F. Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gabregeordis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.	Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, T., Havlak, P., Hawe, M., Hennandez, J., Harvey, M., Harve	Hernaluez, F., mimes, F., misaum, F.L., modgeou, F., modgeo, F., Hollins, B., Howley, S., Hume, F., Tume, J., Idlebiad, D., Jackson, P., Jackson, P., Johnson, B., Johnson, R., Jolivet, P.	Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.	Liu, J., Liu, W., Liu, Y., London, P., Longere, P., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahnoud, M., Malloy, K., Mangum, A.,	Mangulu, b., Maghas, r., Matt., A., Matt., matt., matt., matt., matt., b., mayniney, S., McIeod, M.P., McNeill, T.Z., Meenen, B., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,	Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwackelemet,O., Okwon,G., Olarnpunsagoon,A., Pal,S., Parks,K.,	Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindéxter, A., Popovic, D., Primus, B., Pu, LL., Puazo, M., Quiroz, J., Rachiin, E., Reeves, K., Regier, M.A., Reigh, R. Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131583 AAGAGTCGAGTACTGAAGTCTCCCACTGTTAATGTGTGGGGGTTCATTGTGTGATTTAAGC 131642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131291 ATGAGTTTGTAGGCTTCATGTAGTTTCTGTTGAAG-----TCCAGCTTTAATCCAT 131344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131404 TATGTCTGAGTATATGGCCAATTTTGGAGAAGGTTCTGTGAGATGCTGAGAAGAAGAATT 131463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131464 ATCCCTTTGTGTTTGGGTGAAATGTTCTGTAGATATCTGTTAGTTTTCATTTAAGTCATAA 131523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131814 GCTTCTTGGGTCTATTTGCTTAGAAATCTTTTGTCTAACTCTTTACTCTGAGGTAACAT 131873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131874 CTATAGTGATGTTCAAGTGTGTTTCTTATATGCAGCAGAATGATGATCTTGTTTTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCATTCTGTTACCCAGTATCTTTTTTTTAGAAATTAAGATCATTGAGTCATTGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTATTTCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGTTTGGTTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAAGTTTGTAAGTTTTCTGTTGTTGTTGTTGTTGTTGTTATCTAGATTTAAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 TGTTTTGAAATATGTATTCAATTTTGGAGA-GTTTCATAGGGTGCTGACAAGAAGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A-GICTITIGIGITITIGGIGAAATAGICIGIAAATATICI-CIAGGICCACTIGGITIAIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             648 GAGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGAGG-TCAATATGTGATTTTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131703 ATTGAGACA-----GTGGATTTTTTTTTTGGTGAGTATGAACTGTCTT--CCCATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTAT -- CCATGGTAGGTTGTCTTTTTGGATGCAGCAGTAGGATGTTCTTTTCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGAGACTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTAGCTGTGCTTGTTTTATGAACTTGGGTGACATTGTGTTTTGGTGCATAGACATTAAGA
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Pred. No. 0.12;
0; Mismatches 529; Indels 119;
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clone_end:T7"
complement(14939. .15702)
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/note="wgs_end_extension
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On Nov 19, 2002 this sequence version replaced gi:23678244.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bem.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs acaffold'). Within each contig scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherers, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smais, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Stennie, M., Strong, K., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usman, K., Wang, C., Wallas, R., Walten, D., Walker, B., Wang, J., Wang, C., Walliams, G., Walten, D., Waleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhong, J., Zhou, M., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 168169)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clohe name: CH230-34207
------- Summary Statistics
Assembly program: Phrap: version 0.990329
Consensus quality: 144418 bases at least Q40
Consensus quality: 145485 bases at least Q30
Consensus quality: 145485 bases at least Q30
Estimated insert size: 146785; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Gaps

Length 168169;

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186834 186834 186834 186834 186834 448 186831 187011 563 187011 683 187130 683 187250 187370 187370 187430 187430 187430 187450 1158 187550 1158 187550 1158 187550 1158 187707 1158 187707 1178 187707	ATTG 129  ATTG 186834  GTTG 186834  GTTG 186834  TTGT 186951  TTTC 187130  TTTC 187130  TTTC 187130  TTTC 200  TTTC 300  TTTC 300  TTTC 300  TTTC 300  TTTC 300  TTTC 187250  TTTC 187250		1637 GGTGTTTTGTARGCTTCTTGTACCTTGATAGGCATCTCTTCTCAAGGTTAGGAAATTTT 1696 1697 TCTTTTTGCTTACTTCTTGAAATATTTTCCTGCTTTCTTT	18835 1921 1981 1981 18846 2041 2046	26 IGITIGATIGIATITITCIGIATCITIATACITAGITGCTIACITITIAAIGICICIACC 26 IGITIGATIGIATITITCIGIATCITIATACITAGITCITITIAAIGICICIACC 47TACATITICATAGGITCITIAAIGATITACITITICAGGACC  86 IGITIGAAIGAAIGAAAIGTAAGITCITAAGGATITACICATGITCITITAAGGAC  99 ITITAIGAAIGATACATAAAAIGTAAGGACTITACITACAIGACTCITITAAGGACT  1	RESULT 29 AC101656/c 267360 bp DNA linear HTG 23-APR-2003 LOCUS DEFINITION MUS musculus clone RP23-306M24, WORKING DRAFT SEQUENCE, 47 unordered pieces.
329 1868 1868 1869 1870 1870 1871 1872 1873 1873 1873 1873 1873 1873 1873 1873	329 1868 1868 1869 1870 1870 1871 1872 1873 1873 1873 1873 1873 1873 1873 1873	8 & 8 & 8 & 8 & 8	3 4 8 6 8 6 8 6	3 8 6 8 6 8 6 8	86868686	RES AC1 LOCG DEF
TCTCCTCCCAAACACTCTATTCTTGATTTCTATTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTCTTTTTT	1970 TYCCTCTCTCTCTCAAACTCTAATTCTTCTTAATTCTTCTTTTTCTTC		623 623 1871 1871 742 1872 1872			
ICCCTCTCCAAACACTTCTATTTCTTGATTTCTTTTTTTTT	186395 TTCCCCCTCTCCCAAACCTCTAATTTCTTGATTTC  186395 AGAAGAGCCATTCAAATTTCTTCTTCTTCTTCTTTCTTCTTTCT	raac' FCAT' FIGT' FIGT' FATC' FATC' FAATC' FAATC'	TTTCGTTT TTTTCGTTT TTTTCGTTG TATCTGTG TACTAATG GGGTGACA GGGTGACA GGGTGACA TACTTTGA	 	PAGAAA PAGAAA PTCTTG	TCT TGT TTT
TCTCTCTCCAAACACC TGAGTTTTACAAACTC TGAGTTTTCAAACTC TCTCTCCACCTTCCAGTTTCCAT TCTCTCCACCTTCCAGTTTTCCAT TCTCTCCACCTTCCATTCCA	270 TTCCCTCTCTCTCAAACAC  186835 AGTACACACTTTTACAAACTTTC  186835 AGTACACACTTTCACTTTCCTTTCCTTTCCTTTCCTTTC	THICTTGGCTCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	AGCATTTCTCTG STATTTCTCTG STATTTCTCTG SAGTAGCCCAC SAGGTCTCCCAC TTTTACAATGT TTTTACAATGT TTTTACAATGT TTTTACAAATGT TTGTGGGAATTT TTGGGGAATTT TTGGGGGAATTT TTGGGGGAATTT		AGTATCTTTTCTAC THE	CATTIGAGGATAGATAT 
	270 TTCCCC 330 AGTAG 330 AGTAG 330 AGTAG 330 AGTAG 330 AGTAG 330 TTGTT 186955 AAG- 449 CTTTT 186952 CTTGT 187012 ATGAG 187012 ATGAG 187191 TGGTG 187191 AGTAT 801 CCTAGG 187191 AGTAT 187311 AGTAT 187311 AGTAT 187491 AAGAG 187491 AAGAT 187551 GAATG 1159 ATCTG 1159 ATCTG 1159 ATGTG 1159 ATGTG 1159 AAGATG 11753 AGATG 11753 AGATG 118753 AGATG 118753 AGATG 118753 AGATG 118753 AGATG	TCTATTTCTTGATTTCTATCTTGGCTCATTTT  TAAATTTCTTTCTTTTTTCTTTCCCTAA  ATAAGTTTGTAAGTTTTCTGTTGTTTCTGTTG  TCAAATATGTAGGA-CATAGGTATTTTCTGTTG  TGTGTTGATAGGA-CATAGGATATTTTTTCT  TGTGTTTTGAAATAGTATTTTCAATTTTGGAGAA  TTGTTTTGAAATAGTATTCAATTTTGGAGAA  TTGTTTTGAAATAGTATTGGAGAATTTTGGAGAA  TTGTTTTGAAATAGTATTGGAGAATTTTGGAGAA  TTGTTTTGAAATAGTATTGGAGAATAGTCTG  TAGTTTTGGAAATAGTATTGGAGAATAGTCTG  TAGTTTTGGAAATAGTATTGGAGAATAGTCTG  TAGTTTTGGAAATAGTATTGGAGAATAGTCTG  TAGTTTTGGAAATAGTATTGGAGAATAGTCTG  TAGTTTTGGAGAAATAGTCTG  TAGTTTTGGAGAATAGTCTG  TAGTTTGGAGAAATAGTCTG  TAGTTTGGAGAAATAGTCTG  TAGTTTGGAGAAA	TOTICGITGITALITGGGGATTTCTCTG	AGAALTGGGAIGACCTCTAGTGGATTTTTC CCTCATCTGGGATGAGTTTAGTCTA  [	RATCCATTCTGTTACCCAGTATCTTTTTCTAC	ct tettlaggietgeattigaagalagatai 

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Bookhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Bookhgalter, B., Choepel, Y., Canagolo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Fariztugh, W., Gage, D., Galagan, J., Godge, S., Faro, S., Fariztugh, W., Gage, D., Galagan, J., Gardhan, S., Ginde, S., Goyette, M., Graham, L., Grand-Pherre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Ilev, I., Johnson, R., Jones, C., Kamata, A., Karatas, A., Kalls, C., LaRocque, K., Lamazares, R., Landers, T., Maratas, A., Marquis, N., Matthews, C., Macdonald, P., Major, J., Merpherers, R., Maldrim, J., Mencus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Kiley, R., Stantes, S., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyan, D., Ye, W.J., Young, G., Milson, B., Wu, X., Wyan, D., Ye, W.J., Young, G., Lainoun, J., Zembek, L., Zimmer, A. and Zody, M., Zainoun, J., Zenbek, L., Zimmer, A. and Zody, M., Direct Submission
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 267360)
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Center: Whitehead Institute/ MIT Center for Genome Research
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------- Project Information
----- project name: L17152
Center clone name: 306_M 24
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                 Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-306M24
                     AC101656.2 GI.30018174
HTG; FTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
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COMMENT

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NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                        contig of 606 bp in length of 100 bp contig of 670 bp in length ocntig of 672 bp in length ocntig of 672 bp in length ocntig of 672 bp in length ocntig of 673 bp in length ocntig of 674 bp in length ocntig of 674 bp in length ocntig of 674 bp in length ocntig of 670 bp in length ocntig of 620 bp in length ocntig of 630 bp in length
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of 1027 bp in length
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117183 CAGATAAGATACATGGGGTTATTTCATTTTTATTATGTGTTGAGTTTTGCTTCATGAC 117242
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Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Madonald, P., Marquis, N., McKernan, K., McLaughlin, J., Maldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C.H., No'Connor, T., O'Donnell, P., Stenge-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillav, H., Wo, A., Mheeler, J., Mu, X., Myman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X.,
                                                                                                                                                                                                     Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
Direct Submission
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 31, 2000 this sequence version replaced gi:7387381.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 78450 78499; gap of 100 bp
* 78550 128836; contig of 50287 bp in length.
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Contact: sequence submissions@genome.wi.mit.edu
Contact: project Information
Center project name: 1767
Center clone name: 224_1_12
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/clone="RP21-224112"
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*** SEQUENCING IN PROGRESS ***, 2
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Badwin, J., Barnan, N., Beckerly, R., Bouklagalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus chromosome, clone RP21-224112
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Mus musculus (house mouse)
Mus musculus
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Db 118430 ATGGACCATTGACTTCTTTTTTTTTTTTTTTTTTTTTTT	AC126499/C AC126499  AC126499  LOCUS  DEFINITION Rattus norvegicus clone CH230-202120, WORKING DRAFT SEQUENCE, 8 ACCESSION AC126499  AC12649  AC12649  AC12649  AC12649  AC12649  AC12649  AC12649  AC1264  AC1664  AC1664
654 GGGGTATTGAAGTAGCCCACTATCTGTGTGAGG-TCAATATGTGATTTTAGCTGTAGT 117468  117409 TAGGTGTTGAAATCCGTCACTATCATGTGGGGTTCGATGTGATTTAAGACTCGAT 117468  713 TGTGCTGTTTTATGAACTGGGTGACTTGTGGGGTTCGATGTGATTTAAGATTGCA 772  117529 ACTCCTCTTGTTTATGAACTGGGTGACTTGAGTACTCCCAATTAAG 117528  773 ATGTCTCTCTTGTTATGAATCTGGGTGACTTGAGTATCTTCCCAATTAAG 117528  774 ATGTCTCTCTTGTAGATTTCCTTTGATGTGATATTAAATCTCCCCAATCTCTCTTTTAA 117586  892 TAGGGCATTTGATTTTCCTTTTAATGATTTTAATTCAAATTAAATTCTCTCAAGTTTTACTTTTAATTTTGATTTTCATTTTAATTTTCATTTTAATTTTCATTTTAATTTTAATTTTCATTTTAATTTTAATTTTCATTTTAATTTTAATTTTCATTTTAATTTTAATTTTAATTTTAATTAATTTAATTTAATTTAATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATT	1248 117953 1365 118013 1425 118133 118193 118251 1605 118311 1665 118311

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Submitted (06-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 211245)

38 Rat Genome Sequencing Consortium.

Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23269518.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, with Ns to the estimated size. The sequence contigs with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, R., Karpathy, S., Kally, L., Kovar, C., Kovar, C., Kowis, C., Xaaft, C.L., Lebowh, H., Levais, L., Li, Z., Liu, J., Lorenshhewa, L., Loulseged, H., Lozado, R.J., Lopez, J., Marchari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Milosavi, Jevic, A., Mint, M., Morten, R., Martinez, E., Mordean, M., Morris, K., Morris, S., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Monidasa, M., Murphy, M., Nair, L., Nankeris, S., Munidasa, M., Murphy, M., Nair, L., Pasternak, S., Paul, H., Perez, L., Perankoch, C., Pasternak, S., Paul, H., Perez, L., Peras, D., Pranks, R., Paly, R., Popidexter, M., Rachin, E., Reeves, K., Regier, M., Quiroz, J., Rachin, E., Reeves, K., Regier, M., Cuiroz, J., Schall, R., Reise, R., Ruiz, S. J., Shet, W., Savery, G., Scherer, S., Schelle, R., Statsman, S., Shen, H., Shetty, J., Shvartsbey, M., Scherer, S., Sorelle, R., Shatsman, S., Shen, H., Shetty, J., Shvartsbey, M., Sutton, A., Savelle, R., Walle, R., Yure, S., Walle, M., Yarong, R., Walle, M., Yarong, R., Walle, M., Yarong, R., Walle, M., Warren, J., Walker, R., Walle, R., Wa
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Gabbank draft data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 ATAAGITIGIAAGITITICIGITIGITIGITGITGITGITGITATCIAGAITITAAGCIGI
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                                                                                                                                                                                                                                                                                                                                                                             1861/VCU.
1861/VCU.
1861/VCU.
1861/ST. contig of 75757 bp in length
1868/ST. gap of unknown length
1868/ST. gap of unknown length
1868/ST. gap of unknown length
1868/ST. contig of 25835 bp in length
1868/ST. contig of 25835 bp in length
1868/ST. gap of unknown length
1868/ST. contig of 24699 bp in length
1868/ST. contig of 24699 bp in length
1868/ST. contig of 71470 bp in length
1875/ST. 2028/ST. contig of 71470 bp in length
1889/ST. 2029/ST. gap of unknown length
1895/ST. 2029/ST. gap of unknown length
1896/ST. 2029/ST. gap of unknown length
1897/ST. contig of 1893 bp in length
1898/ST. contig of 1893 bp in length
1898/ST. contig of 5834 bp in length
1808/ST. contig of 5834 bp in length
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30.8%; Score 702.902; DB 1; Lengtl
Best Local Similarity 67.9%; Pred. No. 0.15;
Matches 1362; Conservative 0; Mismatches 576; Indels
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3941. .5860
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/note="wgs_contig"
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Db 112322 ATTTCTGGGCTTTTGACCTGGGTTTCTTCCTTGATTCTTTTTGGTTT 112263  Qy 1780 TGTCTGGCTTCCTGGATGTTTATTGGATTATTTTGGCTTT 112204  Db 112262 GGTCTTTCTTGTCTTGTCTTCATTGTTTTTA-ATTTACATTTTCTTT 112204  Qy 1838 GACCAAGGTATCCATTCTTCTATCTTGTCTTCACTGCCTGAGATTCTTCTTTTTTT 112204  Qy 18203 TACCATGAATCCATTTTTTTTTTTATCTTGTTTCAAGTTTTTTTTTT	Oy 2015 TGAAATGTTTACTCATTTCCTCCCAGTATTTACATTTTCTTAATGGAT 2074	RESULT 32 AC095214 LOCUS AC095214 LOCUS DEFINITION RATUS norvegicus clone CH230-10B9, *** SEQUENCING IN PROGRESS ***, S unordered pieces. ACCESSION AC095214 ACCCT-2002 ACCT-2002	Anyalebechi, V., Aoyagi, A., Ayoegi, M., Barabe, Badewin, Bandwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bulay, C., Burch, P., Burrell, K., Calderon, B., Cardenas, V., Carter, K., Cavaco, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chave, C., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Denger, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Baccotco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagy, N., Forbes, L., Foster, M., Gebregocygis, E., Geer, K., Gill, R., Garcia, A., Garra, M., Guerza, M., Guerza, M., Guerza, M., Guerza, M., Harlen, P., Haaland, W., Hamilton, C., Hamilton, K., Harley, P., Hawes, A., Henderson, N., Hernandez, J., Howels, R., Hoderson, N., Hernandez, M., Hollins, B., Howells, S., Hume, J., Idlebird, D., Jackson, A.,
	113080 TCTTGATGGTGGTTGTTTTTTGGATGGATGGATGGATGGA	TTATTCATATTTCTTGAAIGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGCC	1482 ATTGGAGGTCAGGTGATTCTAATACATCTGCCTTTATGGTTTTTTT 1541  112550 ATTGGAGGTCAGGTTATAATTCTTATATGTCATTATGGTCTTTTTT 112491  1542 CCCTTGCAGTTATAATTCTTTTTTTTTTTTTTTTTTTTT

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Accident, J. Jackson, L. Jacks
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122156 TTTATTTCTTTATTTCTGTTTTTGACCCATTTTTTAATTCAGTAGACAGTTGTTCAATTTCC 122215
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). ONDE: This is a "working draft" sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                               1 97912: contig of 97912 bp in length 98012: gap of unknown length 98013 139433: contig of 41421 bp in length 9834 139533: gap of unknown length 14328: contig of 3695 bp in length 3329 14328: gap of unknown length 5580 235779: gap of unknown length 5780 241255: contig of 92351 bp in length 5780 241255: contig of 5476 bp in length.
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\* NOTE: Estimated insert size may differ from sequence length

Db 12367 ATTTCCCTGCTTTTGACCT GCCTTCTCCCCTTCCT  Qy 1780 TGTCTCGGCTTTTGACCTGGGTTTTTAGCCTGGAT  Db 123627 GGTCTTTCATAGTGCCCGGATTTTTATGCTTGGTT  Qy 1838 GACCAAGGTACCATTTTTTTTTTTTTTTTTTTTTT  Qy 1836 TACCAAGGTATCCATTTTTTTTTTTTTTTTTTTTTTTTT	ACCESSION ALG6996.11 GI:21213362 KERMORDS MAS musculus (house mouse) MAS musculus (house mouse) MAS musculus Eukaryota; Metazoa; Chordata; Craniata MAS manalia; Eutheria; Rodentia; Sciurogn REFERENCE 1 (bases 1 to 227762) AUTHORS 1 (bases 1 to 227762) AUTHORS 1 (bases 1 to 227762) AUTHORS 1 (cambridgeshire, CB10 15A, UK. E-mail er Cambridgeshire, CB10 15A, UK. E-mail er Cambridgesnire, CB10 15A, UK. E-mail er Cambridgesnire, CB10 15A, UK. E-mail er CAMPENT During sequence assembly data is company Where differences are found these are together with a note of the overlapping corresponding to the overlapping clone, only a small overlap as described above This sequence was finished as follows or chemistry or covered by high quality da 30); an attempt was made to resolve all as compressions and repeats; all region one plasmid subclone or more than one N
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11 enquiries:

12 colonerequest@sanger.ac.uk

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abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP; Attabase can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-15J3 is from the RPC1-23 Mouse PAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm

VECTOR: pBAcc3.6
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Pred. No. 0.16;
0; Mismatches 511; Indels 59; Ga
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Similarity 69.1%;
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169058 169345 168938 168998 169108 169168 169226 169402 169462 169701 169521 169581 169641 168884 1957 1301 1421 1481 1601 1661 1837 1897 2077 1123 168885 AGAGAGAGAGG-----GAGAGAGTCTCTTACTTTTGGTTTTTGCTGATGTGTGTTATTTA 168999 TICTGTAGGACTGGATTTGTAGATGGATATTGCTTAAATTTGACTTTTTCGTGAAATATA 169169 GTT-GAGAAGTCAGGCATAATTCTAATAGGTCTGTGTTTATATGTTACTTGGTCTT-TT 169287 GAIGGGAGGA-TITITITITICIGCTCAAICTATITGGIGCTCTGTAAGCTICTTCTACTT GACCAGRGTATCATTTTCTTCTATAATCTTCAATGTCTGAGATTTCCTCTTCCATCTT 169642 TCCAGAATTAACCCTGCTTGTGTTTTCTTTATTGATTCTATTTCATTTTCATGTCTTGA AAAGTATCAATGGACAATGATTGTTAATTTCTGCTATTCTTACGATGTTGTTGGCAATTG TTATTCATATTTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTA--GCC TTTCCTGTGTTTTCATGGATGTAGCTTAACCTGCTTGGGTTAGAATTTTTCTTAACACT TICITIAGGICIGCATITIGAAGATAGATATICITIACATCIGATITIATCITAGAATGIC CCCTTGCATCTTTAATATTCTTTCTTTGTTCTATACTTTTAGTGATTTGATTATTATGC 169346 TCATAGGCATC---TTCTTTAGGTTAGGAAATTTTTCTTGTAGGATTTTGTTGAAAATA rrincagaderringaderidegarnerrerrerrerrearricenagaararaeerregring GACCAAGGTATCCATTTCTTCTTTCTTCTTCACTGCCTGAGATTCTCTCTATCTC 169582 TTGTATTCTGTTGGTGAAACCTGCCTCTGCCATTCCTGTTTGCATACCTAAATTTTCATT AAIGITITACICATITICCICCCAGIATITACATITICATAGGITICITIAAIGGATITA ACAGITITATITICIATGGGTTTTTCTTTGAGGAATTTATTCATTTCCCCTAATCACTTGT TCTGTGTCTTGTGTGTGTGTTCTCCCCCTCTTTTGATTTTTGGCCTGGAATTATTA TTTCTTTCTCCAACTATTGTGACAGAAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGACAT r---rircicrarrigiosica----rirrigcicaciaricidadicicacia CIGIAGICICITGGAGICIGIAGCACAICIGIGCAGGGCCTICITACAITITGAGITICI 169109 CTGTAGTCTCTTAGAATCTGTAGAATATCTGTCCATGCCCTTCTAGCTTTTAGAGTCTCT 1482 ATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATATTAGTTTGGTCTTTTTT 1602 ACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGGTGTTTTGTATGCTTCTTGTACCT TTTTCCCTGCTTTTGACCTGCC-TTCTTCCCCTTCCTCTATTCCTTTGGTT--TTTGCAT <u> AGTGTCTCGCCTTCCTGGATGTTTTATGCCTGGATTATTTTAGACTTAACATTTTTCTTT</u> TTGTATTCTGTCAGTGAGGCTTGTCTCTGAGGTTCCTGTTGGGTTCTTAATTTTTTCATT TCCAGAITTTCCTTCAGTTTGGGGTTTTGTTTAATTAATTCTATTTCCACTTTCAGGTCCTGA 169807 2123 TIGITITITICTAGATTAAAAAAATTATTCATCAATTAATTTATTT 1184 1302 1662 1064 1422 1542 169403 1838 1958 2018 1124 168939 1362 169059 1721 1778 169463 1898 2078 168825 169522 169702 요 ВÞ g 임 g ò 엄 ద 셤 원 8 셤 원 g ð 셤 셤 ò g  $\stackrel{>}{\circ}$ g ò БÞ 8 8

Rat Genome Sequencing Consortium.

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Allen, C. Allen, H. Alberooks, S. Amin, A. Anguiano, D.

Anyalebechi, V. Avogai, A. Ayodeji, M. Baca, B. Baden, H.

Bandaranick, Blait, J. Blankenburg, K. Blyth, P. Brown, B.

Biswalo, K. Blait, J. Blankenburg, K. Blyth, P. Brown, B.

Cardenas, V. Carter, K. Gavazos, T. Chen, R. Calderor, B.

Cardenas, V. Carter, K. Cavazos, T. Chen, R. Calderor, B.

Cardenas, V. Carter, C. Burch, P. Burrell, K. Calderor, B.

Cardenas, V. Carter, C. Burch, P. Burrell, K. Calderor, B.

Cardenas, V. Carter, C. Bretano, C. Coyle, Dinh, J. Davak, B.

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Davila, M. L. Davis, D. Beramo, C. Ding, Y. Dinh, H. Davak, K.

Davis, M. Cabisi, A. Ganta, R. Garcia, M. Guerra, M. Gebregoorgis, B. Geer, K. Gall, R. Cardy, M. Gerra, M. Garza, M.,

Gebregoorgis, B. Geer, K. Gall, R. Cardy, M. Guerra, M.,

Gebregoorgis, B. Geer, K. Hades, A. Handerson, N. Hernandez, J.

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Harray, S. Kally, S. Hadm, S. Hadm, J. Lowas, L. Morgues, M.

Hollins, B. Hwellis, S. Hulk, S. Handerson, N. Manither, D.

Jackson, L. Jacob, L. Jing, H. Johnson, B. Johnson, R. Johnson, R.

Mandgun, B. Hwells, S. McLeod, M. N. Manith, J. Levan, J. Mandon, J. Mando
                       ACL26296 234920 bp DNA linear HTG 13-MAY-2003 Rattus norvegicus clone CH230-53A13, WORKING DRAFT SEQUENCE, 2
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                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_RAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                          AC126296.3 GI:30580982
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ley, K.C.
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Unpublished
RESULT 34
AC126296/c
                                                                                           DEFINITION
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KEYWORDS
SOURCE
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                                                                                                                                                            ACCESSION
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Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23269045.

The sequence in this assembly is a combination of BAC based reads and whole genome shocgun sequencing reads assembled using Atlas (http://www.hgso.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shocgun sequence reads. Both end sequences and whole genome shocgun sequence reads. Both end sequences and whole genome shocgun sequence reads.
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NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 TIGITATCTAGATTTAAGCTGTGGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 698.901; DB 1; Length 234920;
Pred. No. 0.17;
0; Mismatches 561; Indels 123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 180394: contig of 180394 bp in length 180395 180494; gap of unknown length 180495 234920: contig of 54426 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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66.8%;
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Anyalebechi, M. Aoyagi, A. Aydodi, M. Baco, E. Bisdan, H. Brahmed, P. Bisaela, B. M. Bisaela, B. M. Bart, B. M. Barkenburg, M. Bitch, B. Broom, M. Bursell, M. Bird, B. M. Barkenburg, M. Birth, B. Branch, M. Birth, M. Branch, M. Birth, M. Branch, M. Birth, M. Branch, M. Carter, K. Carcase, H. Casar, H. Carter, M. Caurari, M. Cardens, V. Carter, M. Birth, M. Branch, M. Carter, M. Coxesae, H. Coxesae, H. Carter, M. Cardens, M. Carter, M. Distance, M. Branch, M. Carter, M. Distance, M. Branch, M. Carter, M. Carter, M. Distance, M. Branch, M. Carter, M. Carter
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AUTHORS TITLE JOURNAL

REFERENCE

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COMMENT

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NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389
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                                                                                                                                                                                                                                                        Assembly program: Phrap, version 0.990329
Consensus quality: 226894 bases at least Q40
Consensus quality: 229443 bases at least Q30
Consensus quality: 231082 bases at least Q20
Estimated insert size: 231793; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cuery Match 30.7%; Score 698.901; DB 1; Length 243576; Best Local Similarity 66.8%; Pred. No. 0.17; Matches 1377; Conservative 0; Mismatches 561; Indels 123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the apps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238770 238469: gap of unknown length
238470 242092: contig of 2623 bp in length
238470 242192: contig of 3623 bp in length
242193 242192: gap of unknown length
242193 243576: contig of 1384 bp in length.
                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                             Center project name: GRKC
Center clone name: CH230-202N2
------- Summary Statistics
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Db 49266 ATTAGGTTAGGGAAATTTTCTTTAACGTTTTACTTTATCGTAAATTTTTCGTGGCTTTGACC 49325  1739 TGCCTTCTTCCCCTTCCTTTGGTTTTTCGTAAATTTTCTTTGACAAAGGCCC 49385  49326 IGTTCTTCTTCTTCTTATGCCTGAATTTTTTAACTTTTTTTT	RESULT 36 AC129381 C LOCUS LOCUS LOCUS LOCUS EACLES DAY-2003 DEFINITION RATTURE DAY-2003 DEFINITION RATTURE DAY-2003 AC129381.5 G1:30578753 RATTURE AC129381.6 G1:30578753 RATTURE AC129381.7 G1:30578753 RATTURE COURCE ORGANISM RATTURE NOTVEGICUS (NOTWAY TAI) RATTURE NOTVEGICUS (NOTWAY TAI) RATTURE ORGANISM ORGANI
628GAGATGACCTAACTGATGGGGAATTGAAGTAGCCACTATCTGTGTG 684 48225 TTGTCTAAATGATGTCTATTGGCAATTGTGTGAATTGTTTATTGAGGTGT 743 48285 GAGGGCCAATATGACTGTATTGCAATTGTGTGTATTTATT	1259 IGAATGTGGGTAACATCTTAGATTGAAGTTTTTCTCCTAGCCTTCTTTAGGTTGCATT 1318 48856 IGGGTATTGTTAATGTCTTTAGATTGAATTGTTCTTCTTCTTGCTATAGAGTA 48912 1319 IGAAGATAGTCTTTACATCTGATTTTATCTTAGATTTCTTTC

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Gebregeougle, B., Hallon, W., Hamilton, C., Hockson, A., Hacrage, R., Hittes, S., Hiadun, S., L., Hodgeon, A., Hogue, M., Harnede, J., Galen, C., Hamilton, C., Hodgeon, A., Hogue, M., Hockson, A., Hockson, A., Hockson, A., Hockson, A., Hockson, C., Hamilton, C., Hollow, C., Hamilton, C., Hollow, C., Hamilton, C., Hamilton,
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25577 A---rariccadrirraariccarrendagacadaradecrecadedigirarricaarirric 25521
                                                                                             * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       743
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Consensus quality: 237232 bases at least Q20
Estimated insert size: 239244; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25520 TIGIGICIGITGAGGCITGATCT---------TIGGAAAAAGTITCATG
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66.8%; Pred. No. 0.18;
ative 0; Mismatches 561; Indels 123; Gaps
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                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                      243423: contig of 243423 bp in length 245523: gap of unknown length 245548: contig of 1025 bp in length 245705: contig of 1055 bp in length 245705: contig of 1057 bp in length 245705: contig of 1057 bp in length 247051: contig of 1246 bp in length 247051: contig of 1246 bp in length 250030: contig of 2879 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
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Matches 1377; Conservative
                                                                                                                                                                                                                                                                                                                                        be preserved
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M.Lee., Abramzon, S., Adams, C., Alder, J.,
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Ayodejl, M., Baca, E., Baden, H.,
D., Barber, M., Barastead, M., Benahmed, F.,
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Liu, J., 24025 ARBARATGTATGTTARGGTCCTTGCCTT 2144 2024 AGT-TTTTAGATTTAACTTTTTTTTTG-TCTAGG 24144 ACTGCCTGAGATTCTCTTCTATCTTGTATTC 1905 CCTG-TTGGGTTCTTAATTTTTCATTTCCAGAT 1964 a, Craniata, Vertebrata, Euteleostomi, a, Sciurognathi, Muridae, Murinae, TAATTCTATTTCCACTTTCAGGTCCTGAAATGTTT AATGCATTAGATTCTCTCTTTTATCTCCTGTATTT T; HTGS\_ENRICHED.

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ALE SUBMITSENORM

ALE SUBMITTED (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

ON MAY 13, 2003 this sequence version replaced gi:22857433.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
Lorensuhewa, L., Loulesged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, B., Mangua, P., Martin, R., Martine, E.,
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Niederhauseern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinscock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
Submitted (02-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA
3 (Dassel 1 to 228302)
Rat Genome Sequencing Consortium.
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Center code: BCM
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Center clone name: CH230-64N5
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COMMENT

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
NOTE: This is a "working dataft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is

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84824 CCTTTACTCTAAGGCAATGTCTATCTTGTTGCTGAGGTGTGTTTCTAGTATGCAGTAGA 84883
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                  215461: contig of 215461 bp in length 5462 215561: gap of unknown length 5562 218013: contig of 2452 bp in length 218113: gap of unknown length 8014 219376: contig of 1263 bp in length 9377 219476: gap of unknown length 9477 221346: contig of 1870 bp in length 1477 221446: gap of unknown length 1447 228302: contig of 6856 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-64N5"
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981 AGGATGGATCTTGTTATCCATTCTGTTACCCAGTATCTTTTTTTT		1970 TCAGITTGGGTTTTGTTTATTAATTCTATTTCCACTTTCAGGTCCTGAAATGTTTTACTC 2029
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                                                                                                                                                                                                                                         Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On Nov 15, 2002 this sequence version replaced gi:2347788.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bom.tuc.edu/projects/faxt/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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NOTE: This is a "working draft' sequence It currently consists of 3 conties. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                      Submitted (03-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases I to 183078)
Rat Genome Sequencing Consortium.
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Direct Submission
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Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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/note="wgs end_extension
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42972 ACCCTTTAC-CTTGGGTAATGTCTGTCTTGATGTTCAGATTTGTGTCTTTGCTACAGTA 43030
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                                                                                                                                                                                                                                                                                                                                                            Submittee (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23809119.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.igsc.bom.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs scaffold', Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                    Submitted (21-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, O., Wang, C., Warren, J., Warren, R., White, F., White, F., Williams, G., Willson, R., Wieczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, U., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Rat Genome Sequencing Consortium.
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Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGTTATCTAGATTTAAGCTGTGGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Length 199545;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 692.504; DB 1; Length 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.2
Matches 1371; Conservative
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Oy 2138 TGTGCTT  Db 100909 TCTACTT  Qy 2189 AGGACP  Db 100849 GGAGACP  Qy 2249 GTTTGG	RESULT 40 AC129417/C LOCUS DEFINITION Rattus no NCCESSION AC129417 VERSION WERYNORS RATTUS IN RATUS IN RATIS IN RATUS IN RATIS IN RATUS IN RATIS IN RATUS IN RATIS	Williams
1102 TTGCACTT	1257 10174 1317 101716 1377 101656 1437 101600 1497 101742 1617 101319 1737 101319 1737 101319 1838 101319 1898 101319 1898 101319 1898 101319 1898 101319 1958 1011023	100963 TTAATTTCCCTAGAACTCTATCATTTTCATACAGTTGGTTTAAAGTCTTTTCT 100910
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B	<u>අ</u>

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28810 GGGGGTCAATATGTGATTTAAGCTATAGTAGTATTTCTATTACAAATTTGGGTGCTCTTG 28751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 AGTAGTGAGTTGTTTGGTTTTCCATAAGTTTGTAAGTTTTCTGTTGTTTTCTGTTGTTGTTGTTG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       922 TCCTTTTACTCTAAGGTGATGTCTATCCATGGTAGGTTGTCTTTTTGGATGCAGCAGTA 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29108 -TGAAATCCAGCTTTAATCCATGATGGTATAACAGGATGCAGGAAGTTATTTCTATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29049 TTATATCTGTTAACACTTGCTTTCTGTGTATGTGTGCTCAATTTTAGAGGAAGTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28989 TGAGGCATACAGAAGGTTTATTCTTTTGTTTGAATGAAATGTTCTGTAAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TC-TAGGTCCACTTGGTTTATGACATCAGTTAGCTCCAGCATTTCTCTGTTTCGTTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28750 IGCTICGGCCGAAATATTAAGAATTGAAATTCCTTCTTGGTTGAGTTTCCTTGGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510 GGGTGCTGAC--AAGAAGGTACAGTCTTT--GTGTTTTGGTGAAATAGTCTGTAAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28869 rcig-raigaccicarigargagaricegraargagacrececarrarcarierer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGITALCTAGALLTAAGCIGIGGIGGICAGATAGGACATAGAGIATTALTICAALTGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTATCTGTCGAGACTTGCTTTGTATTTGAAATATGTATTCAATTTTGGAGAGTTTCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    625 GTTGAGATGACCTAACTGTTGGAGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             685 -GAGGTCAATATGTGATTTTAGCTGTAGCTGTGCTTGTTTTATGAACTTGGGTGACATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29165 AATAGAGAGTIGTTTACTTTTTATGAGTTTTGTAAGATTTCTAATGTTTCTGTCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 213532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 585; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 692.504; DB 1;
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Best Local Similarity 66.2%;
Matches 1371; Conservative
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Best Local Similarity
           misc_feature
                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                                                                              Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 19, 2002 this sequence version replaced gi:23907989.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/ratt/). Each contig described in the feature table below represents a scaffold in the Atlas seembly (a 'contig-scaffold'). Within each contig scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.twc.edu/docs/Gabbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                              Submitted (30-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center Clohe name: CH230-287M3
------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 195091 bases at least Q40
Consensus quality: 197956 bases at least Q30
Consensus quality: 197956 bases; aum-of-contigs estimation
Q20 bases; sum-of-contigs estimation
Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von hausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2269: contig of 5269 bp in length

2370 5569: gap of unknown length

3370 205785: contig of 200416 bp in length

336 205885: gap of unknown length

386 205942: contig of 4057 bp in length

3943 210042: gap of unknown length

310 21378: contig of 1036 bp in length

310 21178: gap of unknown length

310 21239: contig of 1161 bp in length

340 21239: contig of 1161 bp in length

340 21353: contig of 1093 bp in length

350 21239: contig of 1093 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                             3 (bases 1 to 213532)
Rat Genome Sequencing Consortium.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- Genome Center
                            Niederhausern, A., Weiss, R., Weinstock, G. and Gibbs, R.A. Direct Submission
                                                                                                                                    (bases 1 to 213532)
                                                                                                                                                                                          Direct Submission
                                                                                                           Unpublished
                                                                                                                                                           Worley, K.C.
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205886
209943
211079
211179
212340
212340
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REFERENCE
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449

Gaps

28990

509

28930

624

565

28811

684

28631

861

inton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Lanna,M., Bastien,V., Bloom,T., Boguslavkiy,L.,
Barna,M., Bastien,V., Bloom,T., Boguslavkiy,L.,
Chogel,Y., Calangelo,M., Callins,S., Collymore,A.,
Chopel,Y., Colangelo,M., Collins,S., Collymore,A.,
Ke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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Dahockky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Macdonald,P., Marguis,N., Mathews,C.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Ormor,T., O'Donnell,P., O'Neil,D.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Betta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Savers,M., Travis,N., Trefgilio,J., Vessillev,H.,
A., Wilson,D., Wux,M., Waman,D., Ye,W.J., Young,G.,
Lands,L., Zimmer,A. and Zody,M. GTTGGAATATTCTGGGTCTGCTGTAGAATAGATGGGCTCTACT 27300 A-----cicialcarricaracagricarriaaacicritrici 27360 trcrrcaactatrigcrrgggifrricrggatririrrgagrifca 27414 2137 CTGGTTGTTGTCTGTGTTTTTGCTTTGGCATATAGACGGCTGA 2248 Jaum, C., Lander, E., Abouelleil, A., Allen, N.,
rachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
rachchi, H.M., Conana, N., Chang, J., Choepel, Y.,
Dook, A., Cooke, P., Corum, B., Dakrellano, K.,
ge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
tlcZerald, M., Gage, D., Galagan, J., Gardyna, S.,
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J.L., Hulme, W., Iliev, I., Johnson, R., Jones, C., ITTCCTCCCAGIATTTACATTTTCATAGGITTCTTTAATGGATTTA 2077 GTTGCA-----TTCTCAGGGCCTATTGTAATAGGGTTTTAGC 2188 190947 bp DNA linear HTG 03-FEB-2003 one RP23-442MS, WORKING DRAFT SEQUENCE, 17 unordered zoa; Chordata; Craniata; Vertebrata; Euteleostomi; ria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 190947) PR-2002) Whitehead Institute/MIT Center for Genome harles Street, Cambridge, MA 02141, USA AAGGACCTTTTATGAATTCATAAATGTATGTTAAGGTCCTTGCCT TRATICIAGGIGCIGAT 2279 aum, C. and Lander, E. lone RP23-442M5 1; HTGS\_DRAFT. ouse mouse) 28195960 190947)

COMMENT

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source
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Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Meneus, L., Mihowa, T., Mlanga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasam, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataranan, V. S., Viel, R., Vo, A., Wilson, B.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (03-FEB-2003) Whitehead Institute/MIT Center for Genome
On Feb 3, 2003 this sequence version replaced gi:20219162
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: 120306

Center clone name: 442 M 5

Center clone name: 442 M 5

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 186315 bases at least Q40

Consensus quality: 186315 bases at least Q20

Insert size: 194000; agarose-fp

Insert size: 189347; suu-of-contigs
Quality coverage: 6.4 in Q20 bases; sum-of-contigs
Quality coverage: 6.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
______ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s; contig of 313 bp in length
s; gap of 100 bp
contig of 687 bp in length
contig of 1107 bp in length
contig of 1107 bp in length
contig of 100 bp
contig of 159 bp in length
gap of 100 bp
contig of 1543 bp in length
gap of 100 bp
contig of 6637 bp in length
gap of 100 bp
contig of 649 bp in length
gap of 100 bp
contig of 2449 bp in length
gap of 100 bp
contig of 2449 bp in length
gap of 100 bp
gap of 100 bp
gap of 100 bp
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g of 5946 bp in length
f 100 bp
g of 7635 bp in length
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100 bp
of 66937 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 bp
of 12557 bp in length
100 bp
of 16679 bp in length
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gap of 100
contig of
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gap of 1
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gap of 1
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gap of
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1200:
2307:
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83256
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90991
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120427
132055
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100 bp

132154:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59387 İTGİAİCİĞİTTATGITİTĞCİTİTĞİCICTGAĞİAİAİAİAİAAAİTİTĞĞAĞAAĞĞİTCTĞ 59446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59274 Agradosadrircradrirccardaricreradacriricrorririrrigirigir --- 59329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.2%; Score 688.903; DB 1; Length 190947; 65.5%; Pred. No. 0.16; ative 0; Mismatches 617; Indels 89; Ga
1155 148505: contig of 16351 bp in length 1506 148605: gap of 100 bp 406 169417: contig of 20812 bp in length 169417: contig of 20813 bp in length 189830: contig of 20313 bp in length 18931 199947: contig of 1017 bp in length 160247: contig of 1017 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="assembly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 65.5:
Matches 1343; Conservative
                  148506
148606
169418
169518
189831
189931
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Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
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Jackson,L., Jacobb,L., Jang,H., Johnson,B., Johnson,R.,
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All Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Stat Genome Sequencing Consortium.

Stat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24959759. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/) Each contig described in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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JOURNAL
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AUTHORS
TITLE
JOURNAL
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COMMENT

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213862 TTTGTCTTGAGCCATTTTCATTCACTAGTGAGTTCCTCTGTCTCCATGCACTTACAAGC 213921
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Center project name: GFZX
Center clone name: CFZX
Center clone name: CHZOL185C21
Assembly program: Atlas 3.0;
Consensus quality: 200905 bases at least Q40
Consensus quality: 200905 bases at least Q30
Consensus quality: 201904 bases at least Q30
Consensus quality: 20112 bases at least Q30
Consensus prainty: 20112 bases at least Q30
Consensus diality: 20112 bases at least Q30
Consensus diality: 20210 bases; sum-of-contigs estimation
Q10ality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             663 AAGTAGCCCACTATCTGTGTGA-GGTCAATATGTGATTTTAGCTGTAGCTGTGCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 TCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGTTTGGTTTCCATAAGTTTGTAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.9%; Score 680.301; DB 1; Length Best Local Similarity 69.2%; Pred. No. 0.21; Matches 1258; Conservative 0; Mismatches 477; Indels
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Contact: hgsc-help@bcm.tmc.edu
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Nazny, D.Marie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Anzuy, D.Marie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Anyalebechi, V., Anyagi, A., Ayodeji, M., Baca, E., Baden, H., Badaranaike, D., Barber, M., Barantstead, M., Benahmed, F., Bladwin, D., Bandaranaike, D., Barber, M., Barantstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Banty, J., Chen, Y., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesaar, H., Center, A., Chavez, D., Chen, G., Corden, M., Carter, M., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davia, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Derawo, C., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Derawo, C., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Denson, S., Handle, M., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, K., Havlak, P., Haves, A., Herderson, N., Hernandez, M., Howells, S., Hladun, S.L., Hodgson, M., Hamilton, C., Hamilton, C., Hamilton, C., Mandle, M., Jacob, L., Jacob, H., Lozado, R., Johnson, R., Johnson, R., Johnson, R., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Johnson, R., Johnson, B., Johnson, B., Luly, S., Hulyk, S., Hu

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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the location/qualifiers
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reelily, W., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Riggs, F., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Sharatsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Scdergren, E., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walter, B., Wang, Q., Wallson, R., Walcron, L., Walter, B., Wang, J., Willson, R., Wlacker, R., Weight, D., Willson, R., Walcron, L., Wooden, H., Worley, K., Willson, R., Walch, S., Yen, J., Yoon, L., Yon, V., Vu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Waiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (Dasses 1 to 237087)

Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On Sep 21, 2002 this sequence version replaced gi:21908808.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequency reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entiraly of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both and sequence indicated in the feature table.
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Consensus quality: 218595 bases at least Q40
Consensus quality: 220145 bases at least Q30
Consensus quality: 221163 bases at least Q30
Consensus guality: 221163 bases at least Q30
Estimated insert size: 237881; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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Contact: hgac-help@bcm.tmc.edu
------ Project Information
Center project name: GYBJ
Center project name: GYBJ
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/clone="CH230-33F3"
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75096 TGGTTAATTCTGGGAAAAGTTCCATGCGTTTCTGAGAAAAGGTATATTCTTTTGTGTG
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69.2%; Pred. No. 0.22;
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"Netzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
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"Suwaren, J., Warren, Y., Walren, F., Warren, J., Warr 261378 bp DNA linear HTG 06-NOV-2002 clone CH230-341M21, \*\*\* SEQUENCING IN PROGRESS -2002) Human Genome Sequencing Center, Department Human Genetics, Baylor College of Medicine, One ston, TX 77030, USA u, Chordata, Craniata, Vertebrata, Buteleostomi, 1, Rodentia, Sciurognathi, Muridae, Murinae, HTGS DRAFT; HTGS ENRICHED. (Norway rat) 378)

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95927 TITGLCTTGAGCCATTITCATTCACTAGTGAGTTCCTCTGTCTCCATGCACTTACAAGC 95986
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IGTTTGGTTTCCATAAGTTTGTAAGT
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                                  Submitted (06-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Nov 6, 2002 this sequence version replaced gi:23907833. The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc..bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
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Center clone name: CH230-341M21
Center clone name: CH230-341M21
Assembly program: Phrap; version 0.990329
Consensus quality: 195499 bases at least Q40
Consensus quality: 197131 bases at least Q20
Consensus quality: 198079 bases at least Q20
Estimated insert size: 203971; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bom.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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Center code: BCM
Web site: http://www.hasc.bcm.tmo.e
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Muzny, D.Marie., Matzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
HTG: TOTVEGICUS (NOTWAY rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                               CTGCAGACTCTTAGAATTCATAGAACATCTGTCCAGGTTCTTCTGGCTTTTACAGTCTCC
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Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24819560.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Aclas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold') within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clavez, D., Clavez, D., Clavez, D., Davis, C., Davis, C., Coyle, M., Cree, A., D'Souza, L., Davis, G., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davis, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Davis, D., Davis, C., Paran, C., Peris, C., Hamilton, K., Harrey, Y., Havlak, P., Huld, S., Handilton, C., Hamilton, K., Harrey, Y., Havlak, P., Huld, S., Hune, J., Idlehid, D., Wodels, S., Hulyk, S., Hune, J., Idlehid, D., Wodels, S., Hulyk, S., Hune, J., Idlehid, D., Wodels, C., Varis, C., Liu, Y., Chuly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Morienan, B., Marlon, W., Martin, K., Warten, M., Walle, K., Sterer, M., Wal Morley, K.C.
Direct Submission
Submitted (13-SEP-2001) Human Genome Sequencing Center, Department
Submitted (13-SEP-2001) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 274459)
Rat Genome Sequencing Consortium. Center: Baylor College of Medicine (bases 1 to 274459) Direct Submission Unpublished

AUTHORS TITLE JOURNAL

TITLE JOURNAL REFERENCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

site: http://www.hgsc.bcm.tmc.edu/

Center code: BCM Web site: http://

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TAGAATACTACTTTCACTTCTTTAGGTTTATTTGCTTGAAAATAGCTTTTCCAGCCC 134247
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                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                           Consensus quality: 251930 bases at least Q40 Consensus quality: 253189 bases at least Q30 Consensus quality: 254147 bases at least Q30 Estimated insert size: 263100; sum-of-contigs estimation Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 274459;
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Pred. No. 0.26;
                   Project Information
                               Center project name: GADK
Center clone name: CH230-3B9
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/note="wgs_end_extension
clone_end:T7"
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/db_xref="taxon:10116"
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1928 GGTICCIGITGGGITCT-TAAITTITCAITTCCAGAITTCCTTCAGTTTGGGTTTTGTT 1986
135247 IGATTCTGTTTGCTTATCTAGAITTTCTATCTCAGGAITCCCTCAGITTGTGTTTTCTT 135306
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135067 TTCTATTATTCTTAGGCTTAATCTTTTATGGTTTCCCAAATTTCCTGAATGTTTTGTGT 135126
                                                             1987 TATTAATTCTATTTCCACTTTCAGGTCCTGAAATGTTTTACTCATTTTCCTCCCAGTATT 2046
                                            1808 CTGGATTATTTTAGACTTAACATTTTCTTTGACCAAGGTATCCATTTCTTCTATCTTGTC 1867
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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OM nucleic - nucleic search, using sw model

Run on:

August 25, 2004, 06:30:30 ; Search time 2253 Seconds (without alignments) 3.614 Million cell updates/sec

US-10-664-775-4 2279

1 gatcactcctctagtgaaag......ttgtaattctaggtgctgat 2279 Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapop 10.0 Scoring table:

39 seqs, 1786346 residues Searched:

78

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

rng4.seg:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Mouse Contig 1A co	CV014 c	Partial mouse WRN	Mouse chromosome 1	Mouse chromosome 1	y-rel	y rat hepat	13	Mouse Flt3 carcino	Mouse Flt3 gene.	Mouse Bach2 carcin	ach2	Partial mouse WRN	Mouse Cyp3A11 gene	Cyp3A11	7	Mouse Ptprk genomi	Mouse Ptprk carcin	Mouse Ptprk gene.	Mouse Map3k8 carci	Mouse Map3k8 gene.	Mef2c c	CDNA		Mouse BAC279 clone	encoding	Toxicity-related g	eq	Human breast cance	Human adenosine re	enosi	_	Nucleotide sequenc
		- ABK47192	Ŋ	8	ABN85752	S	7	ADB52444	~	$\alpha$	ADB72365				AAD51996	AAD51995	$\sim$	ADC85257	ADA02777	ADB72515	ADA02837	$\sim$	10	10					an.	$\sim$	AAA35003	AAF21125	ABZ96819	
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Example 10; Fig 9; 120pp; English.

fragments which are capable of modulating an immune response observed with airway hyperresponsiveness and/or bronchalveolar manifestations of asthma. Also included are a method for modulating an immune response of an individual comprising modulating a gene comprising a mucleic acid at least functionally equivalent to a nucleic acid identifiable by a signature sequence (5S) given in the specification such as R1-SO-R1-A11, StO1-A12, and R1-SO-R1-B7, a substance (for use as a medicament) capable of modulating a gene comprising a nucleic acid at least functionally equivalent to a nucleic acid identifiable by SS and the use of a proteinaceous substance derived from a nucleic acid at least functionally equivalent to a nucleic acid identifiable by SS and the use of a proteinaceous substance derived from a nucleic acid at least functionally equivalent to a nucleic acid identifiable by SS for the production of an antagonist (for use as a medicament) against the production of an antagonist and substance are useful for the treatment of an immune response observed with airway hyperresponsiveness and/or bronchoalveolar manifestations of asthma. The method is useful for

Human cDNA differe Human reproductive Mouse dectin-2 gen Mouse tyrosinase g Mouse tyrosinase g Mouse tyrosinase g Human KCNQ5 (KCN6G Chemically pretrea Human breast cance Human breast cance Human breast cance Human breast cance Mouse Ptprk genomi Mouse Ptprk genomi
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## ALIGNMENTS

Nucleic acid library comprising genes which are capable of initiation, progression and suppression of an immune response, especially an immune response observed with airway hyper-responsiveness of asthma. airway hyperresponsiveness; bronchoalveolar manifestation; signature sequence; SS; chronic obstructive pulmonary disease; COPD; allergic disease; rhinitis; atropic dermatitis; urticaria; autoimmune disease; multiple sclerosis; inflammatory bowel disease; allograft rejection; infectious disease; OtS1-B7. ds; nucleic acid library; immune response; asthma; DC-SIGN; Mouse Contig 1A containing a fragment of the Ots1-B7 gene. Van Oosterhout AJM; Groot PC, Van Bergenhenegouwen BJ, ABK47192 standard; DNA; 19619 BP 16-AUG-2001; 2001WO-NL000610. 16-AUG-2000; 2000EP-00202867. 05-JUN-2002 (first entry) (UYUT-) RIJKSUNIV UTRECHT WPI; 2002-241888/29. P-PSDB; AAU88024. WO200214366-A2. 21-FEB-2002. ABK47192; Mus sp. RESULT 1  ~

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modulating the above immune response, where the gene encodes a gene product capable of modulating the immune response. The substance is useful for treating an immune response, particularly asthma, chronic obstructive pulmonary disease (copp), allorgic diseases (thinitis, atopic dermatitis, utricaria), autoimmune diseases (e.g. multiple sclerosis), inflammatory bowel disease, allograft rejection and infectious disease. The present sequence is a genomic DNA sequence (Contig 1A) comprising part of the gene sequence of DC-SIGN (a signature sequence also known as Ots1-B7)
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                                                                                                                                                                 Gaps
                                                                                                                                          Length 19619;
                                                                                                                    Sequence 19619 BP; 6308 A; 4234 C; 4316 G; 4761 T; 0 U; 0 Other;
                                                                                                                                                                545; Indels 119;
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Pred. No. 1.7;
0; Mismatches
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Best Local Similarity 63.2%;
Matches 1138; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411
                                                                Oxytoxin expressed sequence tag; 5'-OT EST; obesity; fertility; male; transgenic animal; human late onset obesity; late onset visceral obesity; and infertility; wasting; anorexis; cachexia; malabsorptive state; catabolic state; inflammatory condition; Crohn's disease; AIDS wasting; burn; cancer; bone disease; vasopressin; oxytocin; ss.
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                                        containing rat vasopressin and oxytocin locus.
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Matches 1173; Conserv
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This sequence represents a fragment of the genomic sequence containing the coding region for the mouse WRN gene (AAX83004). The corresponding human gene (AAX83001) encodes a protein related to Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype, as well as related diseases
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Mouse, Can 1, antiinfertility, gynaecological, infertility, premature ovarian failure; menopause, Sertoli Cell only syndrome; BAC clone RP23-270L8; GenBank reference AC083815; chromosome 11; c

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(BISH/) (AGOU/) (ZHUQ/)

02-NOV-2001; 2001US-00003806 03-NOV-2000; 2000US-0245872P

US2002119929-A1 Mus musculus

29-AUG-2002.

NO 10

SEQ

BAC clone RP23-270L8

chromosome 11

Mouse

(first entry)

14-OCT-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (I) encoding a Can 1 polypeptide used
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The invention relates to a nucleic acid molecule (I) encoding a Can 1 polypeptide. The Can 1 nucleic acid molecule is used to diagnose or treat infertility or premature ovarian failure or Sertoli Cell only syndrome in a mammal. The present sequence is that of a mouse Can 1 encoding chromosome 11 BAC clone RP23-77018 of the invention. Note: The present sequence is not given in the printed specification but was obtained through the GenBank reference AC083815 in treating Sequence 173810 BP; 50474 A; 33519 C; 33994 G; 55823 T; 0 U; 0 Other; Length 173810;

######################################	CONSELVATIVE 0, Mismatches 547; Indels 121; Gaps 18; CHATTCHICATICC 351; CHATTCHICATICC 151; CHATTCHICATICC 151; CHATTCHICATICC 151; CHATTCHICATICC CATACATA AND AND AND AND AND AND AND AND AND AN		Qy 1359 GTCTTTCTTCTCCAACTATTGTGACAGAAAA	1419	1479	1539 160278	Qy 1599 TGCACTGTGGGGAGTTTCTTTCCGGTCCAP 	1659	1719	1765	1825 160578	1885		Qy 2004 CTITCAGGICCTGAAATGITTACTCAITIT 	Oy 2061 TITCTITAATGGATT 2075 	RESULT 6 ADB57960/c ID ADB57960 standard; DNA; 8048 BP.	AX ADB57960; XX X DT 04-DEC-2003 (first entry)	XX DE Toxicity-related gene, SEQ ID 2986. XX	KW Toxic; toxin; gene expression profile; KW drug screening; toxicity assay; ds. XX	OS Unidentified, XX PN WO2003064624-A2.	XX XX 07-AUG-2003.	
	da t t t t t t t t t t t t t t t t t t t	Conservative 0: Mismatches 547; Indels 121; Gaps	MACCINES 1147; CORBEIVACIVE U; MISMACCINES 547; INCELS 121; GAPS 207  292 TCTATITCTTGAITTCTATCTTGGCTCATITITAACTCAGTAGTGAGTTGTTTGGTTTTC 351  150108 PRINCHTPARTTCTTTCTTCACCAGTATTCATCAGAAAAGTGTTGTTCAGTTTTCACCAGTTTGTTCATTCA	352 ATAAGTITGIAAGTITTCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTAAATTTAAGCTGT 411	412 GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTGGAGTTTGCTT 471	472 TGTTTTGAATATGTATTCAATTTTGGAGAGTTTCATAGGGTGCTGACAGAAGGTAC	530 A-GICTITGIGITITIGGIGAAAIAGICIGAAAIALICICI-AGGICCACITGGITTAIGA 1.00246 Anchemptagementalaanaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	159345 AICHTHIGHINGCAIRAGAILCHGAGALCAGLCAGAICAGAICAGAICAGCA 588 CATCAGTAGCTCCAGCATTTCTCTTTTTTTTTTTTAGATGACCTAACTGTTGGA 	648 GAGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGTGAGGT-CAATATGTGTATTTTAGC	707 TGTAGCTGTGCTTGTTTATGAACTTGGGTGACATTGTGTTTTGGTGCATAGACATTAAGA 159524 TTTACTAAAGATGTTAAATGAATGTAGCTGCCTTGCATTTGGAGCGTAGATATCAGA	767 ATTGCAAIGTCCTCTTGGTGGATTTT-CCTTTGATGCCTATGTAGTATTCTTCCCAATCT	826 CAICTGCTTAGTTTTGGGTTTAAGTCTA-TTAGTCAGATATTAAAATGACTGTATCGGGT	885 TGCTTCTTAGGGCCATTTGCTTAGAATA-TCTTTTCCATCCTTTTACTCTAAGGTGATGT 	944 CTATCCATGGTAGGTTGTCTTTTTTGGATGCAGCAGTAGGATGGATCTTGTTTTCAT	1001 ATCATTCTGTTACCCAGTATCTTTTCTACAGAAATTAAGATCATTGATGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	1061 TGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTGTGT 	1121 Gregerger	1181 GIGICIGIGICITGIGIGICIGIGITCICCCCCTCTTTIGAITITIGGCCTGGAATTAT	159971TIGAGGGAT 15997 1291 TTATTATTCATATTTGAAGGAT 15000	159980 TACTITCTTGTTTGTTCTAGGGCGTGATTTCCGTCCTTGTATTGCTTCTTTTCTGTTATA 16003	1301 CTTCTTTAGGTCTGCATTTGAAATAGATAATTCTTTAAATCTTAATTTTTATCTTAGAAT 160040 ATCCTTTGAATGGTTGGTTGAAAATTGTGTGATTTTGGATTTTGGAAA	

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hepatotoxicity; liver;

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LOGIC INC (GENE-) GENE

15-MAR-2002; 30-DEC-2002;

Castle A, щ Higgs Johnson K, Porter M, WPI; 2003-689530/65. 'n Mendrick

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Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.

Claim 1; SEQ ID NO 2986; 1156pp; English.

The present invention relates to a method for predicting a toxic effect
of a compound. The method comprises preparing a gene expression profile
of a tissue or cell sample exposed to the compound, and comparing the
gene expression profile to a database computal, and comparing the
of differential expression of the gene indicates at least one toxic effect.
The method is useful for predicting at least one toxic effect.
The method is useful for predicting at least one toxic effect.
Compound, predicting hepatotoxicity or the progression of a toxic effect.
Compound, identifying an agent that modulates the onset or
progression of a toxic response, predicting the cellular pathways that a
compound modulates in a cell, and identifying an agent that modulates at
compound anothales in a cell, and identifying an agent that modulates at
compound activity of a protein. The method and compositions of the
present invention using a database of genes having liver toxin-induced
differential expression, are useful in identifying toxicity markers in
compounded at for this patent did not form part of the printed
sequence data for this patent did not form part of the printed
cat ftp.wipo.int/pub/published\_pct\_sequences.

The compound modulates in electronic format directly from Wipo 

Sequence 8048 BP; 3068 A; 1764 C; 1532 G; 1682 T; 0 U; 2 Other;

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Length 8048;

17; 3270 3216 GGTGGTCCGATAGCACGCATGGGATTATTTCTATCTTTCTGTACCTGTTGAGGCCCGTTT 3156 3036 2917 3096 cricicinargererecacaicacidini-aariricidirirecardarcigicaridar 2977 587 351 411 471 647 206 TGTTTTGAAATATGTATTCAATTTTGGAG--AGTTTCATAGGGTGCTGACAAGAAGGTAC 529 TGTAGCTGTGCTTGTTTTATGAACTTGGGTGACATTGTGTTTTGGTGCATAGACATTAAGA 766 TCTATTTCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGGAGTTGTTTGGTTTCC TITCITITCITIATITCITCCTIGACCAGGITATCATIGAGIAGAGCATIGITCAATITCC 3269 AGGTATATGTGGGCATTC----Trcccriaricitaricaagaccagririaggccgr TTTGACCAATTATATGGTCAATTTTGGAGAAGTGCCATGAGGAGGTGAGAAGGTAT AGTCTTTGTGTTTTGGTGAAATAGTCTGTAAA--TATCTCTAGGTCCACTTGGTTTATGA GAGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGAGGT-CAATATGTGATTTTAGC GAGAGTGGTGTTGAAATCTCCCACTATTATTGTGTGAGGTGCAATGTGTGTTTGAGC Gaps ATAAGITTIGTAAGITTTCTGTTGTTTGTTGTTGTTGTTATCTAGATTTAAGCTGT GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTTATCTGTCGAGACTTGCTT Indels 136; Query Match 25.4%; Score 578.2; DB 1; Best Local Similarity 62.0%; Pred. No. 2.8; Matches 1160; Conservative 0; Mismatches 574; 292 3329 412 3215 472 3155 530 3095 3035 648 707 588

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2797 2737 2677 1000 2617 1060 2565 1120 1300 1418 2279 1478 2505 2219 1538 2161 1598 2101 1658 2041 1764 1824 1981 1921 825 884 943 TTTAGTAAGGTTTCTTTTACGTATGTAGGTGCCCTTGTATTTGGGGCATAGATATTTAGG TRATTATTCATATTTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGC TIGGITITIGCATAGIGICICIGGCITCCIGGAIGTITIAIGCCIGGAITAITIAGACI 2796 TTTTTGATGACTTTTAGTTGGAAATTGATTTTATTTGATATTAGAATGGCTACTCCAGCT recrircricaecearriscriseaaarrierrirceaecerricaerereaerer CTATCCATG---GTAGGTTGTCTTTTTTGGATGCAGCAGTAGGATGGATCTTGTTTTCAT CTGTCTTTGTCTCTGAGGTGTTTTCCTGTAGGCAGCAGAATGCAGGGTCCTCGTTGTGT TGAGAGATATTAAGGAATAGTGATTATTGCTTCCCGTTATATTCATATTTGGATGTGAGG 1181 GIGTCTGTGTGTGTGTGTGTGTTTCTCTCCCCTCTTTTGATTTTTGGCCTGGAATTAT GTCTTGGTTTCTCCATCAATGTTAATTGAGAGTTTTGCTGGATACAGTAACCTGGGCTGG TGTGACGGGAGGTGTTTCTTTTTTTCTGGTCCAATCTATTTGGAGTTCTGTAGGCTTCTTGTG 767 ATTGCAATGTCCTCTTGGTGGA-TTTTCCTTTGATGCCTATGTAGTATTCTTCCCAATCT CATCTGCTTAGTTTTAGGTCTA-TTAGTCAGATATTAAAATGACTGTATCGGCT TGCTTCTTAGGGCCATTTGCTTAG-AATATCTTTTCCATCCTTTTACTCTAAGGTGATGT ATCCATTCTGTTACCCAGTATCTTTTTTTTAAGATTAAGATCATTGAGTCATTGATGT Arccagringinaarcrangacrininarneeegagricae-----eccannearen TGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTGTGT 2458 TAGTITCTTGCTTCTAGGGTATAGCTTGCCTCCTTATGTTGGGCTTTACCATTTATT CTTCTT--TAGGTCTGCATTTGAAGATAGATATTCTTTACATCTGATTTTATCTTAGAAT 2398 ATCCTTTGTAGTGCTGGATTTGTGGAAAGATATTGTGTAAATTTGGTTTTTGTCATGGAAT GTCTTTCTTTCTCCCAACTATTGTGACAGAAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGA CATCTGTAGTCTCTTGGAGTCTGTAGCACATCTGTGCAGGGCCTTCTTACATTTTGAGTT CATITIGIGITICICITAGGGICIGIATAAACAICCAGGAICCTICIGGCCTICAAGIT TCTATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATGTTAATTGGTCTTT 2218 1CT-GGCGAGAAGTCTGGTGTGATTCTGATAGGTCTCCCTTTATATGTTACTT-GACCTT TTTCCCTTGCATCTTTAATATTCTTTCTTTGTTCTATACTTTTAGTGATTTGATTATTA tricccriacigrititaatatriciriciritaririigigegritigigiririgacaaria TGCACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGGTGTTTTGTATGCTTCTTGTA 2040 IGTCTATGGGTATCTCTTTTTTAGGTTAGGGAAGNTTTCTTCTATGGTTTTGTAGGA TATTTTCCCTGCTTTTGACCTG--------CCTTCTTCCCCCTTCCTATTCCT 2504 Trandrurdrand-------2856 2916 826 2736 2676 1001 2616 1061 2564 1121 1241 1301 1359 2278 1479 2160 2100 885 944 2491 2338 1419 1539 1599 1719 1765 ò 엄 ò 요 셤 ò à g 8 ద 8 요 g 8 8 S B g 8 6 ò 셤 8 8 8 g 8 6 à 8 8 d ò a ò

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CTTCTCTTAIGCTGTCGACATCACTGTTT-AATTTCTGTTTCCATGAICTGTCCATTGAT 2977
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                                                                                                                                                                                     The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                    Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3215 GGTGGTCCGATAGCACGCATGGGATTATTTCTATCTTTCTGTACCTGTTGAGGCCCGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITCITICITIATITCITCCTIGACCAGGITATCATIGAGIAGAGCATIGITCAATITCC
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                                                                                                                                                 Claim 44; SEQ ID NO 2986; 874pp; English
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11-APR-2002; 2002US-0373601P.
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11-APR-2002; 2002US-0373601P.
11-APR-2002; 2002US-0373602P.
11-APR-2002; 2002US-0373652P.
11-APR-2002; 2002US-0378653P.
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2003US-0442900P.
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8759 ICIAGITCCAITTTAGAICCIGGAIGGITTIGITCAITICCTTCACTGITTGAITITG 8700
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9297 ITTCATAGTCTCTGGTGAGAAGTCTAGTCCTATATCTGATAGGTCTGCCTTTATATGTTA 9238
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9060 1763 1814

recombinant nucleic acid encoding carcinoma associated protein, ul for preparing compositions for treating carcinomas.

Claim 1; SEQ ID NO 1145; 245pp; English.

The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host calls comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a blochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism or a random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host of pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host correctionma (especially breast cancer, prostate cancer, lymphoma or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene or by determination of CA gene or by general sequence and in screening and evaluating drug candidates. The consequence of the invention. Note: The complete sequence dit here invention. Note: The complete sequence dit comma directly from MIPO at the printed specification, but was obtained to half-which inthication of the major of the major of the printed specification, but was obtained to be a consequence of the printed specification. ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 47115 BP; 11483 A; 10181 C; 10540 G; 13012 T; 0 U; 1899 Other;

30423 GTGTGTATGTGTGCTTTTCTGTTTT---TTGTTGGTATTTAAGACCAGCCTTAGTCTGT 30479 30480 GGTGATCTGATAGGGTATATGGGATTATTTCAGTCTTCTTGTATCTGTTGAGGCCTGTTT 30539 30659 30660 TTTCTGTTÄGTTTCÄCTGTGTCTCGATTTAG-TTTCTGTTTCCÄTGÄLCTGTCCATTÄGCT 30718 30719 dadagridigierindaadronococitarranidrerocochedaardridicorringado 30778 30838 30899 TTTTTGATAACTTTTGGTTGAAAGTTGATTTTATTCGATATTAGAATGGATACTCCAGGT 30958 30898 20; 411 471 587 825 904 351 TGTTTTGAAATATGTATTCAATTTTGGAGA--GTTTCATAGGGTGCTGACAAGAAGGTAC 529 994 TCTATTTCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGTTTGGTTTCC 352 ATAAGITIGIAAGITITCIGITGITICTGITGITGITGITGITATCIAGAITIAAGCIGI GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGAGACTTGCTT 530 AGTCTTTGTGTTTTGG-TGAAATAGTCTGTAAATATCT-CTAGGTCCACTTGGTTTATGA 30600 ATTCTTTTGCTTTAGGATGAATGTTCTATAATACCTGTTAGATCCATTTGGTTCATAA TTTAGTAAAGTCTCTTTTATGACTGTGGATGCCCTTGCATTTGGAGCATAGATGTTCAGA ATTGCAATGTCCTCTTGGTGGA-TTTTCCTTTGATGCCTATGTAGTATTCTTCCCAATCT CATCTGCTTAGTTTTGGGTTTAAGTCTA-TTAGTCAGATATTAAAATGACTGTATCGGCT Score 555.699; DB 1; Length 47115; Pred. No. 1.6; 0; Mismatches 563; Indels 131; Gaps TGTAGCTGTGTTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGA Query Match
Best Local Similarity 62.5%;
Matches 1159; Conservative 767 292 472 648 707 826 30779 ò g 임 ò g g g a d 8 6 음 ò ò ò

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οp	31079	ccastcretrastcratstritritainssesaatisasrccatisar
ò	1061	TGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTGTGT 1120
qq	31131	ATAGATATTAAGGAAAAGTGATTACTTACTTCTGTTATTTTTGTT
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È	1181	SIGICIGIGICITGIGICIGIGITCICCCCCCTTITIGAITITIGGCCTGGAAITAT 1240
Db	31225 -	TGAAAGATT 31233
ζ	1241 T	TTATTATTCATATTTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGC 1300
g G	31234 P	
ò	1301	CITCITIAGGICTGCATITGAAGATAGATATTCTTTACATCTGATTTTATCTTAGAATGT 1360
දි	31294	rigtaggggtithatggaaagatactgtgtaaattiggtittgtcatggaar
ò	1361	CTITCTITCICCAACIAITGIGACAGAAAGIITITCIAAGIGCAGIAGICIGGCCIGACA 1420
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8	1421 T	TCTGTAGTCTCTTGGAGTCTGTGTAGCACTTGTGCAGGGCCTTCTTACATTTTGAGTTTC 1480
ОÞ	31414 I	JICTCTTAGGGTCTGTATGACATCTGCCCAGGATCTTCTGGCTTTCATAGTCT
ò	1481 T	TATIGGAAAAGICAGGIGIAATICTAATACATCTGCCTTTATATGTTAATIGGTCTTTTT 1540
d d	474	-GAGAAGTCTGGTGTAATTCTGATAGGTCTGTCTTTATATGTTACTT-GACCTTT
δ,	1541 T	CCCTTGCATCTTTAATATTCTTTCTTTGT
Dp	532	CCCTTACTGCTTTTAATATTTTTTTTTTTTTTTTTTTTT
8	601	TTTTGTATGCT
οg	592	TTGGAGTTCTGTAGG
λ	1661 T	TTGATAGGCATCTTTCTCAAGGTTAGGAAATTTTTCTTTTTTGGTTTTTCTTGAAAATA 1720
Db	31652 T	
ζ	1721 T	TITICCTGCTTTTGACCTGCCTTCTTCCCCTTCC
ор	31712 T	-E
δŏ	1767 G	GITITIGCATAGIGICICCIGGCITCCIGGATGITITATGCCIGGATATITAGACITA 1826
qq	31772 G	cricicatroraricredarriccredarerrineserrassascritriccri
δλ	1827 A	A-CAITICITIGACCAAGGIATCCAITICITCIATCITGICITCACTGCCTGAGAITCT 1885
qq	31832 T	GITITICITIAACIGCAGIGCCAAHGITITICIAIGGIATITICIAIACCIAAGAIT
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QQ	31891 -	TCT

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30660 TTTCTGTTAGTTTCACTGTGTCTCGCATTTAG-TTTCTGTTTCCATGATCTGTCCATTGCT 30718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity, and may have a use in gene therapy, or in a vaccine. The recombinant mucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47115 BP; 11483 A; 10181 C; 10540 G; 13012 T; 0 U; 1899 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 555.699; DB 1; Length 47115;
Pred. No. 1.6;
0; Mismatches 563; Indels 131; G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        neoplasm; adenocarcinoma; sarcoma; gene
TAATTTTTCATTTCCAGATTTCCTTCAGTTT
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2001US-00004113.
2001US-00052482.
2001US-00997722.
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llarity 62.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse; ds; cytostatic;
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20-DEC-2001;
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Mouse Bach2 carcinoma associated gene, SEQ ID NO:1019. BP ADA02501 standard; DNA; 96597 (first entry) 06-NOV-2003 ADA02501; gene; ds 

Mouse, murine, carcinoma associated, oncogene, carcinoma, cancer; breast, prostate, lymphoma, leukaemia, cytostatic, gene therapy, drug screening;

26-DEC-2002; 2002WO-US041414 26-DEC-2001; 2001US-00035832 (SAGR-) SAGRES DISCOVERY WO2003057146-A2. 17-JUL-2003 Morris DW Mus sp

WPI; 2003-587068/55.

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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to crecombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a bhochip comprising CA nucleic acid or CA nucleic acid or carcinoma bhochip comprising CA nucleic acid or coopenic retroviruses, which insert into the genome of the host organism or random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host correspond (especially breast cancer, prostate cancer, lymphoma or carcinoma (especially breast cancer, prostate cancer, lymphoma or carcinoma (especially breast cancer, prostate cancer, lymphoma or the sequence of the acids, proteins and antibodies are also useful as therespeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this capent did not forma part of the printed specification, but was obtained control format directly from WIPO at the printed specification, but was obtained control format directly from WIPO at the printed specification, but was obtained control format directly from WIPO at the printed specification. 51244 51304 51364 51598 51424 51483 21; 344 404 464 522 697 757 Seguence 96597 BP; 25792 A; 20376 C; 20447 G; 28650 T; 0 U; 1332 Other; 51129 AAAGTTTTTAATTTCTTTATTTCTTCATTGAGCAAGTTATCATTGAGTAGAGCGTTGTTC 51365 AAGGIACATICATITIGCITITAGGAIGAATGITICIATAAATAATCIGCIAAACCCITTA 51425 GGTTCTTAACTTCTATTAGTTTTCACTGTCTCTCTTTTAG-TTTCTGTTTTCATAATCTG sıs44 deririgader----raadrirererrahdecangidrerreeridearirideadead 285 AAACACTICIAITICIIGAITICIAICIIAGCICATITITIAACICAGIAGIGAGIIGITI 51245 Acreenidationicadiadoarecardoaritatiricaarericingiareridade CTTGCTTTGTTTTTGAATATGTATTCAATTTTGGAGA--GTTTCATAGGGTGCTGACAAG 51305 cerentrigiaaccaaraarareereacririseacaaceraceareacarecare AAGGTACAGTCTTTGTGTTTT--GGTGAAATAGTCTGTAAATA--TCTCTAGGTCCACTT 698 GAITTTAGCTGTAGCTGTGTTTTTATGAACTTGGGTGACATTGTGTTTTGGTGCATAG 51189 AGCTICCATGIGIATGIGIGCTITCCCTIGIT----TICTIGGIATIGAAGACCGGCTTI AAGCTGTGGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGAGA 758 ACATTAAGAATTGCAATGTCCTCTTCGTGGA-TTTTCCTTTGATGCCTATGTAGTATTCT 345 GGTTTCCATAAGTTTGTAAGTTTTCTGTTGTTTCTGTTGTTGTTGTTGTTATTAGATTT 556; Indels 147; Gaps protein, Length 96597; New recombinant nucleic acid encoding carcinoma associated useful for preparing compositions for treating carcinomas. DB 1; Query Match
23.1%; Score 525.898;
Best Local Similarity 61.9%; Pred. No. 1.6;
Matches 1143; Conservative 0; Mismatches Claim 1; SEQ ID NO 1019; 245pp; English, 579 405 465 523 셤 셤 g 임 셤  $\delta$ g 셤 8 g ò ò ò ò ર્જ 8 ₹

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23-CCT-2001, 2001US-00004113.
08-NOV-2001, 2001US-0095482.
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20-DEC-2001, 2001US-0034650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     940
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                                                                                                                                                                    Isolated nucleic acid molecule encoding the WRN gene product - useful for detection and treatment of Werner's syndrome, and related diseases.
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                             Schellenberg
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Pred. No. 2.2;
0; Mismatches
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                          Mulligan
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Best Local Similarity
Matches 1118; Conserv
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5104. .6218
/*tag= a
//ore= "Non repeat region"
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'note= "Non repeat region"
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                                              AAD51996 standard; DNA; 9330 BP.
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Best Local Similarity
Matches 1022; Conserv
                                                                                                                                                                                                                     Mouse Cyp3A11 gene
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Identifying analytes that modulate expression of a reporter sequence mediated by human or mouse transcription control elements in transgenic rodent, comprises administering the analyte and monitoring expression of coding sequence.
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Transcription control element; transgenic; transgenic animal; toxicity; drug metabolism; mouse; Cyp3A11; ds.
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3370 3430 1483 1543 1005 3149 1125 3209 1185 3237 1245 3311 1365 1423 2679 2737 2797 2857 2917 2977 3037 1065 3251 3097 652 711 171 830 889 948 CTIGCATCTTTTAATATTCTTTCTTTGTTCTATACTTTTAGTGATTTGATTATTATGCAC 2620 TTTGTTTTAGGATAAAAGTTTCTGTAGATATCTGTCAAATCCATTTGTTTCATCACTTCT 2680 GITAGITICA -- CIGIGICCIGITIAGITICIGITITCAIGAICIGICCACIGAIGAAG TGGGGTATTGAAGTAGCCCACTATCTGTGTGTGAGGT-CAATATGTGATTTTAGCTGTAG CITAGGGCCATITGCTTAGAATAIC-TITITCCATCCTTTTACTCTAAGGTGATGTCTAIC 3038 TITITCCCTGAGATGGGTTTCCTGTAAGCAGCAGAATGTTGGGTCCTGTTTGTGTAGCCA 3252 rcinecriritciadeecerdararcrerccirerarirrririrciorararccirr TTAGGTCTGCATTTGAAGATAGATATTCTTTACATCTGATTTTATCTTAGAATGTCTTTC 1424 GIAGICITITGAGICIGIAGCACAICIGIGCAGGGCCIICTIACAIIITIGAGITICIAI TGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATGTTAATTGGTCTTTTTTCC TITGIGITITIGGIGAAATAGICTGTAAATATCTCT-AGGTCCACTIGGITTATGACATCA 2858 GAGTICCICITGGAGGATITITACCITIGATGAGTATGAAGTGTCCCTCCTTGTCTTTTT 949 CAT---GGTAGGTIGTCTTTTTGGATGCAGCAGTAGGATGGATCTTGTTTTCATATCCA -----TCCATTGATATTAAGA 3150 garatraaggaaagraarrgrigcriccrarrarrirrgrigiragagriggcarrcrig .-----ritäksakitacit 1246 ATTCATATTTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGCCTTCT 3312 GAAGGGCTGGA-TTCTGGAAAGATAATGTGTGAATTTGGTTTTTGTCATGGAATACTTTGG TITCICCAACTAITGIGACAGAAAGITITTCIAAGIGCAGIAGICIGGCCIGAC--AICI 2738 idereferreaagicreecaciarrarierereagiecaarererererage 712 CIGIGCIIGIIIIAIGAACIIGGGIGACAIIGIGIIIIGGGIGCAIAGACAIIAAGAATIGC 772 AAIGICCICTIGGIGGAITIT-CCITIGAIGCCIAIGIAGIAITCTICCCAAICICI GCTTAGTTTTGGGTTTTAAGTCTA-TTAGTCAGATATTAAAATGACTGTATCGGCTTGCTT 2918 GATAACTTTGGTTTGGAAGTTGATTTTTTTTAGAATTGGTACCCCAGCTTGTTT 1006 ITCTGTTACCCAGTATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGTTGAGA 3098 Grchdrhagrcrandrichtrinarragadahradd-3210 TICITITGGCTGTCTTCTTTTTGGCTTG-1484 1544 890 1306 1366 3371 534 593 653 831 3238

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins. AAB97731 to AAB9734 represent T2R proteins, and AAB97825 to AAB9730 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship to taste centres in the brain. The taste modulators are useful for pharmacological and genetic modulation of taste signalling pathways. Modulatory compounds comprising T2R proteins can therefore be used in decrease the bitter taste of food or drugs
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588 CATCAGITAGCICCAGCATITC  14753 TITCTGIAAGITICACTGIGIC  648 GAGAATGGGGTATTGAGTAGC  14694 GAGAGTGGGGTATTGAGAATC  707 TGTAGCTGTGTTGTAGAATC  707 TGTAGCTGTCTTTTTATTA  14534 TTTAATATGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1057 AIGTTGAGAATTATCAATGAGGAGTGTTTGTGGATTCT 1117 GTGTGTGTGTGTGTGTGTGTGTGTGTTGTTGTTGCTTCC 1117 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT

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binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using on cogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host organism car random. Many of these do not carry transduced host organism component trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence of the invention. Note: The complete sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from MIPPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
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               mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 453.098; DB 1; Length 96595; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mbinant nucleic acid, useful for treating neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 343; 2304pp; English
                                                                                                                                                                                                                                                2001US-00798586.
2001US-00004113.
2001US-00052482.
2001US-00997722.
2001US-00034650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant nucleic acid,
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Best Local Similarity
Matches'1007; Conserv
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23-OCT-2001;
08-NOV-2001;
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a cinvention also encompasses expression vectors and host cells comprising a character acid, a polypeptide (especially an antibody) that specifically comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using concogenic retroviruses, which insert into the genome of the host organism or transform. Many of these do not carry transduced host oncogenes or pathogenic retroviruses, which insert into the genome of the host organism or transform. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host pathogenic trans-acting viral genes, meaning that cancer incidence is a carcinoma (especially breast cancer, prostate cancer, lymphoma or length of the propensity to carcinoma by determination of the sequence carcinoma of especially determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therefore of the invention. Note: The complete sequence data for this sequence of the invention. Once: The complete sequence data for this patent did not format directly from MIPO at the pathned and interestly from MIPO at the pathned and antibode and antibode and interestly from MIPO at the pathned and antibode and antibode are also useful as equence of the pathned and antibode sequence of the pathned and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and antibode and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid encoding carcinoma associated useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse Map3k8 carcinoma associated gene, SEQ ID NO:1355.
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16.8%; Score 381.798; DB 1; Length 41637; larity 60.7%; Pred. No. 8.7; Conservative 0; Mismatches 467; Indels 124; G

Similarity

Query Match Best Local Simi Matches 914;

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in the specification. A polynucleotide of the invention has cycustation activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
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                                                                                                               Sequence 41637 BP; 12049 A; 8888 C; 9032 G; 11648 T; 0 U; 20 Other;
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      CTTTCTTCTCCAACTATTGTGACAGAAGT
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the carcinoma-associated (CA) genes, useful for screening for drug
candidates for diagnosing or treating carcinomas.
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Pred. No. 8.7;
0; Mismatches 4
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60.7%;
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Matches 914, Conservative
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The present invention provides the protein and coding sequences of cDNAs isolated from human, wurtine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a cDNA of the invention
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                                                                                                                                                                                                         New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2920 BP; 1051 A; 666 C; 581 G; 622 T; 0 U; 0 Other;
                                                                                                             Murison JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 328.699;
Pred. No. 47;
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                                                                                                             Sleeman M,
                                                                                (GENE-) GENESIS RES & DEV CORP LTD
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62.38;
                                24-MAY-2000; 2000US-0206650P.
25-JUL-2000; 2000US-0221232P.
24-MAY-2001; 2001WO-NZ000099
                                                                                                                                                                                                                                                            immune responses.
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Best Local Similarity 62.3'
Matches 622; Conservative
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developmental defect; inflammatory disease; dermatological; vulnerary;
immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
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                                                   Murine cDNA isolated from skin cells SEQ ID NO: 572.
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ABL35043 standard; cDNA; 2920 BP.
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    products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype, as well as related diseases
                                                                                                                                                                                                                                                                               TGATTTTATCTTAGAATGTCTTTCTTCTCCAACTATTGTGACAGAAAGTTTTTCTAAGT
                                                                                                                                                                           TTGAAGGATTACTTTCTTATTTTTTTTAGGGCGTGGTTTCTATCCTTGTATTGGGTTTTT
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                                                                Other
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                                                                                            Score 323.899; DB 1; Lengt
Pred. No. 23;
0; Mismatches 296; Indels
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Best Local Similarity 64.1%;
Matches 588; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid molecule encoding the WRN gene product - useful for detection and treatment of Werner's syndrome, and related diseases.
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95US-00580539.
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replace(3749,T)
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replace(3875,G)
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replace(3800,G)
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replace(3829,T)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a transgenic non-human animal which may be used for assessing the behaviour and/or metabolism of a drug in another animal and which expresses a foreign polypeptide associated with drug behaviour and/or metabolism. The invention also comprises a nucleic acid construct for use in producing the invention also comprises a nucleic acid construct of and/or metabolism and/or behavior of a drug in an animal of interest, comprising administering a test agent to the transgenic animal of and conducting analytical tests to determine drug metabolism and/or behaviour. The transgenic animal is useful in studying drug metabolism conducting analytical tests to determine drug metabolism and/or behaviour. The transgenic animal is useful in studying drug metabolism conducting the above transgenic animal and the methods are used for producing, breeding and using transgenic animal and the methods are used for the pharmacokinetic or pharmacodynamic assays) and/or toxicological studies. Nucleic acid sequences used within the invention are serum albumin, alpha-acidic glycoprotein, cytochrome P450 (CYP); uridine albumin, alpha-acidic glycoprotein, cytochrome P450 (CYP); uridine albumin, alpha-acidic sequences used within the invention are serum albumin, alpha-acidic glycoprotein, cytochrome P450 (CYP); uridine albumin, alpha-acidic sequences used within the invention are serum albuming metabolism and (MRP's). The present sequence represents a DNA sequence used to create a transgenic animal within the scope of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New transgenic non-human animal expressing a foreign polypeptide associated with drug behavior and/or metabolism, useful for studying the behavior and/or metabolism of a drug in other animals.
                                                                                                                                                                Human; ss; transgenic; drug metabolism; behaviour; gene; mouse; pharmacokinetic assay; toxicology; serum albumin; alpha-accidic glycoprotein; CYP; multidrug resistance protein; MRP; uridine diphosphoglucuronosy; transferase; UGT; cytochrome P450.
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                                                                                                                                     Mouse BAC279 clone containing alpha-1-acid glycoprotein 1 gene.
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Pred. No. 18;
); Mismatches 222; Indels
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                                              ABX77189 standard; DNA; 41400 BP
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                                                                                          CIGGCCIGACAICIGIAGICICIIGGAGICIGIAGCACAICIGIGCAGGGCCIICIIACA
                                                                                                                                      TITICAGITICIATIGGAAAAGTCAGGIGTAATICTAATACATCTGCCTTTATATGTTAA
                                                                                                                                                                                                                                                                                                                           TIGGICTITITICCCTIGCAICITITAAIAIICTITCTITGIICIAIACTITIAGIGAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Single nucleotide polymorphism"
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New genetic variants of human aldehyde dehydrogenase 5 family, member Al, ALDH5Al gene for treating metabolic diseases and for expressing ALDH5Al protein useful in identifying drugs to treat 4-hydroxybutyric aciduria. / ttag=
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nucleotide sequence which is a polymorphic variant of a reference sequence for the alchyde dehydrogenase 5 family, member Al (succinate sequence for the alchyde dehydrogenase 5 family, member Al (succinate sequence for the alchyde dehydrogenase 5 family, member Al (succinate sequence for the alchyde dehydrogenase 5 family, member Al (succinate polypeptide is useful for screening for drugs targeting it by contacting the ALDH5Al polymorphic variant with a candidate agent and assaying for binding activity. The polypeptide and haplotypes are useful for care also useful for studying expression of the ALDH5Al isogenes in vivo, are also useful for studying expression of the ALDH5Al isogenes in vivo, for in vivo screening and testing of drugs against ALDH5Al protein and for in vivo screening and testing of drugs against ALDH5Al protein and for in vivo screening and testing of drugs against ALDH5Al protein and for the ALDH5Al protein and in vivo, and metabolic diseases in a biological system. Antibodies are useful for diagnostic and prognostic formats and the antibodies are useful for diagnostic and prognostic formats and the antibodies are useful for diagnostic and prognostic formats and contion, for immunoflucrescence techniques. The polymocleotide is useful for gene therapy and antisense gene therapy. This sequence is useful for gene therapy and antisense gene therapy. This sequence sequence on which polymorphic sequences encoding isoforms of the ALDH5Al protein are based, described in the method of the invention invention describes an isolated polynucleotide comprising a Fig 1; 151pp; English 

Sequence 46765 BP; 12395 A; 9903 C; 10380 G; 14087 T; 0 U; 0 Other;

19391 AAAICTAGTGTTTTG-TTAACTTTCTGTCTTGATGACCTGTCTAGTGCTGTCAATGG 19450 19451 AGTATTGAAATCCCCCATTATTATTGTGTTGCTGTCTATCTTCTTAGGTCTAATAG 19510 .9571 ATTTTCCTGTTGAACGAGGCCTTTTÄTCAATATATAATGTCCCTCTCTGTCTTTTTTAAC 19630 .9631 rgcrgrrgcrrraAAGrrrgcrrrrgfcraArArAAAAAAAGAArAGcrACrGCrGCrCACTrrrG 19690 rrecaregrirreaaggriccrirregagricarr---rccagcrirarrccacrered 19211 CTGAGAGAGTGCTTGATATATTTCAATTTTCTTAAATTTTATTGAGGCTCATTTTGTGGC 19271 TCTTGATTCCATTTTTGACCTAATGATCATTCAGGAGCAAGTTATTTAATTTCTATGTAT 19154 595 774 357 417 477 AGGGCCATTTGCTTAGAATATC-TTTTCCATCCTTTTACTCTAAGGTGATGTCTATCCAT 951 TCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGTTTGGTTTCCATAAGT CAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGAGACTTGCTTTGTTTT GAAATATGTATTCAATTTTGGAG--AGTTTCATAGGGTGCTGACAAGAAGGTACAGTTT TGTGTTTTGGTGAAATAGTCTGTAAATATCTCTAGGTCCACTTGGTTTATGACATCAGTT cacciairicearaarcreraaararcreciaacicariricriccaeeererarr AGCTCCAGCATTTCTCTGTTTCGTTTGAGATGACCTAACTGTTGGAGAGAATGG GGTATTGAAGTAGCCCACTATCTGTGT-TGAGGTCAATATGTGATTTTAGCTGTAGCTG TGCTTGTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGAATTGCAAT TAATCATTTTAGAAATTTGGGAGCTCCAGTGTTACATGCATATATTTTAGGATTGTGT GICCICITGGIGGATIT - TCCTTTGATGCCTATGTAGTATTCTTCCCAATCTCATCTGCT TIGEAAGITITICEGITGITICETGITGITGITGITATCIAGAITTAAGCIGIGGIGGI Length 46765; Indels DB 1; 828; Score 288.196; Pred. No. 19; ); Mismatches 8 . 0 12.6%; 51.7%; Best Local Similarity 51.7 Matches 1021, Conservative 536 19332 358 478 893 418 19212 296 715 775 298 19155 19392 19095 19511 g qq 임 Db ઠે g à g ò Dp  $\delta$ 쉽 δ 셤 ઠે g ò ò ò 8 à

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of a compound. The method comprises preparing a gene expression profile
of a tissue or cell sample exposed to the compound, and comparing the
gene expression profile to a database compound, and comparing the
differential expression of the gene indicates at least one toxic effect.
The method is useful for predicting at least one toxic effect of
compound, predicting hepatocoxicity or the progression of a toxic effect of
a compound, identifying an agent that modulates the onset or
progression of a toxic response, predicting the cellular pathways that a
compound modulates in a cell, and identifying an agent that modulates at
least one activity of a protein. The method and compositions of the
present invention using a database of genes having liver toxin-induced
differential expression, are useful in identifying toxicity markers in
liver tissues or cells for drug screening and toxicity assays. Note: The
sequence data for this patent did not form part of the printed
                                                                                                                                                        20950
GTTTCCTGGAGTTTTGATTGTTTTTATTATGCTATCTATTTCATTGAAAACTTCTCCC 20770
                                                                                                     TTTGTTGCCTCCCTGATTAGCTTAATAATAACTATCTGAATTCTTTTTCAGGTAAATCA :20890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
                                                                                                                                                                                                          AAAGAATCTTGTTTTTTTTATTATCAGAGTTGGCTTTCTGGTTTCTTCTTATTG 21005
                         TICAGGICCIGAAAIGIIITIACICATIITICCICCCAGIAITIACAITITICAIAGGIITICI
                                                  20771 CTTATTICTEGRATCTTTTTTTTTTTTTTGTGACTTCCTTAAATTGGGCTTCGCCTTTC
                                                                                                                                                       GGGATTTCTTCTTGGATTCGATCCATTGTTGGTGAGCTCATGTGATTTTGGGGGGGTGTT
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                                                                           AGCAGGGACATATTGTCCTGGTTGTTATTGTCTGTGTTTTTGCTTTTGGCATATAG 2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Elashoff M;
                                                                                                                                                                                                                                                                                                                                                                          c; toxin, gene expression profile; hepatotoxicity; liver; screening; toxicity assay; ds.
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                                                                                                                                                                                                                                                                                                                                                       Toxicity-related gene, SEQ ID 4234
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; 2002US-0364045P.
; 2002US-0364055P.
; 2002US-0436643P.
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                                                                                                                                  Gaps
                                                                                              Length 1632;
                                                                                                                                  103;
specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                        U; 0 Other;
                                                                                                                                Indels
                                                                                            DB 1;
                                                                                          Score 280.299; DB 1;
Pred. No. 96;
0; Mismatches 332;
                                                        Seguence 1632 BP; 700 A; 341 C; 274 G; 317 T; 0
                                                                                          Query Match
Best Local Similarity 60.7%;
Matches 671; Conservative
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12; 351 827 411 773 471 713 529

Gaps

27;

Indels

259;

67;

587 593 647 534 904 474 766 414 825 354 884 294 943 234

653

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TGAGAATTATCAATGAGCAGTGTTTTGTGGATTCTTGTTATCTTGCACTTGTAAGTGTGT
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                                                                           TCTATTTCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGGTTGTTTGGTTTCC
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Best Local Similarity
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                                                                                                       1357
          TITATTATTCATATTTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAG 1299
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                                                                                                                                                                                                     TGTCTTTCTTCTCCAACTATTGTGA 1383
                                                                                                                                                                                                                                 Toxicity-related gene, SEQ ID 4175.
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2002US-0436643P.
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15-MAR-2002;
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ID NO: 850
                                                                         Human breast cancer associated coding sequence SEQ
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                                                      04-DEC-2002
                                ABT10716;
ABT10716/
ID ABT1-
XX
AC ABT1-
XX
DT 04-D:
XX
DE Huma
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Length 3903;

DB 1;

Score 278.099;

12.2%;

Query Match

Sequence 3903 BP; 1598 A; 812 C; 688 G; 805 T; 0 U; 0 Other;

ftp.wipo.int/pub/published\_pct\_sequences

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                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to methods of diagnosing breast cancer in a patient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867-ABT1112, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as adapostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention. Note: The sequence data for this patent directive formed in wellow at the prediction, but was obtained in
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            Human; breast specific gene; breast cancer; differential expression;
cytostatic; gene therapy; gene; ss.
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12.2%; Score 277.897; DB 1; Length 70665;
Best Local Similarity 52.5%; Pred. No. 17;
Matches 895; Conservative 0; Mismatches 726; Indels 83; G
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 850; 260pp + Sequence Listing; English.
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fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present the nucleotide sequences given in the sequence listing from the present the from the previously named sequences. SEQ ID NO:11 to 185, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1600 (AAA32323 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention on match up with their corresponding SEQ ID NO: sequences given in the sequence
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oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antinilammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic

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AAF21125;

(first entry) 14-MAR-2001

Human low adenosine antisense oligonucleotide related sequence #2692

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiaschmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypotroduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss

Homo sapiens.

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WO200062736-A2

26-OCT-2000

24-MAR-2000; 2000WO-US008020.

99US-0127958P 06-APR-1999;

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure; Page 978-991; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a "Universal" or alternative base. (C) can have respiratory bronchodiator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with cativiting peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, cytokines and chemokine receptors, adenosine receptors, binding proteins, adenosine receptors, bradykinin receptors, central cereptors, canditiers, defensions, gradensine receptors, bradykinin receptors, central certors and peripheral nervous and non-nervous system peptide transmitters, defensions and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders and creeptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders and creeptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders and condition selected from pulmonary vasociated with a disease or condition selected from pulmonary vasociated with a disease or condition, emphysema, chronic obstructive pulmonary disease (OPPD), plimonary transplantation rejection, pulmonary infections, bronchitis, and/or encer AAF18434 to AAF21843 represent human polynucleotide fragment invarion the present invention

Sequence 56583 BP; 16610 A; 11169 C; 11927 G; 16877 T; 0 U; 0 Other;

AAF21125 standard; DNA; 56583 RESULT 31 AAF21125 ID AAF2

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Page 38

13029 AATGGGGGTTTCTAATGGCAATTCTCTGGCATTGTTTGTCTGAAAATGCTGTATC 11088  1308) TTTCCTCAATATGATACTAGTTTCTAAGTGCAATAGTTTGGCTGAATATTTT 11148  1428 TGTCTTGAAGTGCTTGACAGAAGTTGCTGCAATAGTTTTGGCTGATATTTTT 11148  1428 TGTCTTGAAGTGCTTAACAGTTGCTGAATAGTTTTGGCTGATTGTTTGATTGTTTGATTGA	RESULT 32 AB296819 ID XX AC AB296819 XX AC AB296819; XX AC AB296819; XX DT 17-OCT-2003 (first entry) XX WHUMAIN; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory; antiallargaic; antinflammatory; antiallargaic; wantiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; wantisense gene therapy; respiratory; lung; adenosine sensitivity; XX Autisense gene therapy; respiratory disease; ds. XX XX XX XX XX XX XX XX XX XX XX XX XX
	Db 30722 TATGTGTAGGGGAGTCTCCTGAAGGCAGATAGTTGGTTGG

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the instraction codon, coding regalon, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dystunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an preventing sensitivity to adenosine, reducing levels of ubiquinone or ceceptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, for reacting bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed or specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                            Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 56583 BP; 16610 A; 11169 C; 11927 G; 16877 T; 0 U; 0 Other;
                                                                                                                                                                                 Aguilar D;
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Tang L, Shahabuddin S;
                                         23-APR-2002; 2002WO-US013135.
                                                                                          24-APR-2001; 2001US-0286137P.
                                                                                                                                   (EPIG-) EPIGENESIS PHARM INC.
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30186 0307 GCAGTIGTIGGALGAAATGTICTGIAATATCIGTIAAGICCAATTGIICTICCAACGTATA 30366 30187 CTGAGAGAGTGTTTGATATATTTCAATTTTCTTAATGTATTGAAGCTCATTTTATGGC 30246 30247 CTATCATATAGTCTATCTTGGAGAAGTTCCATGTATTGTTGAATAGAATGTTTTATTCT 30306 30367 TITAAATCCATTGTTTCTTTG-TTGACTTTCTGCCTTGATGAACTGTCTATGGCTGTCAG 30425 17; 298 TCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGTTTGGTTTCCATAAGT 357 CAGATAGGACATAGAGTATTTCAATTGTCTTTTATCTGTCGAGGACTTGCTTTT 477 593 GTTAGCTCCAGCATTTCTCTGTTTCGTTTTTTTGTTGAGATGACCTAACTGTTGGAGAAA 652 TGGGGTATTGAAGTAGCCCACTATCTGTGTG-TGAGGTCAATATGTGATTTTAGCTGTAG 711 30070 rcircariricaririraacccaargcricarrcregaccaggriariraacriccargrar 30130 TICATGGTTTTGAAGGTTCCCTTTGAAGTTGAT---TCCAGTTTTATTCACTGTGGT 358 TIGTAAGTTITCTGTTGTTGTTGTTGTTGTTATCTAGATTTAAGCTGTGGTGGT --TGTGTTTTGGTGAAATAGTCTGTAAATATCT-CTAGGTCCACTTGGTTTATGACATCA 478 GAAATAIGIATICAATITITGGAG--AGTITICATAGGGIGCIGACAAGAAGGIACAGICTT Gaps Score 269.097; DB 1; Length 56583; Pred. No. 20; 0; Mismatches 739; Indels 99; G 11.8%; (52.7%; Matches 932; Conservative Local Similarity 418 653 Query Match 536

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qq	30486	radraacidririarraarrirideadrirccadidriraddidecrarardriraddirid 30545
ζζ	772	AAIGICCICTIGGIGGAITITICCITIGAIGCCIATGIAGIAITCTICCCAAICIG 831
QQ	30546	GATATTTTCCTGTTGGAAAGGCCTTTTACCATTATATACTGTCCCTCTTTGTA 30605
ò	832	CITACITITICGGITIAAGICIATIAGICAGAIAITAAAAIGACIGIAICGGCITGCITCI 891
qq	30606	Actectatidericaakiritingicraagaatagetaccendereiriri 30661
ò	892	TAGGGCCATITGCTTAGAATAIC-TITICCATCCTTTACTCTAAGGIGAIGICTAICCA 950
DP DP	30662	GGTGTCCATTTGCATGAAATGCCTTTTTTCCACCCCTTTATTTTAAGTTTATGTGAGTCCT 30721
ò	951	T6GIAGGIIGICIIITIIGGAGGAGGAGGAIGGAIGGAIGITIICAIAICCAII 1007
90	30722	ranginadendagiciccidaagddagdagagingdinggigagincinaticani 30781
ò	1008	CIGITACCCAGIAICITITICIAGAGAAAITAAGAICAITGAGICAITGAIGITGAGAAI 1067
QQ Q	30782	CIGCAGTICTGTAICTTTTAAGCGGAGCATTTAGACCATTTATATTCAATGT 30833
ζ	1068	TAICAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTGTGTGT
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ò	1128	Tergrenergrenergrenergrenergrenergrenergrenergrenerg 1187
qq	30875	TIGTIGCTTGTGCTTTGGTTTTTGTTTTTGCTTTTT 30914
λo	1188	TGTCTTGTGTGTGTTCTCTCCCCTCTTTTGATTTTTGGCCTGGAATTATTATTAT 1247
qq	30915	309
λo	1248	TCATATITITICTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGCCTTCTT 1307
Dp	30975	TATGITICCAGGATITGITICAAGATITAGAGAICCTITITAGCAGITCTIGT 31028
č	1308	AGGICTGCATITGAAGATAGATATTCTTTACATCTGATTTTATCTTAGAATGTCTTTCTT
- - - -	31029	AATGGTGGTTTCCTAATGGCAAATTCTCTCAGCATTGTTTGT
ò	1368	TCTCCAACTATTGTGACAGAAAGTTTTTGTAAGTGCAGTAGTCTGGCGCTGACATCTGTAG 1427
QQ	31089	iniccincanalidanacinadinicichganacaaanicinggciganaaniahri 31148
ζ	1428	TCTCTTGGAGTCTGTAGCACATCTGTGCAGGGCCTTCTTACATTTTGAGTTTTGAA 1487
a	31149	Tertragagagagagagagaragaragagacagagacartaragagartaraga 31208
ð	1488	AAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATGTTAATTGGTCTTTTTTCCCTTG 1547
QQ.	31209	AAA-TCTGCTGCTAATCTGATAGGCTTTCCTTTATAGGTAACCTGGT-GCTTCTGTCTCA 31266
λ	1548	CAICTITIAAATAITCITIGITCIATACTITIAGIGATTIGATT
අු	31267	cadeireitaagainetriteeingsietraagitiggataaceigaigacaaagigeerag 31326
à	1608	GGGAGTITCITTICCGGICCAALCIATITGGIGITTIGIAAGCITCTIGIACCITGARAG 1667
qq	31327	GIGAATATCTTTTGCGATGAATTTCCCAGGTGTTCTTGTGCTTCTTGTATTTGGACAT 31386
à	1668	GCATCTCTTTCTCAAGGTTAGGAAATTTTTCTTTTTTTGGTTTTTTTCCC 1727
qq	31387	CTAGGTCTCTCGCAAGGCCAGGAAAGGTTTCCTCGATTATTCCCTTAAACATGTTTTCCA 31446
à	1728	IGCITITIGACCIGCCITCTTCCCCTTCCTCTATTCCTITIGGTITTTTGCA 1776
qq	31447	GGCT1111AGAA11CTCTTCTCAGGTACACTGATTATTCTTAAGTTTGGTCATTTAA 31506

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New beta-tubulin antigen in the membranous structure of the inner ear, reactive with antibodies of patients with Meniere's disease, for diagnosing Meniere's disease and distinguishing this disease from other autoimmune ear diseases.
                                                                                                                          CTTGTATTCTGTCAGTGAGGCTTGTCTCTGAGGTTCCTGT-----TGGGTTCTTAA
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Best Local Similarity Matches 957; Conserv

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Human, ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoitasis; rheumatoid arthritis; glomerulonephritis; atthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

Homo sapiens

83110

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83109 TTGCATGGTTTTGAAGGTTCCTTTTGGAGTTGATTTCCAGTTGTATTCCACTGTGGTT-T 418 CAGATAGGACATATATTCAATTGTTTTATCTGTCGAGACTTGCTTTGTTTT

358 TTGTAAGTTTTCTGTTGTTTGTTGTTGTTGTTATCTAGATTTAAGCTGTGGTGGT

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene (s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the modulating (M2) GA by contacting GC with an agent that alters the capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression of pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (a) detecting (M3) an inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation of especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation in a tissue, by contacting of gene(s) from Gs in the tissue, millammation in a tissue, of modulating GCA preferably in an agent capable of modulating GCA preferably in an exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, confired to pathogen or sterile inflammation in a tissue, and allergic response in a subject to a pathogen or sterile inflammation confired confired confired confired provided in granulocytes. Note The sequence data for this patent did not format directly from the presents aguence expressed in granulocytes. Note The sequence data for this patent did the confit defection format dir
                                                                                                                                                                                                                                                                                                                                         Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
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Human; reproductive system related antigen; reproductive system disorder;
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11-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
28-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0214886P.
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Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32167 BP; 10519 A; 6697 C; 6488 G; 8463 T; 0 U; 0 Other;
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13;

Gaps

Score 256.797; DB 1; Length 32167; Pred. No. 30; 0; Mismatches 772; Indels 82; G

Query Match
Best Local Similarity 51.1%;
Matches 891; Conservative

Db 1418 ACATOGRACITYTTTTCATAMINATORATIOCTRACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	DT 09-NOV-1998 (first entry) XX DE Mouse dectin-2 gene. XX XX XX XX XX XX XX XX XX XX XX XX XX
290 CITCEATTTCTCATTTCTTGATTTTTAACTCATTCTAGGGCGCGTTATTTAATT 17882 350 CATTACTCTCTATTTTTAACCCAALGCTATTTCTAGGGCGCGGTTATTTAATT 17882 350 CATTACTCTCTCTAGATTTCTGTTTTTTAACCCAALGCTATTACTCTAGATTTAATTTCTAGATTTAATTTTAACCTAGGGCGCGGTTAATTCCAGTTTTAATTTCTAGATTTCTTAACTTTAACCTAGGTTCTAACTTCTTAACTTTTTAACCTAGGTTCTAACTTCTTAACTTTCTAACTTTTAACAGTTCTTTAACAGTTTCTTAACTTCTTAACTTCTTAACTTCTTAACTTCTTAACTTCTT	Db 17165 GTJAGTATTGAAATGTGAGGTACTGTTGATCATCATGTTGCTCTTTGTAAACTT 17106  Qy 1118 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG

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TICTROCCCTCCTCTATTCCTTTGG------TTTTTGCATAGTGTCTC 1785
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TCTTTGTTCTATACTTTTAGTGATTTGATTATTATGCACTGTGGGGGAGTTTCTTTTCCGG
                                                                                                                                            TCCAATCTATTTGGTTTTGTATGCTTCTTGTACCTTGATAGGCATCTCTTTCTCAAGG
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                                                 TAATACATCTGCCTTTATATGTTAATTGGTCTTTTTCCCTTGCATCTTTAATATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; tyrosinase; locus control region; LCR; chromosome 7; LCR X; transgene integration; transgene expression variability; protection; chromosomal integration; transgenic animal; gene; transgenic; ds.
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/note= "Locus control region (ABV76781)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the murine dendrin-2 gene that codes for a novel murine dendritic associated C-type lectin. [amily, termed DC-associated C-type lectin.2. (see AAM83010), that is essential for DC-mediated T cell activation. This novel gene is expressed selectively by long-term DC lines (XS series) from murine epidermis. Competion.2 CMN (see AAM42599) has also been isolated. The invention provides: dectin.2 cmN (see AAM42599) has also been isolated. The invention provides dectin.2 cmN (see AAM42599) has also been isolated. The invention provides dectin.2 cmN (see AAM42599) has also been isolated. The invention provides to the for purifying T cells, for detecting automatibodies and for up-regulating immunity e.g. as vaccine adjuvants; dectin DNA (see AAV42598-60); expression vectors; recombinant host cells; probes and primers useful e.g. for identifying human dectin.like molecules (see AAV42569); antibodies; compounds that modulate dectin e.g. for identifying human dectin ligands. Dectin expression and for drug screening; and dectin ligands. Dectin expression and for drug screening; and dectin ligands. Dectin expression and feetin expression is useful for treating allergy and autoimmune disease. Alternatively gene disruption is done in vitro, the call pulsed with an antigen, and returned to the patient to provide long term non-responsiveness to the antigen. The dectin expression is useful for treating the professional antiquen. The dectin dectin expression to DC. Since DC are 'professional' infinite to larget gene expression to DC. Since DC are 'professional' infinite to larget.
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Best Local Similarity 68.0%; Pred. No. 54;
Matches 463; Conservative 5; Mismatches 176; Indels 37; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding dendritic cell specific peptide(s) dectin-1 - useful, e.g. to regulate immune response, as vaccine adjuvants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 159-165; 200pp; English.

    useful, e.g. to regulate im
diagnosis and drug screening.

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2224. .2324
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844 GAAGTGTTATCATGGCTAATTTTTCCTTTGATGAGTATGAAATGTCATTTTCCATCTCTA 903
                                                                                                                                                                                                                                                                                                                                                                         1135 AATATTAATGATCAATGATTCTTCATTTCTGTTATTTTG-----GTGGTGGTGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length LCR (ABV7677) apart from where a 62 bp enhancer has been deleted; Locus control region
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                                                                                                                          TTCTTAGGGCCATTTGCTTAGAATATCTTTCCATCCTTTTACTCTAAGGTGATGTCTAT
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                                                      CTGCTTAGTTTTGGGTTTTAAGTCT-ATTAGTCAGATATTAAAATGACTGTATCGGCTTGC
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generates the full-length LCR (ABV76777)"
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replace(2621. .2684,GGTCATAGTTCCTGCCAGCTGACTTTGTCA
AGACAGTGATGTTCTGTGTTCCAGCAGTTGTTCTG)
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                                                                                                New DNA segment with insulating activity, useful for reducing the variation of transgene expression, in animal cells, caused by integration at different genomic locations.
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                                                                                                                                                                                    Claim 4; Page 54-55; 57pp; Spanish.
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Best Local Similarity 62.2%;
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CC regardless of the site of integration. The present sequence represents a mutant LCR designated LCRmut which retains a protective effect against variable transgene expression. This sequence is dentical to the full-length LCR, apart from deletion of a 62 bp enhancer (denoted as Box AB in the specification) between bases 2622 and 2683 of the full-length LCR, apart from deletion of a 62 bp enhanced the full-length LCR, spart from deletion of a 62 bp enhanced the full-length LCR, spart from deletion of a 62 bp enhanced content and procession variable transgene expression variable transgene expression variable transgene expression variable transgene content of the full-length LCR shown on pages 54-55 (ABV76777) and the conformation given in claim 4
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0; Mismatches 296; Indels 53;
                                                                                                                                                                   r reducing caused by
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                                                                                 Busturia Jimeno AM;
                                                                                                                                                                 DNA segment with insulating activity, useful for lation of transgene expression, in animal cells, c
                                          CONSEJO SUPERIOR INVESTIGACIONES CIENTIF
                                                                               Giraldo Carbajo P,
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at different genomic locations.
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1006 AGTAATGTTTCACTT-CCAAATGTGTTACCCTTGCTTTGGGGACATAGATGTTAAGAACT
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                                                                                                                                       The present sequence represents the human KCNQS (also called KCNGQ) gene, which encodes a voltage-gated potassium channel protein. Human KCNQS has ophthalmological, auditory central nervous system (CNS), cardioactive, anticonvulsant, gastrointestinal and muscular active activities. Sequences and methods from the present invention are useful for identifying activators or inhibitors of KCNQS protein. These activators and inhibitors are useful for treating Stargardt-like macular dystrophy, cone-rod dystrophy, Salla disease, age-related macular degeneration, other forms of macular degeneration, deafness, epilepsy, and different forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders stargardt-like macular dystrophy and cone-rod dystrophies are located at
                 Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying inhibitors and activators which can treat e.g. Stargardt-like macular dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
                                                                                                 99pp; English
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65475 65532 CTGAGAGAGTGCTTGATATATTTCAATTTTCTAAATTTATTGAGGCTCATTTTGTGGC 65592 65772 65892 diradeceasiteridaasereaseraseriseriserisaariteriateariterisea 66127 65652 66007 GTAGGITGTCTTTTTGGATGCAGGAGGATGGATCTTGTTTTTCATATCCATTCTGTT 1012 13; 417 477 537 657 776 836 952 TGTTTTTGGTGAAATAGTCTGTAAATATCTCTCTAGGTCCACTTGGTTTATGACATCAGTTAG 597 Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 0 U; 72 Other; retreatricarititegeceaargaicaricaagagcaggiratriaatricearara crerceiarceiricarceiredadaacircearecaceararacairerararrerares rreirgearicearicricrerarararicrerraacrerarirerreeaggraracrira CTCCAGCATTTCTCTGTTTCGTTTTTTTTGAGATGACCTAACTGTTGGAGAATGGGG 65713 AATCCATTGTTTCATTGTTGACCTTCAGTCTTGATTATCTGTCCAGTGCTGTCGGAG TATTGAAGTAGCCCACTATCTGTGTG-TGAGGTCAATATGTGATTTTAGCTGTAGCTGTG TATTGAAGTCTCCCACTATTATGTTGCCACCTGTCTCATTTCTAAGGTCTGTTAGTA ATTGTTTTATAAATTTGATAGTTCCAGTGTTCAGTGCATATACGTTTAGGATTGTGATGT CCTCTTGGTGGATTTTTCCTTTGATGCCTATGTAGTATTCTTCCCAATCTCATCTGCTTAG rgrigorriaaastricirirgic----raagaaraggiacreccerrigerringerer CCATTTGCTTAGAATATC-TTTTCCATCCTTTTACTCTAAGGTGATGTCTATCCAT---G ccatatriccaaaatgricriririccacaccririaccriraagrirgagacricriangr TCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGTTTGGTTTCCATAAGT TIGIAAGITITICIGITICIGITICITIGITIGITIGITATICIAGATITAAGCIGIGGI riccardecrirgaaadricarringaadridarrirc---agrirrarrecacrorder CAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGAGACTTGCTTTGTTTT CTTGTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGAATTGCAATGT TTTCCTGTTGGACTAGGCCTTTTATCATTATAATGCCCTCTTTGTCTTTTAAAATGC Gaps Score 249.898; DB 1; Length 125910; Pred. No. 15; 0; Mismatches 766; Indels 77; Ga 766; Indels 11.0%; ilarity 51.0%; Conservative Best Local Similarity Matches 878; Conserv 358 298 478 65593 538 598 658 717 65893 80099 Query Match 65416 65476 418 65653 55773 777 837 897 953 56068 65533 65833 65953

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66558 66916 66797 66439 1552 66617 1372 1432 66499 1492 1612 66677 96699 TIGACCTGCCTTCTTCCCCT-----TCCTCTATTCCTTTGGTTTTTGCATAGTG 1781 1961 56618 CCTAAAATTCTTTCCTTTGTCTTAACTTTAGATTACCTGATGACAATGTGCCTAGGTGAT **ACCCAGTATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGTTGAGAATTATCA** TITICITGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGCCTTCTTTAGGTC 1553 TTTAATATTCTTTCTTTCTTCTATACTTTTAGTGATTTGATTATTATTGCACTGTGGGGAG 56678 GATCTTTTGCAATGAATTTCCCAGGTGTTCTTTGTGCTTCTTGTGTATTTGGATGTCTAGG 66738 reteraceaaraceassasiritecrefigiraricecessaararstreeaactr 1782 TCTCTGGCTTCCTGGATGTTTTATGCCTGGATTATTTTAGACTTAACATTTTTGACC s6128 ATTCTATATCTTTT-----AAGTGGAGCATTTAAGCCATTTACATTCAACGTTAGTA 66180 Trdadardrdadgraccarrccarrcarracc----rarrrgrrdccrgraraccr GATTTATGCTTTAAAGAGGTTCTGTTTTGATGTGTTTCCAGGATTTGTTTCAAGAT - - - -------tragacrectritageactericitation 1373 AACTATTGTGACAGAAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGACATCTGTAGTCTCT 56440 TICATATATGAAGCATAGTTTTGTTGGATACAAAATTCTTGGCTGGTAATTCTTTGCTT 1433 TGGAGTCTGTAGCACATCTGTGCAGGGCCTTCTTACAFTTTGAGTTTCTATTGGAAAAGT 66500 GAGGAGGCTGAAGACAAGGCCCCAATACCTTCTAGCTTATAGGGTTTCTGCT-GAGAAT CAGGIGTAATTCTAATACATCTGCCTTTATATGTTAATTGGTCTTTTTTTCCCTTGCATCT crecretraarcraaragetrrrraitrafagetraccaeetacrrriger-creacrecr TTTCTTTTCCGGTCCAATCTATTTGGTGTTTTGTATGCTTCTTGTACCTTGATAGGCATC TCTTTCTCAAGGTTAGGAAATTTTTTTTTTTTTGGTTTTTCTTGAAAATATTTTCCCTGCTT Tragariticicricircercagaacacregairarrarragirificarcraacara ATTCIGTCAGTGAGGCTTGTCTCTGAGGTTCCTGTTGGGTTCTTAATTTTTCATTTTCCA ATTCTATTGCTGAGACT - TTCCAGAGCATTTTGCATTTCTATAAGGGTGTCCAAAGTTT GATTICCITICAGITITGGTTTTGTTTATTATTCTATTCC 2002 ACIGAAGITITGACIGITITITATITATGCTATCIATITCC 1013 56233 1193 1253 1313 1073 1613 1902 1133 1673 1493 56559 1733 86198 1962 56349 66977 67035 g g g g ď g q 셤 ò ò ò à à ò 셤 8 ઠે 음 a à g à ò 8

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RESULT 41 AAS63340 ID AAS63340 standa

AAS63340 standard; DNA; 6207 BP.

Similarity

New nucleic acid, useful for diagnosis and therapy of metabolic disease, solid tumor and cancers, comprises segment of chemically modified genomic sequences of genes associated with metabolism. Human, oytostatic; anti-tumour; metabolism; metabolic disease; liver; solid tumour; cancer; cytosine methylation; epigenetic; eye; kidney; single nuclectide polymorphism detection; SNP; stool; urine; lung; cerebral-spinal fluid; intestine; brain; heart; prostate; breast; DUSP2; EPHX2; ODPR; SGSH; SHWT2; SLC7A2; SLC7A4; TYMS; ds. Chemically pretreated metabolism associated gene #35 Claim 1; Page 100-102; 143pp; English Berlin K; 06-APR-2000; 2000DE-01019058. 07-APR-2000; 200DE-01019173. 30-UTM-2000; 2000DE-01035529. 01-SEP-2000; 2000DE-01043826. 06-APR-2001; 2001WO-EP004016. (first entry) Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2002-010834/01 WO200176451-A2 29-JAN-2002 Homo sapiens 18-OCT-2001 olek A,

930 807 1047 327 583 643 702 762 818 876 687 987 1107 925 1287 524 ò 셤 g g g 셤 g g ठे g ò 셤 ò 셤 8 ઠે 엄 ઠે g  $\dot{\delta}$ ò g 8 ò ઠે 셤 ઠે ò The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases of a segment of the chemically pretreated DNA of genes associated with metabolism such as DUSP2 (NM 004418). EPHX2 (NM 001979), ODPR (NM 000320), SGSH (NM 000419), SHTZ (NM 001971), SGSH (NM 004173) and TYMS (NM 001971) (all undefined). (I) are useful for diagnosis and therapy of metabolic disease, solid tumours and cancers; as primer oligonouleotides for the amplification of DNA sequences, for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPS) in a chemically treated DNA of genes associated with metabolism. An array of (I) is useful for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or single cytosine methylations. The method involves chemically treating genemic cytosine methylations. The method involves chemically treating genemic cytosine methylations. The method involves chemically treating genemic cytosine methylations. The method involves chemically treating genemic cytosine bases which are unmethylated at the 5th-position are such that cytosine bases which are unmethylated at the 5th-position are converted to uracil or another base which is dissimilar to cytosine in chemically pretreated genomic DNA. The genomic DNA is from cells or cellular components which contain DNA, sources of DNA comprising, for chemically pretreated genomic DNA. The genomic DNA is from cells or celluid, tissue embedded in paraffilm such as tissue from eye, inversions and funder, brain, heart, prostate lung, breast or liver, histologic object fully, tissue embedded in paraffilm such as tissue from eye, intestine, brain, heart, prostate lung, breast or liver histologic object solumed to their rombinations. Genetic parameters are in particular cytosine methylations and further chemicall modifications of DNA corpus of genes associated with metabolism. Further epigenetic parameters include for e.g. the acceptation of histones which correated methylation of histones which corrected to inverted G; 3296 T; 0 U; 1 Other; C; 1482 Sequence 6207 BP; 1298 A; 130

Length 6207;

DB 1;

Score 238.198;

Query Match

1346 1046 1106 1166 1226 1044 TGGCCTGGAATTATTATTATTCATATTTCTTGAATGTGGGTAACATCTTTAGATTGAA 1286 1045 TITIAAAATTIGGIAIGITITITGIAGIGGIIGGIATIGGIIGITGITTITIATGITITAGI 1104 12; 345 986 908 998 924 984 149 405 582 446 817 626 875 929 746 206 465 266 523 326 386 701 506 761 566 686 GITITICICCIAGCCITCITIAGGICIGCATITIGAAGATAGATATICTITACATCTGATT 747 TTTTGAGTCGATGTGAGTTTTTTGTAGGTGAGATGGGTTTTTTTGATATATAGTATATTGATG 985 ricarcriacricoriatriroriratrarriraaricrarirririrrarragiatricard CTCTAAGGTGATGT - - - CTATCCATGGTAGGTTGTCTTTTTGGATGCAGCAGTAGGATG 406 AGCTGTGGGTGGTCAGATAGGACATAGAGTATTATTTTCAATTGTCTTTTATCTGTCGAGAC Trecerrerectriradaderacrerererestririraritrirararitreada 267 gigiririaririraariargiggiraaririrgaaraagigirargiggigirargaaga ATGTATATTTTGATTTGGGGGGGGGGGTTTTTGTAGATGTTTAGTTTAGGTTTGGGT 387 GTAGAGTIGAGTITAAGTTITIGGATATITITIGTIAATATITITGTTTTAATAT CCCAATCTCATCTGCTTAGTTTTGGGTTTTAAGTCTATTAGTCA--GATATTAAAATGACT GTATCGGCTTGCTTCTTAGGCCCATTTGCTTAGAATATC-----TTTTCCATCCTTTTA TGAGTCATTGATTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCA GTTAAAGAAGGATGTTTGATTTATGTATTGTTATGTGTGAATTTGATTTTGTTATT 286 AACACTICTATITCTIGATITCTATCTIGGCTCATITITAACTCAGTAGTGAGTTGTTIG GTTTCCATAAGTTTGTAAGTTTTCTGTTGTTGTTGTTGTTGTTATCTAGATTTA Gritinaignagitrigagiritigagigagi---itritiaatritigagitriaaritiga TIGCITINGITITIGAAATAIGTATICAAFITITIGGA--GAGITICATAGGGGTGCTGACAAGA AGGTACAGTCT-TTGTGTTTTGGTGAAATAGTCTGTAAATATCTCTAGGTCCACTTGGTT TIGGAGAGAATGGGGGTATIGAAGTAGCCCACTATCTGTGTGTGAG-GTCAATATGTGAIT Traccigraccigraccingtrargaactragercarrereringerecaragacar TAAGAATTGCAATGTCCTCTTGGTG----GATTTTCCTTTGATGCCTATGTAGTATTCTT GGTTTTGAATTTTAATTTGTTAGTTTATGTTTTTAATTGGGGTATTAGTTCGT 978; Pred. No. 78; 0; Mismatches ilarity 48.6%; Conservative 90 150 346 207 466 Best Local Matches 96 a ò ద 8 g

breast cancer; differential expression;

breast cancer associated coding sequence SEQ ID NO:

(first entry)

04-DEC-2002

therapy; gene; ss

gene

WO200259271-A2

01-AUG-2002

Homo sapiens.

gene;

specific

breast

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Diagnosing breast cancer in a patient comprises detecting the level or expression in cell or tissue samples, where a differential gene

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WPI; 2002-674803/72. Orr MS, Nation M,

25-JAN-2001; 2001US-0263757P. 25-APR-2001; 2001US-0286090P. 23-MAY-2001; 2001US-0292517P.

(GENE-) GENE LOGIC INC.

25-JAN-2002; 2002WO-US002176

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The present invention relates to methods of diagnosing breast cancer in a patient, which comprise detecting the level of expression in a tissue sample of two or more genes salected from those shown in ABT09867-
ABT1112, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients.
The methods are also useful as a coreening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be the onset or progression of breast cancer. The breast cancer genes may be useful as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention. Note: The sequence data for this patent electronic format directly from WIPO at the privation of the print from WIPO at the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the privation of the priva
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The present sequence represents the human KCNQ5 (also called KCN6q) gene, which encodes a voltage-gated pocassium channel protein. Human KCNQ5 has ophthalmological, auditory, central nervous system (CNS), cardioactive, anticonvulsant, gastrointestinal and muscular active activities. Sequences and methods from the present invention are useful for identifying activators or inhibitors of KCNQ5 protein. These activators and inhibitors are useful for treating Stargardt-like macular dystrophy, cone-rod dystrophy, Salla disease, age-related macular degeneration, other forms of macular degeneration, deafness, epilepsy, and different forms of metropsychiatric, heart, gastrointestinal, and muscle disorders. Stargardt-like macular dystrophy and cone-rod dystrophies are located at
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52.9%;
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1217 17665 17725 1188 ô cancer; carcinoma-associated gene; CA; 당 nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnoshing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention. CATTITGITATIT----GTTTTCIAGITGTTTTGGGCTCTTCTTTTTTTTTTTCTTTCC Other; TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCTGTGTTTCTCTCTCCCCTCT TTCTTGTCTTCCTTTCATTGAAAGTGATTTTCTCTGGTGGTATGATTTAGTTTCTTGCTT New recombinant nucleic acid comprising a nucleotide sequence of any the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas. Gaps Sequence 96594 BP; 27993 A; 18068 C; 18732 G; 30838 T; 0 U; 963 ö The invention relates to a recombinant nucleic acid comprising Length 96594; ritaririringreferarccaricarasecririricaririra 70922 Indels TITGATTITIGGCCIGGAATTATTIATTATTCATATTICTIGA 31; Score 71.4; DB 1; Pred. No. 36; 0; Mismatches 31; Cytostatic, gene therapy, vaccine, cancer, secreted, transmembrane, intracellular, ds Claim 1; SEQ ID NO 43; 983pp; English. ВЪ ADC85257 standard; DNA; 96594 Mouse Ptprk genomic sequence 02-DEC-2002; 2002WO-US038582 30-NOV-2001; 2001US-00997722 3.1%; EK; (SAGR-) SAGRES DISCOVERY Local Similarity 74.4 es 90; Conservative Engelhard (first WPI; 2003-513603/48. WO2003045230-A2 G 1189 01-JAN-2004 05-JUN-2003 Morris DW, 1098 1158 1218 1129 71081 71025 70965 ADC85257; 1189 Query Match Sp. Mus RESULT 임 ò g 8 ò 셤 à g ò g ò

Sequence 96595 BP; 27994 A; 18068 C; 18732 G; 30838 T; 0 U; 963 Other; 7.1%; Score 71.4; Di Local Similarity 74.4%; Pred. No. 36; les 90; Conservative 0; Mismatches in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. Claim 1; SEQ ID NO 1295; 245pp; English ADA02777 standard; DNA; 96595 BP. 26-DEC-2001; 2001US-00035832. 26-DEC-2002; 2002WO-US041414 06-NOV-2003 (first entry) (SAGR-) SAGRES DISCOVERY. WPI; 2003-587068/55. WO2003057146-A2. 17-JUL-2003 Morris DW; ADA02777; Query Match Mus sp. RESULT 45 ADA02777 

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0; Gaps

DB 1; Length 96595; 31; Indels

The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA0094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a invention also encompasses expression vectors and host cells comprising to blinds to the protein, and a blochip comprising CA nucleic acid or card the sequences of the invention were identifically card conceptual the sequences of the invention were identified using on cogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or a propensity to carcinoma by determination of the sequence cancer, lymphoma or a propensity to carcinoma by determination of the sequence cancer, lymphoma or a propensity to carcinoma and evaluating draid as the stagence represents and in screening and evaluating draid seaful as therrapeutic agents and in screening and evaluating draid suggested the invention. Note: The complete sequence data for this captured the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears to the parinted appears the complete sequence data for this in electronic format directly from MIPO at Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening; gene; ds. New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas. Mouse Ptprk carcinoma associated gene, SEQ ID NO:1295. 17726 G 17726

17726 Ġ 17726 1189 G 1189 à g g

Search completed: August 25, 2004, 07:09:04 Job time : 2296 secs

us10664775-4.rni

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August 25, 2004, 07:11:15 ; Search time 3651 Seconds (without alignments) 3.978 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                        - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Database : rni4.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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SUMMARIES		S-08-781-891-20	S-09-618-166-20	S-08-781-891-20	8-09-618-166-20	-781-891-20	-09-618-166-20	-08-781-891-20	-09-618-166-2	-09-497-855A-3	-09-497-855A	0-027-983-1	-08-772-440-3	-09-426-290-	-09-818-512-	US-09-751-389-3	-09-245-281-4	-09-340-620A-	-08-742-185-10	-09-734-674-	-09-816-095-	-09-801-87	-10-254-869-	-09-426-290-	-09-377-497-	-09-377-497-6	-10-027-98	-09-816-095-	-09-751-389-	-497-855A	-851-896-	-09-803-671B	-09-393-634-	US-09-220-132-168
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Sequence 4, Appli
Sequence 3, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 604, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-06-781-891-207
1 Sequence 207, Application US/08781891
2 Patent No. 60906207
3 FAPILICANT: Pu, Ying-Hui
3 APPLICANT: Pu, Ying-Hui
4 APPLICANT: Yu, Chang-En
5 APPLICANT: Wulligan, John T.
5 APPLICANT: Mulligan, John T.
5 APPLICANT: Schollenberg, Gerald D.
6 TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
7 TITLE OF INVENTION: WERNER'S SYNDROME
8 NUMBER OF SEQUENCES: 209
9 CORRESPONDENCE ADDRESS:
1 ADDRESSES: SEED and BERRY LLP
1 SCHOLLES STATE: Washington
1 CITY: Scattle
1 COUNTY: USA
21P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,891

FILING DATE: 27-DEC-1996

CLASSIFICATION: 800-000

ATTORNEY/AGENT INPORMATION:

NAME: No. 6090620tenburg Ph.D., Carol

REGISTRATION NUMBER: 39,317

REFERENCE/DOCKET NUMBER: 240052.419

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFORE: (206) 682-690

TELEFORE: (206) 682-690

TELEFORE: 29604 base pairs

TYPE: mucleic acid

TYPE: mucleic acid

TYPE: MUDICAL SINGLE
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                              US-09-525-166B-9
US-09-525-166B-4
US-09-7318-673-3
US-09-010-398-14
US-09-010-398-14
US-09-36-260-14
US-09-736-457-604
US-09-736-457-604
US-09-611-12-8-604
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Best Local Similarity 62.9
Matches 1170; Conservative
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6.8 11 12592
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ATTORNEY/AGENT INFORMATION:

NAME: MCMSSEGTS, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 240052.419C1

TELECOMMUNICATION INFORMATION:

TELEPRONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 207:

SEQUENCE CHARACTERISTICS:

LENGTH: 29604 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
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TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-618-166-207
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Best Local Similarity 62.9
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Pred. No. 0.18;
); Mismatches 576; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OOMPRAING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                            APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Oshima, Junko
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED 1
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
STRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING LASSIFICATION: BUU CLASSIFICATION: ATTORNEY/AGENT INFORMATION: No. 6090620tenburg Ph.D., Carolwam: No. 6090620tenburg Ph.D., Carolwam: No. 700052,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052,419
TELECOMMUNICATION INFORMATION:
      US-08-781-891-209/c
; Sequence 209, Application US/08781891
; Patent No. 6090620
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                              ATCCTTAGGÍTÍTCAÍTÍTCTCÁTTGÍGÍTCCTATATÍTCCTGGATGÍTÍTÍGGGTTAGGÁGC 8940
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           TTGCATAGTGTCTCTGGCTTCCT
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Yu, Chang-En
Oshima, Junko
Muligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS
WERNER'S SYNDROME
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property
STREET: 701_Fifth Avenue, Sulte 6300
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ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERS, DAVID D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRINT APPLICATION DATA:
FILING DATE: 17-Jul-2000
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No. 0.18;
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
                                                                                                                                                                                                                                                                                                                                 Sequence 209, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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62.1%;
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STATE: Washington
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ZIP: 98104-7092
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Best Local Similarity
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US-09-618-166-209/c
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                                                                                                  Version #1.30
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 27-DEC-1996
CLASSIFTCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39.317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPAXI: (206) 622-6031
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 51259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 1118, Conservative
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            1349 ATCTTAGAATGTCTTTCTTCTCCAACTATTGTGACAGAAAGTTTTTCTAAGTGCAGTAG 1408
                                                                                                                                                 9357 CCTGGGCTGGCATTTGTGTTCTCTTTGGGTCTGTATGACATCTGCCTAGGATCTTCTAGC 9298
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Sequence 209, Application US/08781891

Patent No. 6090620

GENERAL INFORMATION:
APPLICANT: Yu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMBR: US/09/618,166
FILING DATE: 17-Jul-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                          APPLICANT: Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED '
WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
                                                     2059 GGTTTCTTTAATGGATTTATTCATTTCCTCTTCAAGGACCTTT
                                                                                     27844 TAATTCTGTAAGGAATTTTTGTGTTTCCTCTTTAAGGGCTTCT
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                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
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Pred. No. 0.3;
0; Mismatches
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                                                                                                                                                        US-09-618-166-209; Sequence 209, Application US/09618166; Patent No. 6583112; GENERAL INFORMATION:
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LENGTH: 31259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 60.77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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                                                                                                                                                 APPLICANT: Fu, Ying-Hui
APPLICANT: Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED ON WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 323.899;
Pred. No. 8.5;
0; Mismatches
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APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-JU1-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 208:
                                                                                             Sequence 208, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 16442 base pairs
TYPE: nucleic acid
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  TICTITAAGGACTIGIA 939
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ilarity 64.1%;
Conservative
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STATE: Washington
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                                                                             US-09-618-166-208
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                                                                                                                                 Score 323.899;
Pred. No. 8.5;
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Best Local Similarity 64.1%;
Matches 588; Conservative
                  LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pai
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US-08-781-891-208
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Gaps

Length 16442;

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Sequence 37, Application US/09497855A

Betent No. 6605432

GENERAL INFORMATION:

APPLICANT: HUANGH,

TILE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION

FILE REFERENCE: UNO1523

CURRENT APPLICATION NUMBER: US/09/497,855A

CURRENT FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: 60/120,592

PRIOR APPLICATION NUMBER: 60/118,760

PRIOR PILING DATE: 1999-02-05

NUMBER: OF SEQ ID NOS: 54

SOFTWARE: Patentin version 3.0

SEQ ID NO 37

TURNENT: 193303

TURNENT: 193303
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US-09-497-855A-37
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Sequence 44, Application US/09497855A
Sequence 44, Application US/09497855A
Sequence 44, Application US/0949785A
GENERAL INFORMATION:
APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
SEQ ID NO 44
LENGTH: 193303
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                                                     TCTTTTCTTTAAGAATGTTGAATATTGGCCCTCACTCTCTTCTGTACTTGTAGAGTTTCTG
   TGTAGTCTCTTGGAGTCTGTAGCACATCTGTGCAGGGCCTTCTTACATTTTGAGTTTTCTA
                                                                                                                                                                                            CIGCGAAA-TCCGCTGTTAGTCTGATGGGCTTCCCTTTGT-GGGTAACCCGACCTTTCTC
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Pred. No. 1.7;
0; Mismatches
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51.9%;
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Best Local Similarity 51.9
Matches 861; Conservative
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CORGANISM: Homo sapiens;
US-09-497-855A-44
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US-09-497-855A-44
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11.1%; Score 252.597; DB 1; Length 392000;
Best Local Similarity 51.9%; Pred. No. 0.87;
Matches 859; Conservative 0; Mismatches 689; Indels 106; Caps
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LOCATION: (186224) ... (186323)
CUCHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (195242) ... (195341)
CUCHER INFORMATION: n = A,T,C or G
NAME/KEY: unsure
LOCATION: 202703
CUCCATION: 202703
CUCCATION: (202703
CUCCATION: (20271) ... (202870)
NAME/KEY: misc_feature
LOCATION: (20271) ... (202870)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (206246) ... (215602)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (220360) ... (22499)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (220360) ... (222816)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (220361) ... (22286)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (220361) ... (2232398)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (220367) ... (230256)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (230359) ... (2332398)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (230359) ... (2302561)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (230359) ... (2302561)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (2305651)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (2305651)
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NAME/KEY: misc_feature
LOCATION: (2305651)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (118288) ...(119101)
OTHER INFORMATION: exon 1C
NAME/KEY: exon:intron junction
LOCATION: (151129) ...(151130)
OTHER INFORMATION: exon 5:intron 5
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LOCATION: (299248)...(299249)
OTHER INFORMATION: exon 9:intron 9
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LOCATION: (238789)...(248788)
OTHER INFORMATION: n = A,T,C or G
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Sequence 11, Application US/10027983
Sequence 11, Application US/10027983
Sequence 11, Application
GENERAL INFORMATION:
APPLICANT: Menth W. Dobie
APPLICANT: Menth W. Dobie
APPLICANT: Menth W. Dobie
APPLICANT: Menth W. Dobie
APPLICANT: Menth W. Mobie
TILLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
FILE REPERENCE: RTS-0340
CURRENT APPLICATION NUMBER: US/10/027,983
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 11
LENGTH: 392000
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                                         111349 TCTGGCTGCCCTTAACATTTTTTTCTTCAA------GACAATTATGTG 111395
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      1543 CCTTGCATCTTTAATATTCTTTCTTTGTTCTATTAGTGATTTGATTATGCA 1602
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NAME/KEY: UNBUIE
LOCATION: 151967
OTHER INFORMATION: UNKNOWN
NAME/KEY: Misc feature
LOCATION: (151967)...(1542066)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: UNBUIE
LOCATION: 154217
OTHER INFORMATION: UNKNOWN
NAME/KEY: Misc feature
LOCATION: (164037)...(164136)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: Misc feature
LOCATION: (164037)...(164136)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: Misc feature
LOCATION: (174557)...(17456)
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LOCATION: 137740

LOCATION: 137740

OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 137742

OTHER INFORMATION: unknown
NAME/KEY: misc feature
LOCATION: (138121)

OTHER INFORMATION: n = A,T,C or
NAME/KEY: unsure
LOCATION: 145507

OTHER INFORMATION: unknown
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ORGANISM: Homo sapiens
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0y 1842 ATTGGAAAAGTCAGTGTAATTCTAATACATGCCTTTAATTGTTAATTGTTTTTT 1541  Db 317401 -CCCAGAACCACCGTGTTTTTCCATCATTCTTTAATTGTTTAATTATTGTTTTTTTT	APPLICATION NUMBER: US/08/772,440 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Parker, David L. REGISTRAINON NUMBER: 32,165 REFERENCE/DOCKET NUMBER: 32,165 REFERENCE/DOCKET NUMBER: 32,165 REFERENCE/DOCKET NUMBER: 32,165 REFERENCE/DOCKET NUMBER: 32,165 REFERENCE/DOCKET NUMBER: 32,165 REFERENCE/DOCKET NUMBER: 312/474-757 INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS: LENGTH: 10409 base pairs INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS: LENGTH: 10409 base pairs IYPE: nucleic acid STRANDEDNESS: single
1318461 ATGTAGTCAGCGCTTTTCAGTCAGTCATTCATCACTCAGTTCTAGTTCATTCA	OY 1242 TATTATTCATATTTCTGAATGTGGGTAACATCTTTAGATTGATT

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TAGACTTCCCTTTATATGTTAATTGGTCTTTTT 1541
                                                                                                                  AGGAAATTTTCTTTTTTGGTTTTCTTGAAAATAT 1721
                                                                                                                                                                        TTCATTTCAACTTTGGTGAATCTGTCAATTATGT 317284
                                                                                           TIGITCIATACITITAGIGATITGATIATIAIGC 1601
                                                                                                                                                          TGACCTGCCTTCCCCTTCCTCTATTCCTTTG 1767
                                                                                                                                                                                                 TGGATGTTTTATGCCTGGATTATTTTAGACTTAA 1827
                                                                            GAGGCTTGT 1921
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GAAGCTTGT 316950
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4452 TTCTTTTTCTTTGTCTATTCCYATAGACTTAGTTTTGTTTGTTTGTTTTTAATCTG 4511
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US-09-426-290-1
Sequence 1, Application US/09426290
Sequence 1, Application US/09426290
PREED NO. 6410712
GENERAL INFORMATION:
APPLICANT: Bergalind Ran Olafsdottir
APPLICANT: Bergalind Ran Olafsdottir
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REPERENCE: 2345-2001-000
CURRENT PELLING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 168575
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ORGANISM: Homo Sapiens
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Best Local Similarity 68.0%; Pred. No. 30;
Matches 463; Conservative 5; Mismatches 176; Indels
                                                                                                                           NAME/KEY: modified base
LOCATION: 3406..6470
CTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mod_base= OTHER
LOCATION: 3564..7896
OTHER INFORMATION: /mod_base= OTHER
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                                   NAME/KEY: modified_base
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NAME/KEY: modified base
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LOCATION: 3457..9998
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4532 TACIGAGITGITGGIGAGGCATACCICTTAGACCTIGITIGICTCCCAAAITATACATT 4691
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Patent No. 653780
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUGAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THERED ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THERED ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: 14000192
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 116592
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Pred. No. 3.1;
0; Mismatches
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OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 51.2%;
Matches 847; Conservative
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NAME/KEY: misc_feature
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ORGANISM: Human
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APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, MUCLEIC
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001067
CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-751-389-3
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US-09-751-139-3
; Sequence 3, Application US/09751389
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10.5%;
Best Local Similarity 51.4%;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6482933
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                       886 GCTTCTTAGGGCCATTTGCTTAGAATATCTT-TTCCATCCTTTTACTCTAAGGTGATGTC 944
                                                                                                                                              768 TTGCAATGTCCTCTTGGTGGATTT-TCCTTTGATGCCTATGTAGTATTCTTCCCAATCTC
                                                                                                                                                                                                                                           827 ATCTGCTTAGTTTTGGGTTTAAGTCT-ATTAGTCAGATATTAAAATGACTGTATCGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1002 TCCATICTGTTACCCAGTATCTTTTTCTAGAGAATTAAGATCATTGAGTCATTGATGTT
                                              708 GTAGCTGTGCTTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGAAA
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APPLICANT: BETTIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
FILE REFERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT FILING DATE: 1999-06-28
PRIOR PLING DATE: 1999-02-05
PRIOR PAPLICATION NUMBER: US 09/245,281
PRIOR PAPLICATION NUMBER: US 09/207,359
PRIOR PRILING DATE: 1999-12-08
PRIOR PLING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/099,042
PRIOR FILING DATE: 1998-02-06
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                                                                                                                                                                                                                                       15487 IGIGGICTGAGAGATAGITTGTIATAATTTCTGTICTTTTACATTTGCTGAGGAGAGAGTTT 15546
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1768 GITTTTGCATAGTGICTCTGGCTTCCTGGATGTTTTATGCCTGGATTATTTTAGACTTAA 1827
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                                                                                                                                                          1828 CATTITCITIGACCAAGGIATCCATITCTICIAICTIGICTICACIGCCTGAGAITCTCT
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COUNTRY: 1828 1888 16912 16852 음 8 ò 원 셤 8 15907 Tiridaictridiiddritaaadictgritraicadagactaggatugaaggecetecer 15966 16027 IGTCTCTGCACGTGAGATGGGTTTCCTGAATACAGCACACTGATGGGTCTTGACTTTA 16086 16087 İCCAACTIGCCAGTCIGIGİLİTİTAAİIGCAGAAİTIAG------TCCAİTIAİAİİ 16138 16199 idcrcairadireaidcagrircriccradicicaaidgrcriracariridgcargair 16258 6139 TAAAGTTAATATTGTTATGTGTGAATTTGATCCTGTCATTATGATGTTAGCTGGCGATTT 16198 TATCCATG---GTAGGTTGTCTTTTTGGATGCAGCAGTAGGATGGATCTTTTCATA 1001 TCCATTCTGTTACCCAGTATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGTT 1061 1062 GAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTGTG 1121 rcrrrradgecagecragregrearanarcrcrcagearrarerrananagerar 16373 16374 ititairicicciricacitaidaagciriadritiggcigganarigaaticigggridaaa 16433 CICIGGCIGCCCTIAACATITITICCTICATITICAACITIGGIGAATCIGACAATIATGI 16611 16612 GTCTTGGAGTTGCTCTTCTCGAGGAGTATCTTTGTGGCGTTCTCTGTATTTCCTGAATCT 16671 16672 GAACGTTGGCCTTGCTAGATTGGGGAAGTTCTCCTGGATAATATCCTGCAGAGTGT 16731 .6732 TTTCCAACTTGGTTCCATTCTCCACATCACTTCAGGTACACCAATCAGACGTAGATTTG 16791 885 1242 TATTATTCATATTTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGCC 1301 16494 Gccóagágá-riccóridrrágricrgárgegerfricchring-agagráacccgaachricr 16551 1302 TICTITAGGICTGCATTIGAAGATAGATATTCTTTACATCTGATTTTATTTAGAATGIC 1361 1482 ATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATGTTAATTGGTCTTTTT 1541 GITITIGCATAGIGICICIGGCITCCIGGATGITITIAIGCCIGGATIAITITIAGACITAA 1827 GCTICTTAGGGCCATTIGCTTAGAATATCTT-TICCATCCTTTACTCTAAGGTGATGTC 944 CTTTGTTCTATACTTTTAGTGATTTGATTATGC 1601 TIGCAAIGICCICTIGGIGGAITI-ICCTITGAIGCCIAIGIAGIAITCTICCCAAICIC 15847 radrragcriccririgridaarragaricccriraccarrargraarggccrircrrrgricri 827 ATCTGCTTAGTTTTGGGTTTAAGTCT-ATTAGTCAGATATTAAAATGACTGTATCGGCTT 1182 TGTCTGTGTGTGTGTGTTGTCTCCCCCTCTTTTGATTTTTGGCCTGGAATTATT 16434 Tricitrichinada Arbit Garante de Cecce de Centre d 16290 ------ATGTTTACCGCTTCCTTCAGAGC TITCTTCTCCAACTATTGTGACAGAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGACAT CTGTAGTCTCTTGGAGTCTGTAGCACATCTGTGCAGGGCCTTCTTACATTTTGAGTTTTCT 1602 ACTGTGGGGGAGTTTCTTTTCCGGTCCAATCTATTGGTGTTTTTGTATGCTTCTTGTACCT CTGCTTTTGACCTGCCTTCTTCCCCTTCCTATTCCTTTG 16259 Trecadedededracagringricetrice---------CCCTTGCATCTTTAATATTCTT 886 1002 945 1122 1422 1768 16314 1362 1542 16552 1722 8 P g d qq ద à ò ò ò 상 원 ò 8 % B 8 8 λ α 상. 음. 8 g 8 8 ò

16792 GTCTTTTCACATAGTCCCATATTTCTTGGAGGCTTTGCTCATTTCTTTTATTCTTTTT 16851 19589 TITCTGCCTICATITIGITATGIACCCAGIAGICATTCAGGAGCAGGTGTTCAGTTTCC 19648 19649 AIGTAGTIGAGTGGTIT -- TAAGTGAGATTCTTAATCCTGAGTTCTAGTTTGATTGCAC 19705 13; CICTABABCTICCCTICTCGCTICATITCATITCATCTTCCATTGCTGATACCCTT CATITICITIGACCAAGGIAICCATITCTACTIGICIICACIGCCIGAGAIICICI 352 ATAAGTTIGTAAGTTTTCTGTTGTTGTTGTTGTTGTTATCTAGATTTAAGCTGT 292 TCTAITICITGATTICIATCITGGCTCATTITTAACTCAGTAGTGAGTTGTTTGGTTTCC Sequence 102, Application US/08742185

Patent No. 6020476

GENERAL INFORMATION:
APPLICANT: Raijo, Renee
APPLICANT: Baxena, Richa
APPLICANT: Reave, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. 785; Indels 106; Gaps DB 1; Length 40328; 3: Hamilton, Brook, Smith & Reynolds, P.C. Two Militia Drive COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOSS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING\_DATE: 30-OCT-1996 criccagrigarcecarcedercereadecrici 16945 CTTCTATCTCTTGTATTCTGTCAGTGAGGCTTGT 1921 Score 227.997; Pred. No. 10; 0; Mismatches 7 PRIOR APPLICATION: 435

APPLICATION NUMBER: US 08/690,734

FILING DATE: 31-011-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429

FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WH194-07A2

TELEPHONE: (617) 861-6240

TELEPHONE: (617) 861-6240

TELEPAX: (617) 861-6240

TELEPAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS: LENGTH: 40328 base pairs

TYPE: INCLESC ACCIDING DNA (genomic) Query Match Best Local Similarity 49.7%; Matches 882; Conservative ( STREET: Two Militia I CITY: Lexington STATE: Massachusetts single linear ; MOLECULE TYPE: US-08-742-185-102 STRANDEDNESS: TOPOLOGY: 1i ZIP: 02173

	706 Db 20951 20005 Qy 1767 766 Db 21011 20065	925 Qy 1827 20125 Db 21071 884 Qy 1887 20185 Db 21131	OY 1944 TTANTITITICAGATICCAGATITICSTITICAGAGATICAGATICAGAAGAAGATICAGAAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGATICAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	1060 RES 20357 ; F 1120 ; G 20417 ;		1300 ; TYPE: DR. 20532 ; ORGANISM 20532 ; EATURE 1360 ; LOCATION 20592 US-09-734-6R	CA 1420 Query Match 9.1%; Score 208.398; DB 1; Length 202001   Best Local Similarity 50.1%; Pred. No. 2.7; AA 20652 Matches 835; Conservative 0; Mismatches 711; Indels 120; G	292   TCTATTTCTAGATTCTAGCTCATTTTTAACTCAGTAGTGAGTTGTTTGGTTTCCCCCCCC
412 GGTGGTCGGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGGACTTGCTTT 19706 TGTGGTCTGAGACATTGTTTTACATTGTCTTTTACATCGTCGGAGAGTTGCTTT 19706 TGTGGTCTGAGAGAGAGAGAGTTCTGTTCTTTTACATCCGCTGAGAGAGA	AGGARATGGGGTATTGAAGTAGCCCACTATCTGTGTGAG-GTCAATATGTGATTTTTTTTTT	767 ATTGCAATGTCCTCTTGGTGGATTT-TCCTTTGATGCCTATGTATCTTCCCCAATCT 20066 ALAGTTAGCTCTTCTTGTTGAATTGATGCCTTTACCATTATGTAAATGGCCTTCTTTGTCT 826 CATCTGCTTAGTTTAGGCTTTAAGTCT-ATTAGTCAGATATTAAAATGACTGTATCGGCT 1	885 IGCTICITAGGGCCAITIGCITAGAATAICIT-TICCAICCITITACICIAAGGIGA 20186 ITTITIGITITCCAITIGCTIGGIAGAICTICCGGCCAICCITITATITIGGGCCTA 944 CIAICCAIGGIAGGIIGCTITITIGGAIGCAIGGAGCAGIAGGAICGAICGAIGGAICTITI 20246 GIGTCTGCACGAGGGAIGGGITTCCTGAATACAGCACTGAIGGGITTGAITTI	1001 ATCCATTCTGTACCCAGTATCTTTTCTAGAGAAATTAAGATCATTGAGGTCATTGATGATGT	20418 THCTTGTTAGTGATGCAGTTTCTTCCTAGTCTCGATGGTCTTTACATTTTGGCTGTGTTTAGCTTGTTTTTGGCTGGATTAT  1181 GTGTCTGTGTGTGTGTGTGTGTTCTTCCCCCTCTTTTGATTTTTGGCCTGGAATTAT  20478 TTTGCAGCGGCTGGTACCGGTTGTTCCTTTCC	1241 TIATTATTCATATTTCTTGAATGGGGTAACATCTTTAGATTGAAGTTTTCTCCTAGC  [	1361 CITTCTTCTCCAACTATTGTGACAGAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGACA 20593 TITTATTCTCCTTCGCTTATGAAGCTTAGTTTGGCTGGATATGAAATTCTGGGTTGAAA	1421 TCTGTAGTCTCTTGGAGTCTGTAGCACATCTGTGCAGGCCTTCTTACATTTTGAGTTTC

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Sequence 3, Application US/09816095
Fatent No. 6664084
GENERAL INFORMATION:
TITLE OF INVENTION:
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THEREOF 146550 CCCAACTTTCTCTGTGGCTGCCCTTAACATTTTTTCCTTCATTTCAACTTTTGGTGAATC 146609 146670 TrircridaArcrigaArgrragccrrgcrragArragagaAgrrcrccrggaraArar 146729 146549 146669 146789 146432 CTGGGTTGAAAATTCTTTTTAAGAATGTTGAATATTGGCCCCCACTCTTCTGGCT 146493 TIGGICTITITICCCTIGCALCTITIAATATICTITCTTIGTTCTATACTTTTAGTGATT 1589 40899 Aigcagiridigcagiririgagigagi---rircritaariccigagricharringaringcar 40843 14; 351 146610 IGAAAHTHATGTGTCTTGGAGTTGGTATTCTCGAGGAGTATCTTTGTGGTGTTCTCTGTA 146492 ighadadiricicci-dagadarccecidriagicigargegerrcccrirgi-gegraa 1756 TCTATTCCTTTGGTTTTTGCATAGTGTCTCTGGCTTCCTGGATGTTTTATGCCTGGATTA 146790 GACGIAGAİTİĞTİCİİİTİCACATAĞİCCCATATİİCTİĞGAĞĞCİTİĞİTTĞİTTÇİLİ TTTTGAGTTTCTATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATGTTAA TGATTATTATGCACTGTGGGGAGTTTCTTTCCGGTCCAATCTATTTGGTGTTTTGTATG -----CIGCITITGACCIGCCTICITCCCCTICC 146730 cchacagadrininicaactragrinchachachachachanda cchachana canacachanda 292 TCTATITICITGATITCTATCTIGGCTCATITITAACTCAGIAGIGAGIIGITITGGIITCC 1816 TITTAGACTIAACATITTCTTTGACCAAGGIATCCATTTCTTCTATCTTGTCTTCACTGC GGIGGICAGATAGGACATAGTATTICAATIGICTITITAICIGICGAGACTIGCIT 352 ATAAGTITGTAAGTITICTGTTGTTTCTGTTGTTGTTGTTATCTAAGCTGT Gaps Query Match 9.0%; Score 204.799; DB 1; Length 99916; Best Local Similarity 50.1%; Pred. No. 5.5; Matches 831; Conservative 0; Mismatches 722; Indels 106; G. 146910 CTGATAACCTTTCTTCCAGTTGATCACATCAGCTCCTGTGGCTTCT 146955 1876 CTGAGATTCTCTTCTATCTCTTGTATTCTGTCAGTGAGGCTTGT 1921 1710 TCTTGAAAATATTTTCC RESULT 20 US-09-816-095-3/c 1470 1590 412 (

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39781 TCTCTGGCTGCCCTTAACATTTTTCCTTCAATTTCAACCTTGGTGAATCTGAATTAG 39722
                                                                                                                                                                                                  39721 TGTCTTGGGGGTTGCTCTTCTCGAGGAGTATCTTTGTGGTGTTCTCTGTCTTTCCTGAATT 39662
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APPLICANT: TS, Jane et al
APPLICANT: TS, Jane et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REPRENCE: CLOOLIGO
CURRENT APPLICATION NUMBER: US/09/801,876B
CURRENT APPLICATION NUMBER: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFWMARE: RastSEQ for Windows Version 4.0
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                                1541 TCCCTTGCATCTTTTAATATTCTTTCTTTGTTCTATACTTTTAGTGATTTGATTATTATG 1600
                                                                                                                                            1601 CACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGGTGTTTTTGTATGCTTCTTGTACC 1660
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; OTHER INFORMATION: n = A,T,C or G
US-09-801-8768-3
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Matches 894; Conservative
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US-09-801-876B-3/c
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18842 TGCGGTCTGAGAGACAGTTTGATGTAATTTCTGTTCTTTTATATTTTGCTGAGCAGTGTTT 40783
                                                                                                              10782 TGCTTCCAATTATGTGGTCAATTTTAGAATAAGTGTGATGTGGGGCTGAGGAAATGTAT 40723
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                                                     TGTTTTGAAATATGTATTCAATTTTGGA--GAGTTTCATAGGGTGCTGACAAGAAGGTAC 529
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RESULT 22 US-10-254-869-3/C US-10-254-869-3/C Sequence 3, Application US Sequence 3, Application US Sequence 3, Application US Sequence 3, Application US Sequence 3, Application US Sequence 3, Application US SEQUENT NUMBRATION: ISOLA TITLE OF INVENTION: ACIII TITLE OF INVENTION: ACIII TITLE OF INVENTION: ACIII TITLE OF INVENTION: ACIII TITLE OF INVENTION: ACIII SEQUENT APPLICATION NUMBER CURRENT FILING DATE: 20 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FASTESQ for WILE SEQ ID NO 3 ILENGTH 148867 SEQ ID NO 3 SEATION: (1)(148867) COTHER INFORMATION: n = AUTHORY ACIII SEAT LOCAL SIMILATILY 50 MATCHES 894; CONSERVATIVE DD 45036 TITLTGTTGTTGTTGC  QY 305 TITLCTGTTGTTGTTGC  QY 425 GACATAGAGTATAA  QY 425 GACATAGAGTATAA	4181 TACTAGGIGACTCCTGAAGGCACATAGTAGGTGGTGATTCTTTTTTTT	8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6
Ouery Match Best Local Similarity Matches 894, Conservat 305 TTCTATCTTGGC	GAATGTGGGTAACATCTTTAGGTTTTTCTCCTAGCCTTCTTTAGGT TTGATGTTTTCCAGGATTTTAAGATTTAGAGTCTCTTTTAGGTTCTTTATAGGT CTGCATTTGAAGATTTGATTT	8 6 6 6 8 6 6 6
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TILLE OF INVENTION: THE FILE REFERENCE: CLOOLIGE CURRENT APPLICATION NUMBER: 2C NUMBERT FILING DATE: 2C NUMBER OF SEQ ID NOS: 8 SOFTWARE: FRREESO FOR WIS	CCAAAAAACCAAAAAAAGAGCTAAAGCTGTTCTTCCCACAAACAGCTTGTGGAAGTTGTGAAGTTGTGAAGTTGTGTGTTCTCCCACAAACAGACCTTCAGCTTCTCCCACAAAAGAGCTGTTCTTCTCCACAAAAAGAGTGTTGTTGTGTGTG	2 4 5 A
US-10-294-869-34) ; Sequence 3, Application 1; Batent No. 6653117 ; GENERAL INFORMATION: ; TITLE OF INVENTION: 157 ; TITLE OF INVENTION: AC.	aattetetaietitiaagtgageaittageeeaittagaateeaiditagaa aatgagegegettetgegattetget aatgagegeareegetegeatteateatgeeeettegeeetgeggettet	9 6 6 6
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43547 1732 43487	GITTARAPATTIGGGACTCCGGTGAGTAGGTTATATGTTTAGGATTGTGACATTTT CTTGGTGGA-TTTCCTTTGATGCCTATGTAGTATCTTCCCCAATCTCATCTGCTTA  CTTGGTGGA-TTTTCCTTTGATGCCTATGTAGTATTCTTCCCCAATCTCATCTGCTTA  CTTGGTGGA-TTTTCCTTTGATGTAGTATTCTTCCCCAATCTCATCTGCTTA  CTTGGTGGA-TTTTCCTTTTGATGTATTTTTTTTTTTTTT	8 8 8
DD 43607 ATACCTITITGCG  QY 1672 CICTITCTCAAGG  DD 43547 AITTCTAGCAAGG	TAAATCCTTCACTATTATTGTGTTGCTGTCTCACTTTCTTAGGTCAATTAGTAATT GTTTTATGAACTTGGGTGACATTGGTTTGGT	2 6 2
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TTCTTTGTTCTATACTTTTAGTGATTTGATTATTATGCACTGTGGGGA 1611 ICTT------CCCCTTCCTCTATTCCTTTGGTTTTTGCATAGT 1780 TICITCIACTIGICITCACIGCGGARITCICICITCIAICICITG 1900 44920 al LLATED HUMAN KINASE PROTEINS, NUCLEIC MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES HEREOF FOLD 188R: US/10/254,869 CTAATACATCTGCCTTTATATGTTAATTGGTCTTTTTTCCCTTGCATC 1551 19; 424 CTGTTGTTGTTGTTATCTAGATTTAAGCTGTGGTGGTCAGATAG 8.8%; Score 200.5; DB 1; Length 148567; 50.8%; Pred. No. 4; ive 0; Mismatches 710; Indels 155; Gaps ndows Version 4.0 GAGGCTT 1919 || || || | |GACACTT 43289 57) = A, T, C or G JS/10254869

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US-09-426-290-1/C
US-09-426-290-1/C
Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
APPLICANT: Begalind Ran Olafsdottir
; APPLICANT: Begalind Ran Olafsdottir
; APPLICANT: Jeffrey Gilcher
; TILLE OF INVENTION: HUMAN NARCOLEPSY GENE
; TILLE OF INVENTION: HUMAN NARCOLEPSY GENE
; CURRENT APPLICATION NUMBER: US/09/426,290
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NOS: 24
; SEQ ID NO 1.
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Best Local Similarity 49.2%;
Matches 816; Conservative
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292 TCTAITTCTTGAITTCTAICTTGGCTCAITTTTAACTCAGTAGTGGTTGTTTGGTTTCC 351  7853 TTTCTGCCTTAATTTCACCCAGTAGTCATTCAGCAGCAGCTGTTTCC 351  7853 TTTCTGCCTTAATTTCATTTTTACCCAGTAGTCATTCAGATTGTTTCC 7794  352 ATAAGTTTGTAAGTTTTCTGTTGTTTCTTTTTATCTGTTACTTTAAGCTGT 411  7793 ATCTAGTTGTAGATAGAGATATTTCTATTCTGTTGAGACTTGCTT 471  7795 GGGGTCAGATAGAGACATAGAGTATTATTCTATTGCTGAGACTTGCTT 471  7795 GGGGTCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AGTCTTTGTGTTTTGGTGAAATAGT-CTGTAAATATCTCTAGGTCCACTTGGTTTATGAC ATTCTATTTATTTGGGGGAGAGTCCTATAGATGTCTATTAGGCCTGGTTTATGAC ATTCTATTTATTTGGGGGAGAGTCCTATAGATGTCTATTAGGCCTGGGG ATCAGTTAGCTCCAGAATTTCTGTTTGTTGAAATAGACTGTTGGAG ATCAGTTAAGCTCCAGATTTCTGTTTTTTTTTT	769 IGCAAIGICCICTIGGIGGAITT-ICCITIGAIGCCIAIGIAGTAITICTICCCAAICTG 827 7377 AGCIAGCIGITICTIGITGAIGCCITIAICAIGCCTTIGIAIGCCCTTIGICTCT 7318 828 ICTGCTIAGITITIGGGITTAAGICIA-TIAGICAGAIATAAAAIGACTGIATCGCTTG 886 7317 ITTGAICTITGTGAGTTTAAGICIA-TIAGAGAIATTAAAAAIGACTGCGCTTG 7258 887 CITCTIAGGGCCATTGCTAAAAIATTTATCAAGAGACTGCAAGATGCAAGCTGCGTT 7258	7257 ATTICCTTICCTTICLININININININININININININININININININI	1124 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
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CANCER-ASSOCIATED GENES
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NUMBER: US/09/377,497
11999-08-20
er. 2.0
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Length 4646;

DB 1;

8.2%; Score 186.899;

Db 3661	RESULT 26 US-10-027-983-11 Sequence 11, Application US/10027983 Fatent No. 6617162 Fatent No. 6617162 Fatent No. 6617162 FAPLICANT: Mark P. Roach FITLE OF INVERMITION: ANTIENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION FILE REFERENCE: RTS-0340 CURRENT APPLICATION NUMBER: US/10/027,983 CURRENT FILING DATE: 2001-12-18 NUMBER OF SEQ ID NOS: 98 SEQ ID NO 11 LENGTH: 39200 FYPE: DNA ORCANISM: Homo sapiens FEATURE: NAME/KEY: unsure
Best Local Similarity 48.5%; Pred. No. 1.38+02; Indels 189; Gaps 292 TCTATTCTTGATTCTACGCCACACACACACACACACACAC	OY 1031 GAGAAATTAAGATCATTGAGTCATTGATGTGAGAATTATCAATGAGCAGTGTTTGTGGA 1090  1

us10664775-4.rni

NAME/KEY: misc\_feature
LOCATION: (232299) ... (232398)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc\_feature
LOCATION: (236552) ... (236651)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc\_feature
LOCATION: (238789) ... (248788) AME/KEY: misc\_feature
OCCATION: (206246)...(215602)
TTHER INFORMATION: n = A,T,C or G
AME/KEY: misc\_feature
COCATION: (218126)...(218225)
THER INFORMATION: n = A,T,C or G OCATION: 202703
THER INFORMATION: unknown
THER INFORMATION: unscriberure
OCATION: (202771)...(202870)
THER INFORMATION: n = A,T,C or G AME/KEY: misc feature OCATION: (222717)...(222816) THER INFORMATION: n = A,T,C or G NAME/KEY: misc\_feature OCATION: (223981) ... (224080) THER INFORMATION: n = A,T,C or G ACATION: (227487) ... (227586) OCATION: (227487) ... (227586) ION: (238789)...(248788) INFORMATION: n = A,T,C or G AME/KEY: misc\_feature OCATION: (151967)...(1542066) THER INFORMATION: n = A,T,C or G OTHER INFORMATION: unknown
NAME/KRY: misc\_feature
LOCATION: (164037)...(164136)
OTHER INFORMATION: n = A,T,C or G
NAME/KRY: misc\_feature
LOCATION: (174657)...(174756)
OTHER INFORMATION: n = A,T,C or G AME/KEY: misc\_feature CCATION: (186224)...(186323) THER INFORMATION: n = A,T,C or G WME/KEY: misc feature OCATION: (195242)...(195341) THER INFORMATION: n = A,T,C or G AME/KEY: misc feature OCATION: (220360)...(220459) THER INFORMATION: n = A,T,C or G AME/KEY: misc\_feature OCATION: (230157)...(230256) THER INFORMATION: n = A,T,C or G ö NAME/KEY: exon LOCATION: (118288)...(119101) OTHER INFORMATION: exon 1C NAME/KEY: exon:intron junction LOCATION: (151129)...(151130) NAME/KEY: unsure
LOCATION: 137742
OTHER INFORMATION: unknown
NAME/KEY: misc\_feature
LOCATION: (138122)
OTHER INFORMATION: n = A,T,C or NAME/KEY: unsure LOCATION: 145507 OTHER INFORMATION: unknown JAME/KEY: unsure JOCATION: 151967 JHER INFORMATION: unknown ON: 137740 INFORMATION: unknown unsure AME/KEY: unsure DCATION: 154217

25044 grichcingeninggagagagacrichanagarchanagarchecingerceagag 25103 25224 cicraadaacirdecirirandaarcidddidcidcidrarigddidiarararradda 25283 25284 TAGTTAGCTCTTCGTTGCATTGATACCTTTACCATTATGTAATGCCCTTCTTTGTCTT 25343 1061 TGAGAATTATCAATGAGCAGTGTTTGTGGAITCTTGTTATCTTGCACTTGTGAAGTGTGT 1120 24811 Tricigectiaaricugueatitaeaelagiagicarieagaageaegiraricaeririee 24870 25104 GİGAĞİİCAAGIÇCIGAAİAICÜTGİİAAİTİİCIĞİCICATİĞAIĞİĞITİAAİATIĞ 25163 25043 1001 ATCCATTCTGTTACCCAGTATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGT 1060 411 88344 Tirigaicrrichigarihaaagichgrihrarcagagachagachgcaccchacti 24871 Arcraghtgrachthraghdagh---fretharcraaghtgrachannaarthaan 25404 TTITTTGCTCTCCATTTGCTTGGTAAATCTTCCGCCATTCCTTTATTTTGAGCCTAGT 25524 Archartraccharcrarcrartrancrasachirancrar-----24984 TACTICIAATIAIGIGGICAATITITAGAATAAGICIGATGIGGIGCIAAGAAGAATGITAT 530 AGTCT-TIGIGITITIGGIGAAATAGICTGTAAATATCTCTAGGICCACTIGGITTAIGAC 25164 Acadridadengriaaadrendedeerarranidrerdadaarenaadeerringraden GTAGCTGTGTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACATAAGAA 886 GCTTCTT-AGGGCCATTTGCTTAGAATATCTT-TTCCATCCTTTTACTCTAAGGTGATGT 24928 IGTGGICTGAGAGACTGI----TAGGATTTCCATTCTTTTGCATTTGCTGAGGAGTGTTT TGTTTTGAAATATGTATTCAATTTTGGAG--AGTTTCATAGGGTGCTGACAAGAAGGTAC 649 AGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGAG-GTCAATATGTGATTTTAGCT 768 INGCAANGICCICINGGIGGATIT-ICCITIGAIGCCIAIGIAGIAITICTICCCAAICIC 827 ATCTGCTTAGTTTTGGGTTTAAGTCT-ATTAGTCAGATATTAAAATGACTGTATCGGCTT 352 ATAAGTTTGTAAGTTTTCTGTTGTTGTTGTTGTTGTTATCTAAGATTTAAGCTGT GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGAGACTTGCTT 589 ATCAGTTAGCTCCAGCATTTCTCTGTTTCGTTTGTTGAGATGACCTAACTGTTGGAG Indels 113; Gaps Length 392000; 292 TCTATTTCTTGATTTCTTGGCTCATTTTTAACTCAGTAGTGAGT Query Match
8.2%; Score 186.1; DB 1;
Best Local Similarity 50.5%; Pred. No. 1.8;
Matches 838; Conservative 0; Mismatches 709; NAME/KEY: exon:intron junction COCATION: (299248)...(299249) OTHER INFORMATION: exon 9:intron 9 NAME/KEY: exon:intron junction COCATION: (348578)...(348579) OTHER INFORMATION: exon 10:intron 10 NAME/KEY: intron COCATION: (348579)...(381838) OTHER INFORMATION: intron 10 NAME/KEY: intron:exon junction COCATION: (386185)...(386186) US-10-027-983-11 INFORMATION: exon 5:intron 708 412 472 g g q d 8 6. ò 셤 d ò d ð ò ઠે  $\delta$ ઠે Б ò 셤 ઠે 심 ò 엄  $\delta$ g ò

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22143 TTTCTGTTGATTTGGGGTGGAGAGTTCTTTAGATGTGTATTAGGTCGGCTTGGTGCAGAG 22202
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                                                                                                                                                                                                                                                                                                  292 TCTATITCTIGATITCTATCTIGGCTCATITITAACTCAGTAGTGAG
                                                                                                                                                                                                                 Score 177.9; DB 1;
Pred. No. 7.4;
0; Mismatches 306;
; SEQ ID NO 3
; LENGTH: 99916
; TYPE: DNA
; ORGANISM: Human;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(99916)
; OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 58.3%;
Matches 449; Conservative
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                                                                                                                                                                                                                                                    TACCAGTTTTACCTTTCCAT--------ATTTAGTGTTTTAGGA 25748
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Sequence 3, Application US/09816095
Patent NG. 6664084
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001147
CURRENT APPLICATION NUMBER: US/09/816,095
CURRENT APPLICATION NUMBER: 2001-03-26
NUMBER OF SEQ ID NOS; S
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                  CTATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATGTTAATTGGTCTTTT
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US-09-816-095-3
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US-09-751-389-3/c
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITILE OF INVENTION: THEREOF
FILE REPERENCE: CLOOLOGY
CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 186431
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## Patent No. 6605432
| GENERAL INFORMATION:
| APPLICANT: Huang, Tim
| APPLICANT: Huang, Tim
| TILE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
| FILE REFERENCE: UMO1523
| CURRENT APPLICATION NUMBER: US/09/497,855A
| CURRENT FILING DATE: 1999-02-04
| PRIOR APPLICATION NUMBER: 60/120,592
| PRIOR APPLICATION NUMBER: 60/118,760
| PRIOR APPLICATION NUMBER: 60/118,760
| PRIOR APPLICATION NUMBER: 60/118,760
| PRIOR PILING DATE: 1999-02-05
| NUMBER OF SEQ ID NOS: 54
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 40
| LENGTH: 161652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
7.4%; Score 169; DB 1; Length 161652;
Best Local Similarity 48.3%; Pred. No. 5.1;
Matches 857; Conservative 0; Mismatches 800; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: HOMO
US-09-497-855A-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54374
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                                                                                                                                                                                                   GENERAL INCOMESTATION:

GENERAL INCOMESTATION:

APPLICANT: WEBSTER,

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOODI61

CURRENT APPLICATION NUMBER: US/09/803,671B

CURRENT FILE APPLICATION NUMBER: 2001-03-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PREKESEQ FOR WINDOWS Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652 ATGGGGTATTGAAGTAGCCCACTATCTGTGTGAG-GTCAATATGTGATTTTAGCTGTA
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   24985 GIGATITICICIGGIGGIAIGITITIAATITICITICITITITITITITIGI 25034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 64467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 531;
                                                                                                                                            Sequence 3, Application US/09803671B Patent No. 6582946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; LCATION: (1)...(64467); COTHIEN: INFORMATION: n = A,T,C or GUS-09-803-6718-3
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Best Local Similarity 50.9
Matches 595; Conservative
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ORGANISM: Human
                                                                                              RESULT 31
US-09-803-671B-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569 AGGICCACTIGGITTAIGACATCAGITAGCICCAGCATTICTCGITTIGITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24451 GGATGAACTGTCTAATGCTGAAAGTGGAGTATTGAAGTCTCCAGCTATTATTGTATTGAG
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Pred. No. 14;
0; Mismatches 322;
Sequence 3, Application US/09851896
Patent No. 6410325
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Fraier
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHC
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 56.0%;
Matches 431; Conservative
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ORGANISM: Homo sapiens
PEATURE:
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Factor No. 6558910

Factor No. 6558910

FAPTICANT: Adver, Charles S.

APPLICANT: Adver, On Elliot

APPLICANT: Adver, On Elliot

APPLICANT: Adver, On Elliot

APPLICANT: Mueller, Ken

APPLICANT: Hoon, Marx

APPLICANT: The Regents of the United States of America

APPLICANT: The Government of the United States of America

APPLICANT: The Government of the United States of America

APPLICANT: The Government of the United States of America

APPLICANT: The Government of Health and Human Services

TITLE OF INVENTION: SF, and No. 6558910el Family of Taste Receptors

TITLE OF INVENTION: 19900008

CURRENT FILING DATE: 1999-09-10

WINDERS OF SEQ ID NOS: 92

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 8

LENGTH: 1540
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US-09-393-634-8
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1115 ACCTGTTAGTTTCTCTGTGTGTTTAG-TTTCTGTTTCCATGATCTGTCCATTGATG 1173

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827 ATCTGCTTAGTTTTGGGTTTAAGTCTA-TTAGTCAGATATTAAAATGACTGTATCGGCTT

945 TAICCAIG---GIAGGIIGICITITIGGAIGCAGCAGTAGGAIGGAICTIGITITICAIA

1473

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Sequence 169, Application US/09220132

Patent No. 6506607

GENERAL INFORMATION:

APPLICANT: Shyjan, Andrew W.

TITLE OF INVENTION:

TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT

TITLE OF INVENTION: OF PROGRATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 07334-07401

CURRENT APPLICATION NUMBER: US/09/220,132

CURRENT APPLICATION NUMBER: US 60/079,303

PRIOR PILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-25

NUMBER OF SEQ ID NOS: 1912-24

NUMBER OF SEQ ID NOS: 1912-24

SEQ ID NO 168

LENGTH 5573

LENGTH 5573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
US-09-220-132-168
                                                 1002 TCCATT 1007
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Query Match 6.3%; Score 142.8; DB 1; Length 1540; Best Local Similarity 67.1%; Pred. No. 6.3e+02; Matches 286; Conservative 0; Mismatches 132; Indels 8;

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Sequence 9, Application US/09525160B
Sequence 9, Application US/09525160B
Sequence 9, Application US/09525160B
Sequence 9, Application US/09525160B
SETTING OF INVENTION WETHODS OF IMPROVING HOMOLOGOUS RECOMBINATION FILE REPERENCE: 10278/016001
CURRENT APPLICATION NUMBER: US/09/525,160B
CURRENT APPLICATION NUMBER: US/09/525,160B
SOFTWARE OF SEQ ID NOS: 10
SOFTWARE: FASTERQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/146,053A; CURRENT FILING DATE: 1998-09-02; EARLIER FILING DATE: 1997-09-02; NUMBER OF SEQ ID NOS: 7; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 4; LENGTH: 50000
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Patent No. 656681
Patent No. 656681
Patent No. 10 Color Sequenci
TITLE OF INVENTION: METHODS OF IMPROVING HOMOLOGOUS RECOMBINATION
FILE REFERENCE: 10278/016001
CURRENT APPLICATION NUMBER: US/09/525,160B
CURRENT PILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 11 NOS: 11 NOS: 11 NOS: 10 NOS: 11 NOS: 10 NOS: 11 NOS: 10 NOS: 11 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 
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Best Local Similarity 58.5
Matches 340; Conservative
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ORGANISM: Homo sapiens
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-09-525-160B-4/c
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LENGTH: 3213
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                                                                                                              RESULT 37
US-09-818-312-3/C
| Sequence 3, Application US/09818512
| Patent No. 6537780
| GENERAL INFORMATION:
| TILLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
| TILLE OF INVENTION: THEREOF
| TILLE OF INVENTION: THEREOF
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| TILLE OF INVENTION: THEREOF
| TILLE OF INVENTION: THEREOF
| TILLE REFERENCE: CLOO1192
| CURRENT APPLICATION NUMBER: US/09/818,512
| CURRENT FILLING DATE: 2001-03-28
| NUMBER OF SEQ ID NOS: 4
| SOGTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 3
| LENGTH: 116592
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5.1%; Score 116; DB 1; Length 11
Best Local Similarity 51.8%; Pred. No. 12;
Matches 565; Conservative 0; Mismatches 465; Indels
1544 GAATAT-TITITCCATCCCTITACCTTCAGTCTATATGTGTC 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 TAGTGAGTTGTTTGGTTTCCATAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; LCCATION: (1)...(116592)
; OTHER INFORMATION: n = A,T,C or G
US-09-818-512-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 510
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CTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGAATTGCAATGTCCTCTTGGTGGAT

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GTCTA-TTAGTCAGATATTAAAATGACTGTATCGGCTTGCTTCTTAGGGCCCATTTGCTTA

GAATAICTITICCAICCTITIACTCTAAGGTGAIGTCTAIC 948

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                                                                                       Gaps
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US-09-010-398-14

Sequence 14, Application US/09010398

Sequence 14, Application US/09010398

Sequence 11, Application

APPLICANT: An. Gang

APPLICANT: Veltri, Robert W.

APPLICANT: Veltri, Robert W.

TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,

TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
Length 38564;
                                                                                       9
                                                                                                                                                                                    TCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGTTTGG
                                                                                       Indels
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STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEADELIN PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,398
Score 115.3; DB 1;
Pred. No. 36;
); Mismatches 197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Corder, Timothy S.
REGISTRATION NUMBER: 38,414
REFERENCE/DOCKET NUMBER: URC:015
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          774 IGICCICITGGIGGATITICCITI
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    59.1%;
                                                                                                 Conservative
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STREET: P.O. Box 4433
CITY: Houston
                                                Similarity
                                                                                            298;
    Query Match
Best Local S
Matches 298
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Sequence 3, Application US/09734673

Patent No. 6410294

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1020
CURRENT PAPPLICATION NUMBER: US/09/734,673
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANIEN: Human
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(38564)
CTHER INFORMATION: n = A,T,C or G
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LENGTH: 38564
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Sequence 604, Application US/09702705; Patent No. 6504010; GENERAL INFORMATION:
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
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Best Local Similarity 59.2
Matches 218; Conservative
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ORGANISM: Homo s
FEATURE:
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US-09-702-705-604
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SEQ ID NO 604
LENGTH: 468
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Patent No. 6171796

GENERAL INFORMATION: An, Gang

APPLICANT: An, Gang

TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,

PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
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                                                                                                                                                                                                                                                                                                                      Length 8224;
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,260
FILING DATE: 03-Aug-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                  Score 108.3; DB 1; Length
Pred. No. 1.7e+02;
0; Mismatches 147; Indels
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ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
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**PRELICATION UNBER: 09/010,398
**FILING DATE: <UNKNOWN-)
ATTORNEY/AGENT INFORMATION:
                             INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 8224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 59.2
Matches 218; Conservative
512-474-7577
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US-09-366-260-14
TELEFAX:
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59.2%; Pred. No. 1.7e+02;
tive 0; Mismatches 147;
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APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR 'TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
NUMBER OF SEQ ID NOS: 1833
REGISTRATION NUMBER: 38,414
REFERENCE/DOCKET WUMBER: UROC:015
TELECOMMUNICATION INFORMATION:
TELEFAX: 512-418-300
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGHH: 8224 base pairs
TEMPER: mucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Panger, Gary
APPLICANT: Vacter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: 105/09/614,124B
CURRENT FILING DATE: 2001-07-11
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4.7%; Score 106.2; DB 1; Length 468;
Best Local Similarity 57.7%; Pred. No. 2.9e+03;
Matches 239; Conservative 0; Mismatches 171; Indels 4;
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 604, Application US/09614124B Patent No. 6630574
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LCCATION: (1) ... (468)
COTHER INFORMATION: n = A,T,C or G
US-09-614-124B-604
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ORGANISM: Homo sapien
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Vetvick, Tom
APPLICANT: Retter, Darrick
APPLICANT: Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Mang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: 1864
SEQ ID NO 604
LENGTH: 468
TYPE: DN"
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Pred. No. 2.9e+03;
0; Mismatches 171; Indels
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4.7%; Score 106.2; DB 1;
Best Local Similarity 57.7%; Pred. No. 2.9e+03;
Matches 239; Conservative 0; Mismatches 171;
) NAME/KEY: misc_feature

) LOCATION: (1)...(468)

) OTHER INFORMATION: n = A,T,C or G

US-09-702-705-604
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) LOCATION: (1)...(468)
) OTHER INFORMATION: n = A,T,C or
US-09-736-457-604
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Best Local Similarity 57.7%;
Matches 239; Conservative
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RESULT 45
US-09-589-184-604
IS-09-589-184-604
; Sequence 604, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
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; LOCATION: (1)...(468)
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US-09-589-184-604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marrick
APPLICANT: Retter, Marrick
APPLICANT: Fan, Lidgun
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
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TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION NUMBER: 105/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 604
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 604, Application US/09671325
Patent No. 6667154
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LCCATION: (1)...(468)

OTHER INFORMATION: n = A,T,C or G

US-09-671-325-604
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Patent No. 6667154
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 44
US-09-671-325-604
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                                                                       TGTGTGTGAG-GTCAATATGTGATTTTAGCTGTAGCTGTGCTTTTATGAACTTGGGT
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4.7%; Score 106.2; DB 1;
Best Local Similarity 57.7%; Pred. No. 2.9e+03;
Matches 239; Conservative 0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Warnich, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.479C8
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
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Search completed: August 25, 2004, 08:12:44 Job time: 3688 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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August 25, 2004, 08:14:16; Search time 4409 Seconds (without alignments) 3.936 Million cell updates/sec

US-10-664-775-4 2279

1 gatcactcctcagtgaaag...........tgtaattctaggtgctgat 2279 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

41 seqs, 3807569 residues Searched:

Total number of hits satisfying chosen parameters:

82

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

rnpb4.seq:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	G	-4 Sequence 4, Appli	equence 1,	Sequence 5,	Sequence 3,	77 Sequence 577	3 Sequence 166	29 Sequence 129	945 Sequence 194	80 Sequence 58(	Sequence 68!	90 Seguence 790	20 Sequence 720	7 Sequence 20	15 Sequence 119	7 Sequence 57,	0 Sequence 10,	71 Sequence 273	0 Sequence 10,	-223 Sequence 223	-224 Sequence 224	-682 Sequence 682	-720 Sequence 72(	-785 Sequence 78!	-808 Seguence 808	-547 Sequence 547	-1033 Sequence 103	7 Sequence 57,	029 Sequence 203	Sequence 58	1 Seguence 61,	9 Seguence 79, Ap	61 Sequence 1861
SUMMAKIES			64-775	64-775	64-77	-10-087-192	-10-087-192	69-214	87-192	-10-388-934	-10-388-934	-10-388-934	-10-191-803	-10-374-077	-10-322-281	-10-175-523	-10-003-806	-10-322-281	-10-003-806	-10-388-934	-10-388-934	-10-388-934	-10-388-934	-10-388-934	-10-388-934	-10-087-19	-10-087-192	-10-175-52	-10-087-192	-10-175-523	US-10-175-523	-10-175-523	-10-087-19
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6 5 3 55 1 9 5 3 55 9	Φ	B 1; -06; 0;	CCCAA'	gaaca'	VATAC
12-13 13-14 14-14 15-14 16-17 16-17 17-17	MENTS Recombinant 775 cation PA 2 6	.1 e	PAGGC 	TCTG 	1166C
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RESULT 3 US-10-664-775-5 Sequence 5, Application US/10664775 ; Publication No. US20040115776A1	ζγ Op	TGAAGTAGCCCACTATCTGTGTGTGAGGTCAATAT 
; GENBRAL INFORMATION: ; APPLICANT: Simesen, Ruth B ; APPLICANT: Pedersen, Anette A ; APPLICANT: Faisst, Steffen	QV Ob	721 TTTTATGAACTTGGGTGACATTGTGTTTTGGTGCATAGACATTAAGAATTGCAATGTCCTC 780 
<pre>; APPLICANT: Jensen, Jan J ; APPLICANT: Wellyuny, Dietmar ; TITLE OF INVENTION: Method for Making Recombinant Proteins ; FILE REFERENCE: 6448.200-US</pre>	Qy Db	781 TTGGTGGATTTTCCTTTGATGCCTA1GTAGTATTCTTCCCAATCTCATCTGCTTAGTTTT 840
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Publication No. US20040115776A1
GENERAL INFORMATION:
APPLICANT: Simesen, Ruth B
APPLICANT: Pedersen, Anette A
APPLICANT: Pedersen, Anette A
APPLICANT: Pedersen, Anette A
APPLICANT: Pedersen, Anette A
TITLE OF INVENTION: Method for Making Recombinant Pro;
FILE REFERENCE: 6448.200-US
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/416,566
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                                                                                        Sequence 577, Application US/10087192
| Fublication No. US20020182586A1
| GENERAL INFORMATION |
| APPLICANT: MORTIS, David W. |
| APPLICANT: Engelhard, Eric K. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVER: US 09/10/087,192 |
| CURRENT FILING DATE: 2000-02.03-01 |
| PRIOR PILING DATE: 2000-12-22 |
| PRIOR APPLICATION NUMBER: US 09/747,377 |
| PRIOR APPLICATION NUMBER: US 09/798,586 |
| PRIOR FILING DATE: 2010-03-02 |
| NUMBER OF SEQ ID NOS: 2059 |
| SEQ ID NOS: 2059 |
| SEQ ID NOS: 2159 |
| LENGTH: 41219
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65.8%; Pred. No. 1.8;
tive 0; Mismatches 476;
1981 TCTTCAAGGACCTTTTATGAATT 2003
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; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-577
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Best Local Similarity 65.8
Matches 1223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mus musculus
                                                                             JS-10-087-192-577
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Oy 1765 TIGGITITIGCATAGIGICICCIGGAIGITITIATGCCTGGAITATITIAGACT 1824  Db 153654 TIGGICTICATIGACCAGGITICCIGGAIGITITIAGATAGGAICTITIAGAT 153713  Oy 1825 TAACATITICATIGACCAGGIAICCATTCATCAGTAGTAGGAICTITIAGATT 153713  Oy 1885 TCCTTCTATCATTGACCAGGIAGATACTTCATCAGAATCTCAGGATTC 1884  Db 153714 TICCATTTTATCATTGACTAGAGGATACTCAGAGATTCAGGATTC 153773  Oy 1944 TIAATTTTTCATTCCAGATTCCTTCAGTTGAGGATCTCAGGATTC 153833  Oy 1944 TIAATTTTTCATTCCAGATTCCTTCAGTTGAGGATCTCTTCTTCAGGATTC 153833  Oy 2004 CTTTCAGGATTCCAGATTTCCTTCAGTTTGGATTCTTTTTTTATTCTATTCCA 153833  Oy 2004 CTTTCAGGACTTTAACTCCATTTACTCATTTCTTTTTTTT	RESULT 7 US-10-369-114-129/C  i Sequence 129, Application US/10369214  i Sequence 129, Application US/10369214  i Sequence 129, Application No. US20030232037A1  i GENERAL INFORMATION:  i APPLICANT: Genes involved in immune related responses observed  i TITLE OF INVENTION: Genes involved in immune related responses observed  i TITLE OF INVENTION: With asthma  i TITLE OF INVENTION: With asthma  i TITLE OF INVENTION: WINBER: US/10/369,214  CURRENT APPLICATION NUMBER: BF 00202867.8  PRIOR FILING DATE: 2000-08-16  i PRIOR FILING DATE: 2000-08-16  i PRIOR FILING DATE: 2010-08-16  i PRIOR FILING DATE: 2010-08-16  i ROGANISM: Mus musculus  reature:  i CATTURE: DNA  i CREATURE:  i NAME/KEY: misc_feature  i COTHER INFORMATION: //10-619)  i OTHER INFORMATION: //10-619	Query Match
100 TGTAGCTGTGCTTTATGAACTTGGGTGACATTGTGTTTGGTGATAGACATTAAGA 766 152656 TTTACTAAAGTTCTTTAATGAACTTGGGTGCCTTGTTTTGTGGATAGAATTCAGA 152715 767 ATTGCAATGTCTCTTTAATGAATTT-CCTTTGATGCTTATTGAAGTTGCCTTGTTCTTCCCAATCT 825 152716 ATTGATAGTTCTCTTGGGGATTTTACCTTTGATGAATATAAAGTGATTTCTTCCCAATCT 15275 826 CATCTGGTTAGTTTTGGGATTTTACCTTTGAAATAAATAGATATAAAATGACTGTATCGGT 152835 152776 TTTTTGATGATTTGGTTGGAATATTAATAAGATATAAAATGACTGTATCGGT 152835 885 TGCTTCTTAGGGCCATTTGCTTAGAATA-TCTTTCCAACTTTACTCTAAGGTGATGT 943 152836 TGCTTCTTAGGGTTGGAAAATTTTATTAGATATAACTTCTAAGGTGATGT 152895 944 CTATCCATGGTAGGTTGGAAAATTTTCTTCCATCTTCTTTCATTCATT	1061 TGAGAATTATCAATGAGCAGTGTTTGTGCATTCTTGCACTTGTGAAGTGTGT 1120 153008 TAAGAGATATTAAGGAAAAGTAATTGTTGTTGCTGTTGTTTTTTTT	1479 TCTATTGGAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATTGTTAATTGGTCTTT 1538  153356 TCTGGT GAAAATTCTGATAGGCTTGCCTTTATTATTTTTTTTTT

92208	Sequence 580, Application US/10388934 Publication No. US20040005547A1 GENERAL INFORMATION: APPLICANT: Boess, Franziska APPLICANT: Surer-Dick, Laura APPLICANT: Wolf, Detlef APPLICANT: Wolf, Detlef TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
15.1-10-1588 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	<b>ω</b> Δυ · · · · · · · · · · · · · · · · · ·
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Pred. No. 5.8;
0; Mismatches 560;
FILE REFERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
FRIOR APPLICATION NUMBER: 02005336.9
FRIOR FILING DATE: 2002-03-14
FRIOR APPLICATION NUMBER: 02015657.6
FRIOR FILING DATE: 2002-07-17
FRIOR FILING DATE: 2002-07-17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 580
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.7%;
Matches 1173; Conservative
                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Rattus norvegicus
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US-10-388-934-580
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APPLICANT: Suter-Dick, Laura
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, DetLeb
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
TITLE REFERENCE: 21199
CURRENT APPLICATION NUMBER: 02014
PRIOR PILING DATE: 2003-03-14
PRIOR PLICATION NUMBER: 02005336.9
PRIOR PLICATION NUMBER: 02015657.6
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PRIOR PRIOR DATE: 2002-07-17
SOFTWARE: PARENTIN VERSION 3.1
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                                                 Sequence 685, Application US/10388934 Publication No. US20040005547A1 GENERAL INFORMATION:
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1126	ULT 12  10-191-803-720/c iequence 720, Application US/10191803  iequence 720, Application US/20191803  wbbication No. US20040014040a1  APPLICANT: MENDRICK, Donna  APPLICANT: PORTER, Mark  APPLICANT: GASTER, Mark  APPLICANT: CASTER, Mark  APPLICANT: CASTER, Mark  APPLICANT: CASTER, Mark  APPLICANT: CASTER, Mark  APPLICANT: CASTER, Mark  APPLICANT: CASTER, Mark  APPLICANT: CASTER, Mark  TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling  FILE REFERENCE: 44921-5090US  FURENT APPLICATION NUMBER: US 60/303,819  PRIOR PELING DATE: 2001-07-10  PRIOR PELING DATE: 2001-07-10  PRIOR PELING DATE: 2001-07-17  PRIOR APPLICATION NUMBER: US 60/369,351  PRIOR PILING DATE: 2002-04-03  PRIOR APPLICATION NUMBER: US 60/369,351  PRIOR PILING DATE: 2002-06-06  SOFTWARR: PARCHELIN VENTER: 1140  SOFTWARE: PARCHELIN VENTER: 2010-07-10  BRIOR PILING DATE: 2002-05-06  SOFTWARE: PARCHELIN VENTER: 1140  SOFTWARE: PARCHELIN VENTER: 2010-07-10  ENGO 720  LENGTH: 6335	TYPES DNA MARCHUS norvegicus PERTURE: ODRGANISM: Rattus norvegicus FEATURE: ODRGANISM: Rattus norvegicus FEATURE: ODRGANISM: Genbank Accession No. US20040014040A1 X53581  10-191-803-720  25.8%; Score 588.5; DB 1; Length 6335; Batches 1173; Conservative 0; Mismatches 560; Indels 137; Gaps 18; Batches 1173; Conservative 0; Mismatches 560; Indels 137; Gaps 18; C292 TCTATTCTTCTATCTATCTTGGCTCATTTTTAACTCAGTAGTGGTTGTTTGGTTTCC 2536  1

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Oshima, Junko
Wulligan, Junko
Wulligan, John T.
Schellenberg, Gerald D.
INVENTION: ANTIBODIES AGAINST GENE PRODUCTS RELATED
WERNER'S SYNDROME
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UGA.

ZIP: 98104-7092

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA: US/10/374,077
FILING. DATE: 25-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 207, Application US/10374077; Publication No. US20040006779A1
GENERAL INFORMATION: APPLICANT: Fu, Ying-Hui
                                                                                                                                      TATTTTCCCTGCTTTTGACCTG
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Pred. No. 3;
0; Mismatches 567;
                     NAME: Rosenman, Stephen
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 100107,401D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        207:
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear seq ID NO: US-10-374-077-207
                                                                                                                                     TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     LENGTH: 29604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 62.9%;
Matches 1170; Conservative
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TYPE: DNA
ORGANISM: Mus musculus
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  US-10-322-281-115
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                                                                            APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Met
FILLE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SEQ ID NO 115
Sequence 115, Application US/10322281 Publication No. US20040126762A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(289190)
OTHER INFORMATION: n = A,T,C or G
US-10-322-281-115
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	RESULT 16 US-10-003-806-10/C US-10-003-806-10/C Sequence 10. Application US/10003806 POUDIcation No. US20020119929A1 GENERAL INFORMATION: APPLICANT: Bishop, Colin E. APPLICANT: Alexander I. APPLICANT: Alexander I. APPLICANT: Alexander I. APPLICANT: Alexander I. APPLICANT: Alexander I. APPLICANT: Solu Colina C. TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY FILE REFERENCE: 2002-6021/10024824 CURRENT FILING DATE: 2001-11-02 PRICR FILING DATE: 2000-11-03 NUMBER: OF SEQ ID NOS: 14 SEQ ID NO 10 SEQ ID NO 10 SEQ ID NO 10 SEQ ID NO 30 CORGANISM: Mouse US-10-003-806-10	Query Match Best Local Similarity 62.8%; Pred. No. 1.4; Matches 1168; Conservative 0; Mismatches 569; Indels 123; Gaps 18; Matches 1168; Conservative 0; Mismatches 569; Indels 123; Gaps 18;  Qy 292 TCTATTTCTTATTCTTACTTGCTCATTTTAACTCAGTAGTGTTTTACTTCAGTTCC 123573  Qy 352 ATAAGTTTCTTATTCTTCGTTGTTCTTTGTTGTTTATTCAGTTTCTTTAACTCAGTTCC 123573  Qy 412 GGTGGTCAGATGTTTCTTTATTTGTTATTGTAATTCTGTCGAGTTCTTTAAGTCTCT 411  Db 123572 ATGGAATGTTTCTTTATTTGTTATTGTAATTCTGTCGAGATTTCAGTTTC 123516  Qy 412 GGTGGTCAGATAGGACAATTGAATTTTTTTTTTTTTTTT
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Qy         1719 TJ           Db         122284 TJ           Qy         1765 TJ           Db         122224 TJ           Qy         1825 TJ           Qy         1885 TJ           Qy         1885 TJ           Qy         122164 TJ           Qy         1944 TJ           Qy         2004 CJ           Qy         2004 CJ           Qy         2061 TJ           Qy         2061 TJ           Db         121984 TJ           Db         121924 TJ	RESULT 17 US-10-322-281-27 Sequence 271, Publication No. SCHERAL INFORM SCHELL INFORM HELE REPERENCY CURRENT APPLICANT: CURRENT APPLICANT: CURRENT APPLICANT: CURRENT APPLICANT: SOFTWARE: Faz SOFTWARE: Faz SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWARE: No. SOFTWAR
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) CTHER INFORMATION: n FEATURE: NAME/KEY: misc feature LOCATION: (3503)(3503) COTHER INFORMATION: n US-10-388-934-223	Query Match 25.4%; Score 578.2; DB 1; Length 8048; Best Local Similarity 62.0%; Pred. No. 5.8; Matches 1160; Conservative 0; Mismatches 574; Indels 136; Gaps	OY 292 TCIATTTCTTGATTTCTATCTTGGGTCATTTTTAACTCAGTAGTGGGTTGGTT		DD   3215 GGTGGTCCGATAGGATTATTTTTTATCTTTCTGTACCTGTTGAGGCCCGTTT 3156	530 AGTCTTTGTGTTTTGGGGAAAAGTCTGGAATATCTCTAGGTCCACTTGGTTTATGA 587 3095 ATCTTTTGCTTTTAGGAAAAATTTCTAAAAATATCCGTTAGGTCACTTGGCTTATGA 3095	588 CATCAGTTAGCTCCAGCATTTCTCTGTTTCGTTTTTTTTT	Oy 648 GAGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGTGAGGT-CAATATGTGATTTTAGC 706	Oy 707 IGTAGCIGIGCITGITITATGAACTIGGGIGACATIGIGITITGGIGCATAGACATTAAGA 766  Db 2916 ITTAGIAAGGITICTTITACGIAIGTAGGIGCCCTIGIATTIGGGGCATAGATATTAGG 2857	Qy 767 ATTGCAATGTCCTCTTGGTGGA-TTTTCCTTTGATGCCTAAGTAGTACTCTTCCCAA1CT 825	TCGGCT         CCAGCT	Qy 885 IGCITCTIAGGCCATTIGCITAG-AATAICTITICCATCCITTIACTICTAAGGIGAIGT 943	Qy 944 CTATCCATGGTAGGTTGTCTTTTTTGGATGCAGCAGTAGGATGGATCTTGTTTTCAT 1000  Db 2676 CTGTCTTTGTCTCTGAGGTGTTTCCTGTAGGCAGCAGAATGCAGGGTCCTCGTTGTGT 2617	QY 1001 ATCCATTCTGTTACCAGTATCTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGT 1060	QY 1061 TGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTGTGT 1120	Qy         1121         GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	Qy 1181 GTGTGTGTGTGTGTGTGTGTTCTCCCCCTCTTTTGGTTTTTGGCCTGGAATTAT 1240

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PROFILES

EXPRESSION

APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
FILE COFINVENTION: BIOWARKERS AND EXPRESSIO
FILE REPERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: Patentin version 3:1
SEQ ID NO 224
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Query Match
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CRGANISM: Rattus norvegicus (No. US20040005547Alway rat ORGANISM: Rattus norvegicus (No. US20040005547Alway rat FEATURE: MANEKEY: misc feature I.OCATION: (2005)...(2005) OTHER INFORMATION: n FEATURE: NAMEKEY: misc feature ; LOCATION: (3503)...(3503) ; CCATION: (3503)...(3503) ; UCATION: (3503)...(3503)

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US-10-388-934-720/C
i Gequence 720, Application US/10388934
i Publication No. US20040005547A1
sequence 720, Application US/10388934
i Publication No. US20040005547A1
i GENERAL INFORMATION:
    APPLICANT: Boess, Franziska
    APPLICANT: Boess, Franziska
    APPLICANT: Wolf, Detlef
    TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
    FILE REFERENCE: 2199
    CURRENT PAPLICATION NUMBER: US/10/388,934
    CURRENT FILING DATE: 2003-03-14
    PRIOR FILING DATE: 2002-03-14
    PRIOR PLICATION NUMBER: 02015657.6
    PRIOR FILING DATE: 2002-07-17
    NUMBER OF SEQ ID NOS: 862
    SOFTWARE: Patentin version 3.1
    SEQ ID NO 720
    LENGTH: 8048
    TYPE: DNA
    ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)
    COCATION: (2005)...(2005)
    COTHER INFORMATION: n
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    NAME/KEY: misc feature
    LOCATION: (3503)...(3503)
    COTHER INFORMATION: n
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Sequence 755, Application US/10388934

Sublication No. US20040005547A1

GENERAL INFORMATION:

APPLICANT: BOES: Franziska

APPLICANT: Wolf, Detlef

ITILE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY

FILE REPERENCE: 21199

CURRENT APPLICATION BIOMARKER: US/10/388,934

CURRENT APPLICATION NUMBER: US/10/388,934

CURRENT APPLICATION NUMBER: 0203-03-14

FRICH FILING DATE: 2002-03-14

FRICH FILING DATE: 2002-07-17

FRICH FILING DATE: 2002-07-17

SOFTWARE: PALENTING DATE: 2002-07-17

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Fublication No. U820040005547A1
GENERAL INFORMATION:
APPLICANT: Boess.
APPLICANT: Boess.
APPLICANT: Boess.
APPLICANT: Wolf. Detlef
TITLE OP INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
FILE REFERENCE: 2119
CURRENT PEPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-033-4
PRIOR PLING DATE: 2002-03-14
PRIOR PLING DATE: 2002-03-14
PRIOR PLING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: Patentin version 3.1
SEQ ID NO 808
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ORGANISM: Rattus norvegicus (No. US20040005547Alway
PEATURE:
NAME/KEY: misc_feature
LOCATION: (2005)...(2005)
FEATURE:
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COCATION: (3503)..(3503);
CTHER INFORMATION: n
US-10-388-934-808
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RESULT 24 US-10-388-934-808/c : Sequence 808, Application US/10388934

TITITGATGACTITITAGTIGGAAATIGATITTATITGATATIAGAATGGCTACTCCAGCT 826 CATCTGCTTAGTTTTGGGTTTAAGTCTA-TTAGTCAGATATTAAAATGACTGTATCGGCT

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1827 1767 36125 1887 2006 2063 412 472 35945 TYPE: DNA д 8 8 g 8 8 ò à ò g ò g ò 셤 ठे a ò 37114 TTTACTAAAGTTTCTTTAATGAATGTGGCTGCATTTGCATTTGGAGCATAGATATTCAGA 37055 36877 cherchranecergaderdeerhrecheraacadekaaarernegereerdrinener 36818 36673 TIGATAACITIGGGIIGGAAGICAAT ---TITAIIIGATATIAGAAIGGCIACICCAGCI 36938 ------TTAAAGGAT 36664 36663 AACTITCITGCTITITCIAGGGIGIAATITCCAICITIGGGITAGIGITITCCCTTIAIT 36604 36543 ACTITICATITICICCATCIAIGGIAATIGAGAGITITGGCIGGGIATAGIAGCCIGGGCIGG 36484 36483 AATTIGIGITCTCTTAGIGICIATAACAICIGICCAGGAICTICIGGCITTCAIAGIC 36424 ATCCATTCTGTTACCCAGTATCTTTTTCTAGAGAAATTAAGATCATTGAGGTCATTGATGT 1060 TGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTGTGT 1120 1241 TTATTATTCATATTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGC 1300 1359 GTCTTTCTTTCTCCCAACTATTGTGACAGAAGTTTTTTTAAGTGCAGTAGTCTGGCCTGA 1418 CATCTGTAGTCTCTTGGAGTCTGTAGCACATCTGTGCAGGCCTTCTTACATTTTGAGTT 1478 ---GCCTTCTTCCCTTCTTATTCCTTT 1766 ATTGCAATGTCCTCTTGGTGGATTTT--CCTTTGATGCCTATGTAGTATTCTTCCCAATC TCATCTGCTTAGTTTTGGGTTTAAGTCTATTAGTCAGATATTAAAATGACTGTATCGGCT CTATCCAT - - - GGTAGGTTGTCTTTTTGGATGCAGCAGTAGGATGGATGTTTTTCAT TGCACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGGTGTTTTGTATGCTTCTTGTA 1181 GIGTCTGTGTGTGTGTGTGTTCTCTCCCCCTCTTTTGATTTTTGGCCTGGAATTAT CTICITI - - AGGICTGCATTTGAAGATAGATATTCTTTACATCTGATTTTATCTTAGAAT 1539 TITCCCTIGCATCTTTAATATTCTTTGTTCTATACTTTTAGTGATTTGATTATTA TCTATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATGTTAATTGGTCTTT 36705 Arciditorrandecrerorrorrangerrage-36672 ------TATITICCCIGCITITIGACCI;-167 825 944 36817 1301 707 36994 1001 1001 1479 1599 1719 셤 8 & B gg g 8 6 쉽 ò 셤 ያ ያ ያ ò 8 8 8 δ 6 8 9 8 8 8 8 8 8 g ò

157369 157426 36006 35946 35886 36185 TATTTGCTGGCCCTTTAAGTTAAATCTTCATTCTCATCTACTACTATTATCCGTAGGTTT 36126 471 TGTTTTGAAATATGTATTCAATTTTGGAG--AGTTTCATAGGGTGCTGACAAGAAGGTAC 529 36065 ACATITICALIGATIGATATATCCATGCTCCCTATGGAATCTICTGCACCTGAGATTCTC TTCAGGTCCTGAAATGTTTTACTCATTTTTCCT----CCCAGTATTTACATTTTCATAGGTT AGGGTTTCTATCTCCAGAGTTGTCTTCCTTTGGGTTTTCTTCATTGTTTCTACTTCTATT 157315 TITCTITCTIAATTICCTAACTAATTIC----AGAGTAGAGAGTIGTICAGTTICC ACATTITICITIGACCAAGGIAICCAITICITCIAICTICITCITCACIGCCIGAGAITCIC 1946 AATTITICATTICCAGATITCCTICAGTITGGGTTTTGTTTATTAATTCTATTTCCACT 157370 ACGTGTATGTGGGCTTTTTTGTCGTTTTTTGCTGTTATTAATGA----CCAGCCTTAAGCCAT GGTTTTTGCATAGTGTCTCTGGCTTCCTGGATGTTTTATGCCTGGATTATTTAGACTTA 157427 GGTGATCTGGATGCATGGATTATTTCTGTCTTCTTGTATCTGTTTAGGGTTGTTT 292 ICTATITICITICATITICIATICITIGCCICATITITIAACTCAGTAGTGGTTGTTTGGTTTCC 352 ATAAGITTGTAAGITTTCTGTTGTTGTTGTTGTTGTTATCTAGATTTAAGCTGT GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGAGACTTGCTT 126; Gaps Length 200400; Indels US=U0-07-192-1033
; Sequence 1033, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: CANCEL COMPOSITIONS AND METHODS FOR;
; TITLE OF INVENTION: CANCEL COMPOSITIONS AND METHODS FOR;
; TITLE OF INVENTION: CANCEL COMPOSITIONS AND METHODS FOR;
; CURRENT FILING DATE: 2001-22
; CURRENT FILING DATE: 2001-12-22
; PRIOR FILING DATE: 2001-03-02
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2069
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1030 Query Match 25.2%; Score 573.4; DB 1; Best Local Similarity 63.4%; Pred. No. 1.5; Matches 1164; Conservative 0; Mismatches 546; 35825 TCTTTAAGGGATTTTTGTGTTTCTTCTAC 35797 ICTITAATGGATITATTCATTTCCTCTTC 2091 NAME/KEY: misc\_feature | LOCATION: (1)...(200400) | OTHER INFORMATION: n = A,T,C or G US-10-087-192-1033 ORGANISM: Mus musculus

157487 TGTGACCAATTATATGGTCAGTTTTGGAGAAAGTACCATGAGGTGCTAAGAAGAGGTGT 157546 530 AGTC-TTTGTGTTTTGGTGAAATAGTCTGTAAATATCT-CTAGGTCCACTTGGTTATGA 587	Qy 1601 CACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGGTTTTGTTATGCTTCTTGTACC 1660
ATTCTTTTGTTTTAGGGGGAATGTTCTATAGATATCTGTTAAATCGTTTGGTTCATAA	1720
588 CATCAGTIAGCICCAGCATITCTCTGTTTTTTTTTTTTGGATGACCIAACTGTIGGA 647 	Db 158599 TTTATGGCCACTTCTTCTTCAGGTGGGGAAGTTTTCTTCTATGATTTTGTTGAAGACA 158658
648 GAGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGT-GAGGTCAATATGTGATTTTAGC 706	1/21 IIIICCIGIIIIIGCIG 186659 TITITAGGICCTTICAGAIGGGAACCTTCATTCCCTCTATTCCAATTATTCTTAGATTT
707 IGTAGCIGTGCTTGTTTTATGAACTTGGGGACATTGTGTTTGGTGCATAGACATTAAGA 766 	1767 GGTTTTTGCATAGTCTCTCTGCATGTTTAGGCTTGCGGATGTTTTAGGCTTGCATGTTTTGCATGTTTTGCATGTTTTGCATGTTTTGTAGTTTTGTAGTTTTGTAGTTTTGTAGTTTTGTAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGTAGAGGTTGGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGTAGGTTGGTAGGTTGTAGGTTGTAGGTTGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTTGGTAGGTAGGTAGGTTGGTAGGTAGGTAGGTTGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGT
767 ATTG-CAATGTCCTCTTGGTGGATTT-CCTTTGATGCCTATGTAGTATTCTTCCCAATC 824	н
825 TCATCTGCTTAGTTTTAGGTTTAAGTCTA-TTAGTCAGATATTAAAATGACTGTATCGGC 883 	1887 TCTTCTATCTCTTGTATTCTGTGAGGGGGTTGTCTGAGGTGGTTCTGGGGTTGTGTTGTTGTTGTTGTTGTTGTTGT
884 ITGCTTCTTAGGCCATTTGCTTAGAATATCTTTTCCATCCTTTTACTCTAAGGTGATGT 943	1946 AAIITIICATIICAANICAAAATIICAAAAAAAAAAAAAA
944 CTATCCATGGTA-GGTTGTCTTTTTGGATGCAGCAGTAGGATGGATGTTTTCATAT 1002	2006 TTCAGGTCCTCAAATCTTTACTCATTCCCCCCAAATTACTAGATTTCTTCTTCTTCTTCTTTTCTTTTCTTTTCTTTTCTTTT
1003 CCATTCTGTTACCCAGTATCTTTTCTAGAAAATTAAGATCATTGAGTCATTGATGTTG 1062 	OY 2066 THATIGGATHATICATITICATION 2101  DD 159015 THCAGGAGTHATTAATAICCICCTTTAAGGACTGT 159050
1063 AGAATTATCAANGAGCAGTGTTTGTGATTCTTGTTATCTTGCACTTGTGAAGTGTGT 1122 	RESULT 27 US-10-175-523-57 ; Sequence 57, Application US/10175523
1123 GIGTGIGTGIGTGIGTGIGTGIGTGIGTGIGTGIGTGIG	; PUDICACION NO. USZUGOSOZOWAI; GENERAL INFORMATION; APPLICANT: Brockman; Jeffrey; APPLICANT: Evans, David;
1183 GTCTGTGTGTGTGTGTGTCTTCTCCCCCTTTTGATTTTTGGCCTGGAATTATT 1242 	; APPLICANT: Hook, Desek ; APPLICANT: Kimczak, Leszek ; APPLICANT: Laeng, Pascal ; APPLICANT: Laeng, Michael ; APPLICANT: Pailreyman, Michael
1243 ATTATTCATATTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGC 1300 158181 ATATCTTGTCCTTTCTAGGTGCAGATATCTCTTCTTGAGTTTTCCTTCTAGGAT 158240	# AFPLIANI
1301 CITCTIAGGICTGCAITIGAAGAIAGATATICTITACAICTGAITTIATCTIAGAATGT 1360 	FRIOR APPLICATION WINNER: US 60/299,151  PRIOR FILING DATE: 2001-06-18  PRIOR FILING DATE: 2001-06-18  PRIOR FILING DATE: 2001-06-18
1361 CTTTCTTTCTCCAACTATTGTGACAGAAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGACA 1420 	FAIOR FILLING DATE: 2001-09-25  PRIOR FILLING DATE: 2001-09-25  PRIOR FILLING DATE: 2001-09-25  PRIOR FILLING DATE: 2001-1333,047
1421 TCTGTAGTCTCTTGGAGTCTGTAGCACATCTGTGCAGGCCCTTCTTACATTTTGAGTTTC 1480	FAIOT FILLING DATE: 2002-01-18 ; PRIOR APPLICATION WINBER: US 60/349,936 ; PRIOR FILING DATE: 2002-01-18 ; PRIOR APPLICATION WINBER: US 60/361,834 ; DELIOP FILING DATE: 2002-03-04
. 1481 TATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTATATGTTAATTGGTCTTTTT 1540 	, NUMBER OF SEQ ID NOS: 197 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 57 
1541 TCCCTTGCATCTTTAADATTCTTTGTTCTATACTTTTAGTGATTTGATDATTAG 1600 	; TYPE: DNA ; CRGANISM: Mus musculus US-10-175-523-57.

173066 CTTTCTTGCTTGTTCTAGGGCGTGATTTCCGTCCTTGTATTGCTTCTTTTCTGTTATTAT 173125 172530 172531 AAGTGGTGTGTTGAAGTCTCCCACTATTATTGTGTGAGGTGCAATGTGTGCTTTGAGCTT 172590 172591 TACTABAGTGTCTTTAATGAATGTGGCTGCCCTTGCATTTGGAGCGTATATATTTAGAAT 172650 reagagricarctriceaegarrirraccarreaegarareaegrerecerecererer 172710 172770 172831 GICTTTTTCCCTGAGATGGGTTTCCTGTAAGCAGCAGAATGTTGGGTTCTGTTTGTGTAG 172890 -----TCCATTGATATTA 172942 173036 ----TrititititidGTTTGTTGAGGGATTA 173065 172351 172412 CCTTTTGTTTTAGGATAAAACGTTCTGTAGATATCTGTCAGATCCATTTGTTTCATAACT 172471 172352 TGACCAATTATATGGTCAATTTTTGGAGAAGGTCCTGTGAGGTGCTGAGAAGAATTTATAT 172411 172175 TTTTTCATTATTCCTTCCTTGACCAAGGTATCATTGACAAGAGTGTTGTTGTTCAGTTTCCAT 172234 GICTGTGTCTTGTGTGTGTGTGTTCTCTCCCCCTTTTTGATTTTTTGGCCTGGAATTATTT 1242 ATCCAT --- GGTAGGTTGTCTTTTTGGATGCAGCAGTAGGATGTTGTTTTTCATAT 1002 CCATTCTGTTACCCAGTATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGTTG 1062 19; 886 473 413 GAATGGGGTATTGAAGTAGCCCACTATCTGTGTGTGAGGT-CAATATGTGATTTTAGCTG 708 172472 TCTGTTAGTTTCACTGTGTCCTTGTTTAG-TTTCTGTTTCCATGATCTGTCCATTGTAGA 1243 ATTATICATATITICITGAATGIGGGTAACATCTITAGATTGAAGTITTTCTCCTAGCCT 172292 TGGTCTGATAGGATACATGGGACAATTTCAATATTTTTGTATCTGTTGAGGCCTGTTTTG TCTGCTTAGTTTTAGGTCTA-TTAGTCAGATATTAAAATGACTGTATTGGCTTG TGGTCAGATAGGACATAGAGTATTATTTTCAATTGTCTTTTATCTGTCGAGACTTGCTTTG TITIGAAATAIGIATICAATITIGGAGA - GITICATAGGGIGCIGACAAGAAGGIACAG TC-TTTGTGTTTTTGGTGAAATAGTCTGTAAATATCTCT-AGGTCCACTTGGTTTATGACA TCAGTTAGCTCCAGCATTTCTCTGTTTCGTTTTTTTTGTTGAGATGACCTAACTGTTGGAGA TAGCTGTTTTTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGAAT TGCAATGTCCTCGTGGTGGATTTT-CCTTTGATGCCTATGTAGTATTCTTCCCAATCTCA CTTCTTAGGGCCATTTGCTTAGAATA-TCTTTTCCATCCTTTTACTCTAAGGTGATGTCT 294 TATTICITGALITICIATCITGGCICALTITITAACTCAGIAGIGAGITGITIGGITICCAT 354 AAGITIGIAAGITITICIGITGITICIGITGITGITGITGITATCIAGAITITAAGCIGIGG Indels 101; Gaps Length 225883 cicircriciccciciriririririririri Score 572.9; DB 1; Pred. No. 1.4; 0; Mismatches 596; 172891 CCAGTCTGTTAGTCTATGTCTTTTATTGGGGAATTGAG 25.1%; Query Match
Best Local Similarity 62.7
Matches 1171; Conservative 650 887 946 1003 1183 532 290 709 169 172651 828 1063 172943 1123 474 172711 .73003 173037 414 8 8 g q 상 원 ò d  $\delta$ g 8 8 ò g ò Dp ò a ò g ò g ò g ò g S S S ò දු දු à

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Sequence 2029, Application US/10087192

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Sequence 2029, Application US/10087192

SETILATION OF US COMPOSITIONS OF US COMPOSITIONS OF US TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER

FILE REPERENCE: 52945200122

CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT FILING DATE: 2002-03-01

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Pred. No. 2.1;
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PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2029
                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(95982)
CTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 62.3%;
Matches 1158; Conservative (
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                                                                         APPLICANT: BLOCKMEN, VELLEY
APPLICANT: BLOCKMEN, VELLEY
APPLICANT: Hook, Derek
APPLICANT: Klinczak, Leszek
APPLICANT: Klinczak, Leszek
APPLICANT: Rajan, Pithi
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APPLICANT: Rajan, Pithi
ETIE REFERENCE: 3235/1J795-US3
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,151
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-25
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PRIOR FILING DATE: 2001-11-14
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Pred. No. 1.4;
0; Mismatches 580;
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Best Local Similarity 62.2%;
Matches 1157; Conservative (
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; ORGANISM: Mus musculus
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237046 236772 236712 236592 236532 236414 236926 236874 236474 236234 236114 236783 236354 236294 1240 1418 1120 1478 1598 1718 1658 1824 TAACATTITICITIGACCAAGGIATCCATTICITATCTTGTCTTCACTGCCTGAGATTC 1884 943 AGCCAGTTTGTTAGTCTATGTCTTTTCATTGGGGAGTTGAG------TCCATTGATAT TGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTGTGT rciggi-daaaarciggigiaarrcigaraggcrigccirrarargiracri-gaccri CTATCCAT --- GGTAGGTTGTCTTTTTGGATGCAGCAGTAGGATGTTTTTTCAT TAAGAGATATTAAGGAAAAGTAATTGTTGCTTCCTGTTATTTTTGTTGTTAAAGTTGGCA ----TTGAGGGAT arcciticaaccecicatriccicacacacataarcccicaatriacititurcceccaar CCTTGATAGGCATCTCTTTCTCAAGGTTAGGAAATTTTTTCTTTTTGGTTTTTCTTGAAAA rerrearesecarerrirrrasarrrassas arrirrerrana arrirrarranda renderas reirirecrescriridaerreaaarcrrcarrcrcarccacrecrarrarcrerager crarctritricicadardacitriccidraaddadaaaarritgdgricrigirgricri TTATTATTCATATTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCCTAGC CTICITI - - AGGICTGCATITGAAGATAGATATTTTTTTACATCTGATTTTATCTTAGAAT actritectritetecheraliceratricadadeniecereciariatadadeerec 236591 AATTTGTGTTCTCTTACTGTCTGTATAACATCTGTCCAGGCTCTTCTGGCTTTCATAGTC rrrccerrgcrecrirragrarrcrarcrirarrragecarrraargricrgarrarra TTGGTTTTTTGCATAGTGTCTCTGGCTTCCTGGATGTTTTATGCCTGGATTATTTTAGACT riggiciirciyarigigiçerganrirecigangirirganınaganerriringearr 237105 TTTTTTATTATTTTGGGTTGGAAGTCAATTTTGTTAGATGTTAGAATGGCTACTCCAGCT TGCTTCTTAGGGCCATTTGCTTAGAATA-TCTTTTCCATCCTTTTACTCTAAGGTGATGT GTGTCTGTGTGTCTGTGTCTGTGTTCTCTCCCCTCTTTTGATTTTTGGCCCTGGAATTAT CATCTGTAGTCTCTTGGAGTCTGTAGCACATCTGTGCAGGGCCTTCTTACATTTTGAGTT TCTATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATATTAATTGGTCTTT TTTCCCTTGCATCTTTTAATATTCTTTCTTTGTTCTATACTTTTAGTGATTTGATTATTA TGCACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGGTGTTTTGTATGCTTCTTGTA TATTTTCCCTGCTTTTGACCTG--------CCTTCTTCCCCCTTCTATTCCT rrecarriricirridarrerrergeagarerrererargeaarerrerecaeereagarre rerricricaraccaririscirosaaaarrerririccasccirricarricreasscasisr TTCTAGAGAAATTAAGATCATTGAGTCATTGATGT

Oy 530 AGTC-TITGIGITITGGTGAALAGTCTGTAALTCT-CTAGGTCCACTTGGTTTATGA	Qy         707 IGTAGCTGGTTGTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGA           Db         237225 ITTACTAAAGTTTTTTTTATGAATGTGGCTGCCCTTGTATTCGAGCATAGATATTCAGA           Qy         767 ATTGCATGTCCTTTGGTGGATTTTC-CTTTGATGCCTATGTAGTATTCTTCCCAATCT           Db         237165 ATTGAAGGTTCCTTTGGAGGATTTTATCTTTGATGAGTATTCTTCCCAATCT	Oy 826 CATCTGCTTAGTTTTGGGTTTAAGTCTA-TTAGTCAGATATTAAAATGACTGTATCGGCT	Oy 944 CTATCCATGGTAGGTTGTCTTTTTGGATGCAGCAGTAGGATGGATTGTTTTCAT	1061 236873 1121 236813	Oy 1181 GIGICIGGICTIGGGGGGGGGTCTCCCCCTCTTIGATITITGGCCTGGAATIAN  Db 236780TIGAGGAI  OY 1241 TIATIATICATATITICTIGAATGTGGGTAACATCTTTAGAGGTTGAAGTTTTTCCTAGC  Db 236771 TATCTTGTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Oy 1301 CTTCTTAGGTCTGCATTTGAAGATAGTTTTACATCTTTACATCTTTAGAAT	Oy 1419 CATCIGTAGTCTTGAGACTGTGTAGCACATCTGTGCACGCCTTCTTACATTTTGAGTT
Oy 1885 TCTCTTCTATCTCTGTCAGGGGTTGTCTCTGAGGTTCCTG-TGGGTTC 1943  Db 236113 TCTCTTCTTCTTGTTGTTGTTGTTGTTGTTTTTTTTTT	Qy 2061 TITCTTTAATGGATTTATTCATTTCTTCAAGGACCTTTTATGAATTCATAAAATGTA 2120	; Sequence 61, Application US/10175523 ; Publication No. US20030096264A1 ; GENERAL INFORMATION . ; APPLICANT: Brockman, Jeffrey ; APPLICANT: Hook, Derek ; APPLICANT: Hook, Derek ; APPLICANT: Alinczak, Leszek	APPLICANT: Palfreyman, Michael APPLICANT: Rajan, Prithi TILLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS) FILE REFERENCE: 3.235/10795-US3 CURRENT APPLICATION NUMBER: US/10/175,523 CURRENT FILING DATE: 2002-06-18 PRIOR APPLICATION UNMER: US 60/299,151 PRIOR APPLICATION UNMER: US 60/299,151	PRICR APPLICATION NUMBER: US 60/317,828 PRICR FILING DATE: 2001-09-07 PRICR PLING DATE: 2001-09-25 PRICR PLING DATE: 2001-09-25 PRICR PLING DATE: 2001-11-14 PRICR PLING DATE: 2001-11-14 PRICR PLING DATE: 2001-11-14 PRICR PLING DATE: 2001-11-14	PRIOR APPLICATION NUMBER: US 60/361,834 PRIOR FILING DATE: 2002-03-04 NUMBER OF SEQ ID NOS: 197 SEQ ID NO 61 SEQ ID NO 61 FIRIGH: 251364 TYPE: DNA ORGANISM: Mus musculus	-10-175-523-61  24.9%; Score 567.5; DB 1; Length 251364;  Query Match Best Local Similarity 62.2%; Pred. No. 1.4;  Matches 1157; Conservative 0; Mismatches 580; Indels 123; Gaps  Matches 127; Conservative 1: Mismatches 580; Indels 123; Gaps  292 TCTATTTCTAGATTTCTAGGCTCATTTTAACTCAGTAGGTGATTTGGTTTCC	Db 237641 THICTTICTTICTTIANIGACCAAGGTAICATTGAGAAGAGTGTIGTTCATTICC 237582  Oy 352 ATAAGTTGTAAGTTTCTGTTGTTCTTGTTGTTGTTGTTATTTAT

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Query Match
Best Local Similarity 62.2%;
Matches 1157; Conservative
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GREEKAL INFORMATION:

APPLICANT: Brockman, Jeffrey

APPLICANT: Brockman, Devid

APPLICANT: Hook, Derek

APPLICANT: Hook, Derek

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APPLICANT: Hook, Derek

APPLICANT: Hook, Derek

APPLICANT: Palfreyman, Michael

APPLICANT: Palfreyman, Michael

APPLICANT: Rajan, Prithi

TITLE OF INVENTION NUMBER: US(10/175,523)

CURRENT PALING DATE: 2002-06-18

PRIOR FILING DATE: 2001-06-18

PRIOR FILING DATE: 2001-06-18

PRIOR FILING DATE: 2001-09-07

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Publication No. US20030096264A1
GENERAL INFORMATION:
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; ORGANISM: Mus musculus
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Pred. No. 1.7;
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RESULT 33 US-10-374-077-209/c

10353 10293 10292 GGTCTGATGATGATGGCATGGGATGATTTCCATCATCTTGAATCTGTAGAAGTCTGTTT 10233 10113 10112 ATCTGTTAGTTTCACTGTGTCTCTGATTAGTTTCTGTTTCCGTGATCCTGTCCATTGCTG 10053 18; 588 351 411 471 TGTTTTGAAATATGTATTCAATTTTGGAGA--GTTTCATAGGGTGCTGACAAGAAGGTAC 529 648 707 10352 ATATGTATGTGTGTTTCCGTTGTTTGTGTTTGGTATTTAAGACCAATCTTAGGCCGTGGT 530 AGTCTTTGTGTTTTGGTGAAATAGTCTGTAAATATCT-CTAGGTCCACTTGGTTTATGAC 10412 refreatrireatriciocetroaceaagraficarioagragagoceroficagerice 589 ATCAGITAGCICCAGCAITICICIGITITCGITITITIGITGAGAIGACCIAACIGITGGAG TOTATTICTIGATTICTATCTTGGCTCATTITTAACTCAGTAGTGAGTTGTTTGGTTTCC 352 ATAAGTTTGTAAGTTTTCTGTTGTTTCTGTTGTTGTTGTTGTTGTTATCTAGATTTAAGCTGT 412 GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGAGACTTGCTT 10172 ATTTATTGCTTTTGGATGACATGTTCTATAAATATCTGTTAGGTCCATTTGGTTCATAAC AGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGTGAGGT-CAATATGTGATTTTAGCT Gaps Yu, Chang-Bn
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: ANTIBODIES AGAINST GENE PRODUCTS RELATED
WERNER'S SYNDROME Length 51259; Law Group Version #1.30 DB 1; ADDRESSEE: Seed Intellectual Property STREET: 701 Fifth Avenue, Suite 6300 NAME: Rosenman, Stephen REGISTRATION NUMBER: 43,058 REFERENCE/DOCKET NUMBER: 100107.401D1 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,077
FILING DATE: 25-Feb-2003
ATTORNEY/AGENT INPORMATION: Score 565.399; Pred. No. 2.9; 0; Mismatches TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 209: Application US/10374077 5. US20040006779A1 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900 LENGTH: 51259 base pairs TYPE: nucleic acid ELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 209: SEQUENCE CHARACTERISTICS: 24.8%; 62.1%; SEQUENCES: 209 Sequence 209, Application US/11 Publication No. US20040006779A1 GENERAL INFORMATION: APPLICANT: Fu, Ying-Hui CORRESPONDENCE ADDRESS: CITY: Seattle STATE: Washington Conservative COUNTRY: USA Best Local Similarity Matches 1155; Conserv NUMBER OF US-10-374-077-209 292 472 649 Query Match

TGTATCGGGTGTGATGTGTGCTTTGAGAT 9993  CCTTGCATTTGTGGTGCATAGAAA 767  CCTTGCATTTGTAGCATAGATGTGTGTTCAGAA 9933  CGATGCATTTGTAGCATAGATGTTCAGAA 9933  CGATGCATTTGTAGCATACATGTTCAGAA 9933  CTATTAGTCAGATATTAAAATGCTTATCTT 9873  TAGAATA TCTTTTCCATCTTTTAGTTC 911  ATTTCCAGATGATTAAAATGCTTAGTT 991  ATTTCCTAGAAATTTACAAATGCTTGAGTC 963  CTTTTTCTAGAAATTTACAAATGCTGGTC 963  CTTTTTCTAGAAATTTACAAATGCTGGTC 963  CTTTTTCTAGAAATTACAAATGCTGGTC 963  CTTTTTTTGAGAATTACAAATGCTGGGTC 963  CTTTTTTTGAGAATTACAAATGCTGGGTC 110  ATTTCCTAGAAATTACAAATGCTGGTGTC 1110  CTTTTTTTGAGAATTACAAATGCTGGGTC 963  CTTTTTTTGAGAATTACAAATGCTGGTGTC 110  ATTTCTTTTGGGTTTG	0y 1764TITIGETITITICATION CONGREGATION TO B999 ATCCTIAGGITTCATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATION CONGREGATIO	RESULT 34 US-10-087-192-1861/c i Gequence 1861, Application US/10087192 sequence 1861, Application US/10087192 publication No. US20020182586A1 GENERAL INFORMATION: APPLICANT: Morits, David W. APPLICANT: Engelhard, Eric K. TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER TITLE REFERENCE: 52942200122 CURRENT APPLICATION NUMBER: US/10/087,192 CURRENT APPLICATION NUMBER: US 09/747,377 PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR APPLICATION NUMBER: US 09/798,586 PRIOR FILING DATE: 2010-01-02 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1861 CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: Musculus FEATURE:	Query Match
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Oy 1590 TGATTZ  Db 52703 TGATTZ  OY 1650 CTTCTT  OY 1706 GTTTTT  Db 52583 TTTTT	1759 1759 1819 52463	. 52403 1938 52343 1998 52283 2055	RESULT 35  US-10-322-281-495  Sequence 495, Appl Sequence 495, Appl Sequence 495, Appl Senseal INFORMATIC APPLICANT: David APPLICANT: David APPLICANT: Marc TITLE OF INVENTIC FILE REPREBUCE: CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FILING DD CURRENT FOSSA  CURRENT FOSSA  CONTRES FOSSA  CONTRES INFORMATIC CURRENT INFORMATIC CURRENT INFORMATIC CURRENT INFORMATIC CURRENT INFORMATIC	Ouery Match Best Local Similar Matches 191 from Qy 292 TCTATT Qy 129540 TTTCTT Qy 352 ATAAGT Db 129600 ACGTGAR Qy 412 GGTGGT
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52583 TTTTGTTGTTTTTGCATAGTGCCTTTAAGTGCTAATTATCC  97 1759 ATTCCTTTGGTTTTTGCATAGTGCCTTTAAGTGCTAATTATCC  1819 TAGATTTGGTTTTTGCATAGTGCTCTGGATGTTTTTAGGTTTGCTTTGCTTTTGCTTTGCTTTGCTTTGCTTTGGTTTTTGCTTGGTTTTTGCTTGGTTTTTGCTTGGTTTTTGCTTGGTTTTTGCTTGGTTTTTGCTTGGTTTTTT
UNKERN AFFILING DATE: 2002-12-17  UNMER OF SEQ ID NOS: 866  OFTWRER: FESTSEQ for Windows Version 4.0.  OFTWRER: FESTSEQ for Windows Version 4.0.  OFTWRER: FESTSEQ for Windows Version 4.0.  OFTWRE: NAME AFFILING SEQ ID NOS: 866  LENGTH: 176594  NAME/KEY: misc feature  LOCATION: (1)(176594)  OFTHE INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OTHER INFORMATION: n = A.T.C or G  OT

; SEQ ID NO 75 ; LENGTH: 85548 ; TYPE: DNA ; ORGANISM: Mus musculus US-10-175-523-75

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24.4%; Score 556.899; DB 1; Length 8554
Best Local Similarity 62.1%; Pred. No. 2.5;
Matches 1142; Conservative 0; Mismatches 571; Indels 125; 530 588 768 988 945 1002 412 472 33559 648 34083 34122 g g g ò g *∂* 8 g QQ ò g 8 a 8 6 g ò ò 8 8 8 ò ò 6 6 6 g

2064 CITTAAIGGAUTTAITCAITICCICTICAAGGACCITI 2
Db 35025 CTTTAAGGGATTTTTGTGCTTCCTCTTTAAGGTCTTCT 35062

RESULT 37 US-10-052-482-133

Sequence 133, Application US/10052482
Publication No. US20040072264A1
GENERAL INFORMATION:
APPLICANT: Engelhard, Eric
APPLICANT: Morris, David
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REFERENCE: A-71087,RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15

34168 GGTTTGTTGCGGGATACCTTTTTTTTTTTTGGACATGGTTTCTGTCTTGTATTGTT

TLING DATE: 2000-12-22 PPLICATION NUMBER: US 09/798,58	<b>д</b>	30899 TTTTTGATAACTTTTGGTTGAAAGTTGATTTTATTCGATATTTAGTGGATACTCCAGCT 30958
RIOR FILING DATE: 2001-03-02 UMBER OF SEQ ID NOS: 241 OFTWARE: Patentin version 3.1	දු ස	
O ::	δ	944 CTATCCATGGTAGGTTGTCTTTTTTGGATGCAGCAGTAGGATGTTTTTCAT 1000
TYPE: DNA SOMANISM: Mus musculus	DÞ	
FEATURE: LOCATION: (1171)(1270) OTHER INFORMATION: "n" at positions 1171 to 1270 can be any base	S G	1001 ATCCATTCTGTTACCCAGTATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGT 1060
FERTURE: NAME/KEY: misc_feature LOCATION: (28066)(28402) OTHER INFORMATION: "n" at positions 28066 to 28402 can be any base	& 8	1061 IGAGAATTATGAATGAGGAGTGTTTGTGGATTCTTGTTATCTTGGACTGTGT 1120 
FERTURE: NAME/KEY: misc_feature LOCATION: (34655)(34891) OTHER INFORMATION: "n" at positions 34855 to 34891 can be any base	& A	1121 GIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGI
FERTURE: NAME/KEY: misc_feature LOCATION: (37116)(37389) OTHER INFORMATION: "n" at positions 37116 to 37389 can be any base	& 8	1181 GIGICTGIGICTTGIGICTCTGIGITCTCTCCCCTCTTTTGATTTTTGGCCTGGAATTAT 1240 31225TGAAAGAIT 31233
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%; Score 555.699; DB 1; Length 47115;	& g	1301 CITCITIAGGICIGCATITGAAGAIAGAIAITCITIACAICTGAITITAICITAGAAIGI 1360 11294 CCITIGTAGGGGIGGAITIAIGGAAAGAIACIGIGAAAITIGGIITITGICAIGGAAIAI 31353
nservative 0; Mismatches 563; Indels 131; Gaps TTCTTGATTICTATCTTGGCTCATTITTAACTCAGTAGTGAGTGTTTGGTTTCC	<i>5</i> 5 62	1361 CTITCTTCCCAACTATTGTGACAGAAAGTTTTTCTAAGTGCACTAGTCTGGCCTGACA 1420
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; Sequence 1765, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
    APPLICANT: Morris, David W.
    TITLE OF INVENTION: CANGER
    TITLE OF INVENTION: CANGER
    TITLE OF INVENTION: CANGER
    TITLE OF INVENTION: CANGER
    TITLE OF INVENTION: CANGER
    TITLE OF INVENTION: CANGER
    TILE OF INVENTION: CANGER
    FILE REFERENCE: 5245200122
    CURRENT APPLICATION NUMBER: US 09/747,377
    PRIOR APPLICATION NUMBER: US 09/747,377
    PRIOR PILING DATE: 2000-12-22
    PRIOR APPLICATION NUMBER: US 09/747,377
    PRIOR PILING DATE: 2000-12-22
    PRIOR APPLICATION NUMBER: US 09/747,377
    PRIOR PILING DATE: 2000-12-22
    NUMBER: OF SEQ ID NOS: 2059
    SOFTWARE: FastESQ for Windows Version 4.0
    LEWGHT. 69-77
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LOCATION: (1)...(68370)

OTHER INFORMATION: n = A,T,C or G
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US-10-087-192-1765
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TTAACATTTTCTTTGAACCAAGGTATCCATTTCTTCTATCTTGACTTCATGCTTGAGATT  TTGAACATTTTCTTTGAACTTGTGCCGATGTCTTCTTCTATGCAATCTTCATGCAAGATT  TTGAATTTCTTTGAATGTTGTGCCGATGTTCTCTTATGGAATCTTTGAAGAATT	3 & g	GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTATCTGTCGAGACTTGCTT GATGATCTTTATAGATACACGGACAATTTCAATATTTTGTATCTTTTGAGGTTTGTT GATGATCTTATAGGATCACGGGACAATTTCAATATTTTTGTATCTTTTGAGGCTTGTTT
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Qy 1943 CTTAATTTTTCATTTCCAGATTTCCTTCAGTTTTGGGTTTTGTTTAATTCTATTTCC 2002		530 AGTC-TTTGTGTTTTGGTGAAATAGTCTGTAAATATCT-CTAGGTCCACTTGGTTTATGA 587 
OY 2003 ACTITCAGGICCTGAAATGITITACTCATTTTCCTCCCAGTATTTACATTTCATAG 2059  47632 CTITITAGITCTAGIATGITTTGITCATTTCCATCACCTGTTTGGAIGTGITTTCCTGT 47691	o da	588 CATCAGTTAGCTCCAGGATTTCTCTGTTTTGTTTGAGATGACCTAACTGTTGGA 647
OY 2060 GITTCITIAAIGGAITIATICATITCCICTICAGGACCITITAIGAAITCATAAAAIGI 2119	yy da	648 GAGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGTGAGGT-CAATATGTGATTTTAGC 706
Qy 2120 A 2120. Db 47752 A 47752	& 43	707 TGTAGCTGTGCTTGTTTTATGAACTTGGGTGACATTGTGTTTGTGTGCATAGACATTAAGA 766 
RESULT 39 US-10-175-523-97	<b>상</b> 점	767 ATTGCATGTCCTCTTGGTGGATTTTCC-TTTGATGCCTATGTAGTATTCTTCCCAATCT 825
2, 12, 11	o d	826 CATCTGCTTAGTTTTGGGTTTAAGTCTA-TTAGTCAGATATTAAAATGACTGTATCGGCT 884
	oy op	885 IGCITCITAGGGCCATTIGCTTAGAATA-ICTITICCAICCTTTACCTCAGGTGATGT 943
; APPLICANT: Palfreyman, Michael ; APPLICANT: Rajan, Prithi ; TITLE OF INVENTION: MULT-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS) ; FILE REFERENCE: 3235/1J795-US3	5 d	944 CTATCCATGGTAGGTTGTCTTTTTGGATGCAGCAGTAGGATGGATCTTGTTTTCAT 1000
<pre>IT APPLICATION NUMBE) IT FILING DATE: 200: APPLICATION NUMBER: PILING DATE: 2001-0</pre>	Oy Dp	1001 ATCCATICIGITACCCAGTATCTITICIAGAGAAATTAAGATCATIGAGTCATIGATGT 1060
APPLICATION NUMBER: US FILING DATE: 2001-09-07 APPLICATION NUMBER: US FILING DATE: 2001-09-25	oy ea	1061 IGAGAATTATCAATGAGCAGTGTTTGTGAATTCTTGTTATCTTGCACTTGTGAAGTGTGT 1120 
; PRIOR APPLICATION NUMBER: US 60/333,047 ; PRIOR FILLNG DATE: 2001-11-14 ; PRIOR PILLNG DATE: 2002-01-18 ; PRIOR FILING DATE: 2002-01-18	& 8	1121 GrGrGrGrGrGrGrGrGrGrGrGrGrGrGrGrGrGrGr
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; SEQ ID NO 97 ; LENGTH: 106664 ; TYPE: DNA ; ORGANISM: Mus musculus domesticus	% A	1241 TTATTATTCATATTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTTCTCC 1296
US-10-175-523-97  Query Match 24.0%; Score 547.299; DB 1; Length 106664;	ð 6	1297 TAGCCTTCTTTAGGTCTGCATTTCAAGATAGATATTCTTTACATCTGATTTTATCTTAGA 1356 03.05.6 TTDATCTTAGGTCTGCGATTTTGAGGATAGGTAAAATTGGGTCTTTTGGGA 94015
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   GCATTTGTGTTCTCTTTAGTGTCTGTATAACATCTGTCCATGCTCTTCTGGCTTTTCATAG
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Publication No. US20040126762A1;
GENERAL INFORMATION:
APPLICANT: David W. Morris;
APPLICANT: David W. Morris;
APPLICANT: David W. Morris;
APPLICANT: David W. Morris;
APPLICANT: David W. Morris;
APPLICANT: David W. Morris;
CURRENT APPLICATION WUMBER: US/10/322,281;
CURRENT APPLICATION WUMBER: US/10/322,281;
CURRENT FILING DATE: 2002-12-17;
NUMBER OF SEQ ID NOS: 866;
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 123.
LENGTH: 104399
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| ORGANISM: Mus musculus
| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(104399)
| OTHER INFORMATION: n = A,T,C or
| US-10-322-281-123
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 Pred. No. 2.5;
0; Mismatches 581; Indels 133; Gaps
Best Local Similarity 61.7%;
Matches 1152; Conservative
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Score 546.799;
Pred. No. 1.9;
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CURRENT APPLICATION NUMBER: US/10/175,523
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,151
PRIOR PILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR PLICATION NUMBER: US 60/325,150
PRIOR PLING DATE: 2001-09-25
PRIOR PLING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR FILING DATE: 2002-01-18
PRIOR PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-03-04
PRIOR FILING DATE: 2002-03-04
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Best Local Similarity 62.2%;
Matches 1156; Conservative
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LENGTH: 185548
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APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, David
APPLICANT: Hook, Derek
APPLICANT: Almczak, Leszek
APPLICANT: Lang, Pascal
APPLICANT: Palfreyman, Michael
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANT: Palfreyman, Michael
APPLICANT: Palfreyman, Michael
APPLICANT: Palfreyman, Michael
APPLICANT: Palfreyman, MICHI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/1J795-US3
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Publication No. US20030096264A1
GENERAL INFORMATION:
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CY , 2061 TITCITIAAIGGAITTAITCATTCCTCTTCAAGGACCTTTTATGAATTCATAAAAIGTA 2120	RESULT 42 US-10-087-192-235  JOURNAL 2020 US20020182586A1  FUBLICATION NO. US20020182586A1  JOURNAL INFORMATION:  APPLICANT: Morris, David W.  APPLICANT: Morris, David W.  APPLICANT: MOYEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION COMPOSITIONS (CONCER.)  TITLE OF INVENTION: UNVER. US/10/087,192  CURRENT APPLICATION NUMBER: US 09/747,377  FRICH REPERBNCE: 529452000122  CURRENT FILING DATE: 2000-12-02  FRICH APPLICATION NUMBER: US 09/747,377  FRICH APPLICATION NUMBER: US 09/747,377  FRICH RILING DATE: 2001-03-02  NUMBER OF SEQ ID NOS: 2059  SOFTWARE: FEASTSEQ for Windows Version 4.0  SEQ ID NO 235  LENGTH: 91071  TYPE: DNA  NAME/KEY: misc_feature  COTHER INFORMATION: (1)(91071)  COTHER INFORMATION: (1)(91071)  US-10-087-192-235	Ouery Match 23.6%; Score 537.888; DB 1; Length 91071; Best Local Similarity 63.0%; Pred. No. 2.9; Matches 1180; Conservative 0; Mismatches 551; Indels 143; Gaps 24;	OY 292 TCTATTTCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGGTTTCG 351	OY 352 ATAAGITTGTAAGITTTCTGTTGTTGTTGTTGTTGTTATCTAGATTTAAGCTGT 411	Qy 412 GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTATCTGTCGAGACTTGCTT 471  Db 24718 AGTGGTCTGATAGGATACATGGTATTATTTCAGTTTTTCGTATCTGTTGAGGGTTGTTT 24777	OY 472 TGTTTTGAAATATGTATTTGGAGAGTTTCATAGGGTGCTGACAAGAAGGT-A 528  Db 24778 TTTGACTAATTATAGGTCATTTTGGAGACAGTACCATGAGGTGCTAAGAAAAAGATGT 24837	OY 529 CAGTCTTTGTGTTTTGGTGAAAAGTCTGTAAATGTCT-CTAGGTCCACTTGGTTTATGA 587	Qy 588 CATCAGTTAGCTCCAGCATTTCTCTGTTTTTTTTGTTGAGATGACCTAACTGTTGGA 647	Qy 648 GAGAANGGGGTATTGAAGTAGCCCACTATCTGTGTGTGGGG-TCAATATGTGATTTTAGC 706	OY 707 IGIAGCIGCITGITITATGAACTIGGGIGACATIGIGITIGGGGGATAGACATIAAGA 766	Qy 767 ATTGCAATGTCCTCTTGGTGGATTTTCCTTTGATGCCTATGTAGTATTCTCCCAAT 823
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23.1%; Score 525.898; DB 1; Length 96597;
Best Local Similarity 61.9%; Pred. No. 3.1;
Matches 1143; Conservative 0; Mismatches 556; Indels 147; Gaps
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LOCATION: (8196).,(8446)
OTHER INFORMATION: "n" at positions 8196 to 8446 can be
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MAME/KEY: misc_feature
LOCATION: (43067)..(43340)
OTHER INFORMATION: "n" at positions 43067 to 43340
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LOCATION: (59328)..(59671)
OTHER INFORMATION: "n" at positions 59328 to 59671
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26352 GAATTTTAGGTCCT 26365
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LOCATION: (64349)..(64381)
OTHER INFORMATION: "n" at
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LOCATION: (29221)..(29240)
OTHER INFORMATION: "n" at
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FEATURE:
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0; Mismatches 637; Indels
    Version #1.30
                                                                                                                                NAME: Rosenman, Stephen
REGISTRATION NUMBER: 43,058
REGISTRATION NUMBER: 100107.401D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
SOFTWARE: Patentin Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/374,077
FILING DATE: 25-Feb-2003
CLASSIFICATION: <universelection of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of 
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TYPE: nucleic acid
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Best Local Similarity 60.7%;
Matches 1118; Conservative
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22.9%; Score 521.599; DB 1; Length 96602;
Best Local Similarity 61.8%; Pred. No. 3.3;
Matches 1157; Conservative 0; Mismatches 579; Indels 136; G
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2059 GGTTTCTTTAATGGATTTATTCATTCCTCTTCAAGGACCTTT
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Sequence 61, Application US/10085117
Sequence 61, Application US/10085117
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Sequence 61, Application US/10085117
Sequence 61, Application US/2003022334A1
SPELICANT: MORIFIC COMPOSITIONS AND METH
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METH
FILE REFERENCE: 529452000121
CURRENT FILING DATE: 2002-02-27
FRICH APPLICATION NUMBER: US/9/798,586
PRIOR APPLICATION NUMBER: US/9/798,586
PRIOR PALIOR DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 96602
TYPE: DNA
CREANISM: Mus musculus
FRATURE:
NAME/KEX: variation
LOCATION: (1)...(96602)
GOGATION: (1)...(96602)
GOGATION: (1)...(96602)
                                                                                     RESULT 45
US-10-085-117-61/c
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

August 25, 2004, 09:30:42; Search time 151 Seconds (without alignments) 2.623 Million cell updates/sec Run on:

Title: US-10-664-775-4 Perfect score: 2279 Sequence: 1 gatcactccttagtgaaag......ttgtaattctaggtgctgat 2279

IDENTITY NUC Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 45 seqs, 86898 residues Searched:

90

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

rst4.seq:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1

3843 hr mPN2 linear HTC 19_CFD_2003	Mus misculus 3 days neonate thymus CDNA, RIKEN full-length enriched library, clone:A630050F23 product:Rho-associated coiled-coil full intert. Sequence.	AK041981 AK041991.1 GI:26334838 HTC: CAD Francer	Mus musculus (house mouse) Mus musculus	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.	1 Carninci D and Havachiraki V	High-efficiency full-length cDNA cloning	92200		<pre>Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.</pre>	Normalization and subtraction of cap-trapper-selected cDNAs to	General ress. 10 (10), 1617-1630 (2000)	20499374 11042159	E,	Shibata, K., Itoh, M.; Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,	Konno, H., AKIYama, U., Nishi, K., Kitshnai, I., Iashiro, H., Iton, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Endinake S. Trone V. Torene V. Trane V. Ohara R. Matshiki M.	Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	KIKEN INCEGIACEG SEGUENCE analysis (KISA) system384-Iormac seguencing pipeline with 384 multicapillary seguencer	Genome Res. 10 (11), 1757-1771 (2000)	20530913 11076861	7	The RIKEN Genome Exploration Research Group Phase II Team and the	FANIOM CONSOLLIUM. Functional annotation of a full-length mouse cDNA collection		5 The RANTOM Consortium and the RIKEN Genome Exploration Research	Group Phase I & II Team.	Analysis of the mouse transcriptome based on functional annotation of 60.770 full-length cDNAs	Nature 420, 563-573 (2002)	6 (bases 1 to 3843) Adachi.J., Aizawa.K., Akimura.T., Arakawa.T., Bono.H., Carninci.P.,	Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,	Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
AK041981	DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE		REFERENCE	TITLE	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	1			Ē	371.T.I	JOURNAL	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	CHOIL DE	TITLE	JOURNAL	REFERENCE AUTHORS		

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Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nahai, K., Namura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission Hayashizaki, Y. Direct Submission Rasahizaki, Y. Direct Submission Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:Genome-res@georiken.go.jp, URL:http://genome.georiken.go.jp/, Tel:81-45-503-9222,
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forming kinase 1 (MGD|MGI:107927, GB|NM_009071, evidence:
BLASIN, 100%, match=1716)
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Itsues were provided by Dr. John Todd (Dept. of Medical Genetics Fisues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose Trust/MRC building Addenbrookes Hospital Cambridge) whose passistence we gratefully exchowledge.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/.

URL:http://fantom.gsc.riken.go.jp/.

I. 3843 [Walfield Br. John Trust Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432
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Pred. No. 0.69;
0; Mismatches 554; Indels 122; Gaps
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clone="A630050F23"
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Matches 1152; C
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MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS  TITLE  AUTHORS AUTHORS AUTHORS	TITLE JOURNAL	COMMENT COMMENT FEATURES SOUFCE	misc_feat Query Match Best Local & Matches 114	3 8 8 8 8
2300 TTAGGTTGGGGCAGTTTTTTCTATAATTTTGTTGAAGATATTTACTGGCCTTTTAATTT 2359 1740 G	2082 TITCCTCTTCAAGGACCTTTTATGAATTCATAAAATGTATGT	RESULT 2  AK087425  LOCUS  Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130020L12 product:unknown EST, full insert sequence.  ACCESSION AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AK087425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  AKO87425  A		AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Xashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izwa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A., and Hayashizaki,Y. TITLE SKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
8 6 8 6 8 6 8 6 8 6 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 2 AK087425 LOCUS DEFINITIC ACCESSION VERSION KEYWORDS SOURCE ORGANIE AUTHOR TITLE JOURNAL	REFE REFE AC GO ME PE	14 LT 05

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/strain="C57BL/6J"

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/dbox ref="Haxon:1000"

/dlone="E130020L12"

/dlone lib="RIKEN Uill-length enriched mouse cDNA library"

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1. .3887

/note="unknown EST (GB|BB797679, evidence: BLASTN, 96%, match=243)"
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ed (16-APR-2002) Yoshihide Hayashizaki, The Institute of
ed (16-APR-2002) Yoshihide Hayashizaki, The Institute of
l and Chemical Research (RIKEN), Laboratory for Genome
tion Research Group, RIKEN Genomic Sciences Center (GSC),
skohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
a 330-0045, Japan (E-mail:genome-resegsc.riken.go.jp,
1//genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 orary was prepared and sequenced in Mouse Genome deadia Project of Genome Exploration Research Group in Riken Sciences Center and Genome Science Laboratory in RIKEN.

of Experimental Animal Research in Riken contributed to
                                                                                                                                                      TOM Consortium and the RIKEN Genome Exploration Research hase I & II Team.
s of the mouse transcriptome based on functional annotation 70 full-length CDNAs 420, 563-573 (2002)
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Genome Exploration Research Group Phase II Team and the
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ity 62.0%; Pred. No. 0.7;
servative 0; Mismatches 574; Indels 127; Gaps
                                                         al annotation of a full-length mouse cDNA collection 09, 685-690 (2001)
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isit our web site for further details.

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Location/Qualifiers
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1536 TTITTCCCTTGCATCTTTTAATATTCTTTGTCTAATATTTAGGGCATTTGATTA 1595  1888 CCCTTCCCTTAGCATCTTTAATATTCTCTTTTGTCCAATTTGTTGTTGTTTTTTTT	RESULT 3 AKO46480 LOCUS Mus musculus adult male corpora quadrigemina cDNA, RIKEN Lull-length enriched library, clone:B230397K24 product:Similar to LI RETROPOSON, ORF2 MRNA (FRAGMENT) [Rattus norvegicus], full insert sequence. AKO46480 LI RETROPOSON, ORF2 MRNA (FRAGMENT) [Rattus norvegicus], full insert sequence. Mus musculus Nus musculus (house mouse) ORGANISM Enkaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus. REFERENCE Carninci,P. and Hayashizaki,Y. AUTHORS AUTHORS AUTHORS AUTHORS TITLE DOURNAL PORMED D329255 AUTHORS TITLE Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. TITLE Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. TITLE PUBMED D10349536 AUTHORS TITLE Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., TITLE PUBMED D1042159 REFERENCE AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashiro,H., Itoh,M., Konno,H., Nishi,K., Kiteunai,T., Tashiro,H., Thoh,M., Suna, N., Nishi,K., Kiteunai,T., Tashiro,H., Thoh,M., Suna, N., Nishi,K., Kiteunai,T., Tashiro,H., Thoh,M., Suna,K., Suna,M., Nishi,K., Suna,M., Nishine,T., Harada,A.,
472 TGTTTTGAAATATGTATTCAATTTTGGAGAGTTTCATAGGGTGCTGACAGAAGGTAC 529 897 TGTGCCAATTATATGGTGATTTTGGAGAAGGTACCATGGTGAGAAGAAGATT 956 530 AGTC-TTTGTTTTTGGTGAATATGTTGTAATATCT-TTAGGTGAAAAATTGAAATATGGTTAATATGAAAAAATATGTTGT	1061   TGAGATTATCAATGGCAGTGTTTGTGGATTCTTGTATCTTGCAGTGTGT   1120

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	Vamamoto D Materimoto U Galamichi C Ilbacami T Kachiwaci K	-	2065 JTTSTTSTAGAGTEGATTAGAGGAAGGAAATCAATGAGGAAATCAATAGAGTAGAGTAGTAGTTGATTGA
	Fujiwake,S., Incue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda V. Ishikawa,T. Ozawa,Y., Tanaka,T. Matshiki,M.,	8 8	GGTTTCCATAAGTTTGTAAGTTTTCTGTTGTTGTTGTTGTTGTTATCTAGATTT
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	sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913	λ <sub>O</sub>	AAGGIGGIGGIGAGALAGGACATAGAGTATTATTICAATIGICTITTATCTGICGAGA
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AUTHORS TITIE	The RIKEN Genome Exploration Research Group Phase II Team and the AbyTrOM Consortium. Princtional amoration of a full-length mouse cDNA collection	<i>ò</i> €	465 CTIGCTITGTITGAAAIAIGTATITCAAITTIGGAGAGTITCAIAGGGGGCIGACA 520 2087 CIIGTITIGGAACCAAITGIGGGCCAIGGTGAAIAGGIACCAIGGAGC 2028
JOURNAL REFERENCE	Nature 409, 685-690 (2001)	l &	AGAAGGTACAGTC-TTTGTGTTTTGGTGAAATAGTCTGTAAATATATCTCTAGGTCCACTTG
SS	æ	qa	2027 AGAAGGAAIATCCTTITGTTTTAGAIAAAATGTTCTGTAGAIATCTAITACATCATTT 1968
TITLE TOTRNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 56.573 (2002)	ò	580 GTITATGACATCAGTTAGCTCCAGCAITTCTCTGTTTTGTTT
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	Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Havashida,K., Bavatsı,N., Hirancto,K., Hiraoka,T., Hirozane,T.,	ò	
	Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kolima, Y., Kondo, S., Konno, H., Kouda, M.,	ପ୍ର	
	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,	07	TGATTTTAGCTGTAGCTGTGCTTGTTTATGAACTTGGGTGACATTGTGTTTGGTGCGTA
	Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano H., Sasaki,D., Shibata.K., Shinaqawa,A., Shiraki,T.	qq	
	Sogabe, Y., Tagami, M., Tagawa, A., Takabashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,	δ	GACATTAAGAATTGCAATGTCCTCTTGGTGGATTTT-CCTTTGATGCCTATGTAGTATTC
TTT.E	Muramatsu,M. and Hayashizaki,Y. Direct Submission	QQ	1788 GATATTCAGAATTGAGAGTTCCTCTTGGAAGATTTTACCTTTGATGAGTATGAAGTGCCC 1729
Æ	Submitted (16-UL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome	š	816 IICCCAARTTCATTGGTTTTGGGTTTAAGTCTA-TTAGTCAGATATAAAATGAC 874
	Exploration Research Cropp, 77LKB Genomic Sciences Center (GSC), 87KRN Vokchama Institute: 1-72 Suchiro-cho. Teurumi-ku. Yokohama.	d d	
	Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jb/, Tel:81-45-503-9222,	ò	
COMMENT	Fax:81-45-503-9216)	qq	
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	Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	qq	GAGGIAGICITITICCLIGAGGIGGGITICCTGIAAGCAACAAAATGITGAGTC
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Radchi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Harshizume, W., Frizozane, T., Harozane, T., Harozane, T., Harozane, T., Harozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Milyzaki, A., Muraca, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, M., Sakai, M., Tagama, M., Tagama, A., Tanaki, T., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Makahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330109E13 product:unclassifiable, full AK033883.1 Gf:26083632 HTC; Mus musculus full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched full enriched
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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RESULT 4 AK033883 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED

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GIGICIGIGICITGIGIGICIGICITCICCCCCICITITGATITITIGGCCIGGAATHAT 1240
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24.0%; Score 547.599; DB 1, Length 3235;
Best Local Similarity 62.2%; Pred. No. 0.9;
Matches 1144; Conservative 0; Mismatches 594; Indels 100;
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Encyclopedia Project of Genome Exploration Research Group in Riken
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-650 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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hote="unknown BST (GB|BF020883, evidence: BLASTN,
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Pred, No. 0.98;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus

cloning

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REFERNCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS AUTHORS AUTHORS	TITLE JOURNAL
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,710 full-length cDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,710 full-length cDNAs

As Nature 420, 563-573 (2002)

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Adchi, J., Aizawa, K., Akimura, T., Hara, A., Hashizune, W., Hayatau, N., Hirancoka, T., Hiraokar, T., Harozane, T., Hayatau, N., Hirancoka, T., Hiraokar, T., Kauda, M., Kadah, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nishi, W., Nishi, Y., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sajoe, H., Sasaki, D., Shibata, K., Shinaka, T., Takahashi, P., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y. Shinaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Saitoka, Shinaka, Y., Tanaka, Y., Tanaka, Y., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Saitoka, Shinaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y., Tanaka, Y.,
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
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AK089507. G1:26104836
HTC; CAP trapper.
Mus musculus (house mouse)
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RESUÍT 6 AKO88507 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE 'ORGANISM

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Submitted (16-APR-2002) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.go.jp, Raxi81-45-503-9216)

Fax: 81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 6enome Res. 10 (10), 1617-1630 (2000)
                  AKO85877 3204 bp mRNA linear HTC 20-SEP-2003
Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
library, clone:D830021017 product:unknown EST, full insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Functional annotation of a full-length mouse cDNA collection
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High-efficiency full-length cDNA
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/organism="Mus musculus"
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C AK008913 1644 bp MRNA Nus musculus adult male stomach cDNA, RIKEN library, clone:2210413A13 product:unclassi	sequence. AKO08913.1 GI:12843388 HTC; CAP trapper. Mus musculus (house mouse) Mus musculus					Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S. Konno,H., Akiyama,J., Nishi,K., Kitsunai,T. Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Vamanoto P. Mateumoto H. Sakamurhi S.	raman.O.C., racaman.O.C., Dagawa,Y., Izawa,M., Yoneda,Y., Ishikawa,T., Ozawa,X., Tanaka,T. Okazaki,Y., Muramatcu,M., Inoue,Y., Kira,A. PIKEN integrated seminon analysis (RISA)			Nature 409, 685-690 (2001)  S ANTOM CONSORTIUM and the RIKEN Genome	Group Fines 1 % 1 cam. Analysis of the mouse transcriptome based of 60,770 full-length cDNAs Nature 420, 563-573 (2002) Chases 1 to 1644	Adachi, J., Aizawa, K., 'Akahira, S., Akimura, Arakawa, T., Bono, H., Carninci, P., Fukuda, S. Fukuno, M., Hanagaki, T., Hara, A., Hayatsu, M. Piraoka, T., Tahii, Y.	Rasukawa,T., Rato,H., Kawai,J., Kojima,Y., Koya,S., Kurihara,C., Matsuyama,T., Miyaza Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y.	Shibata,K., Shibata,Y., Shinagawa,A., Shir Suzuki,H., Tagami,M., Tagawa,A., Takahashi Tejima,Y., Toya,T., Yamamura,T., Yasunishi Yoshino,M., Muramatsu,M. and Havashizaki,X	Direct Submission Submitted (10-JUL-2000) Yoshinide Hayashiz Physical and Chemical Research (RIKEN), La Physical Research Groun. RIKEN Genomic	RIKEN Yokohama Institute; 1-7-22 Suehiro-c Kanagawa 230-0045, Japan (E-mail:genome-re URL:http://genome.gsc.riken.go.jp/, Tel:81 Fax:81-45-503-9216)
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tissue type="activated spleen"
clone lib="RIKEN full-length enriched mouse cDNA library"
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                           prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/.

URL:http://fantom.gsc.riken.go.jp/.
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| db_xref="MG1:4428751"
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Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830032109 product:unclassifiable, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komlo, H., Okazaki, Y., Muramatsu, M. and Hayathizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Kokaki, Y., Muramatsu, M., Inoue, Y., Kirah, and Hayshizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 565-573 (2002)
( Dases 1 to 2436)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P. and Hayashizaki, Y.
Ish efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
Mus musculus (house mouse)
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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	ଶ ଧ ଶ	
Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Cana Albharay was prepared and sequenced in Mouse Genome	6 6 6 6	TIGCTICTIAGGGCCATTIGCTIAGAATAICTITICCATCCTTTIACTCTAAGGTGATGT TIGCTICTIAGGGCCATTIGCTIAGAATAICTTTCCATCCTTTIACTCTAAGGTGATGT TIGCTICTIAGGTCCATTIGCTTAGATGCTTTCCAACGTTGTTTTTGGATGCATGGATGG
Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our we sice for further details. URL:http://genome.gsc.riken.go.jp/. URL:http://fantom.gsc.riken.go.jp/.	3 6 6 6	
organism="Mus musculus"  "and type="mRNA"  "strain="C57BL/6"  "db_xref="FANTOM DB:B830013D20"  "db_xref="FANTOM DB:B8330013D20"  "db_xref="raxon:10090"  "clone="B8330013D20"  "clone="B8330013D20"  "clone="Redulla oblongata"  "clone="Ib=RIKEN full-length enriched mouse cDNA library"  "dev_stage="10 days neonte"	6 6 6 6 6	GIGICAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
4832 note="unknown BST (GB BM120546, evidence: BLASTN, 100%, latch=704)" 22.6%; Score 515.998; DB 1; Length 4832; y 61.4%; Pred. No. 0.83; rvative 0; Mismatches 486; Indels 296; Gaps 28;	. AG AG AG	
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Direct Submission

Submitted (16-UJU-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fx:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

UKL:http://fantom.gsc.riken.go.jp/.

UKL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                                                                                      Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hirozane, T., Hori, F., Imoteni, K., Ishin, Y., Itch, M., Kagawa, I., Ksukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyasaki, K., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Mumazaki, A., Murata, M., Okazaki, Y., Saito, H., Sakai, C., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogobe, Y., Tagami, M., Tagawa, A., Takashashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Tayanishi, A., Toya, T., Yasunishi, A.,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev sfage="adult"
                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 3375)
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                  Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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/db_xref="MG1:2411246"
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/dlone="B230315G06"
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/mol_type="mRNA"
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   FANTOM Consortium.
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                                                                                                                                                                                                                                                                                     1997 ATTICC-ACTITCAGGICCIGAAAIGITTIACICATTITICCICCCAGIAITIACAITITC 2055
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1290 TTT-----CCTGTTTAACATCTGAGGTATCCATTTCTTCCATCATGTCTTTAATGCCT 1238
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                          1237 GAGATTCTCTTTCCATCTCTTGCATTCTATTGGTAAGGCTTGCCCTCTGAGGTTCCTGT
                                                                                                                                                                                                                TGGGTTCTTAATTTTTTCATTTTCCAGATTTCCTTCAGTTTTGGGTTTTGTTTAATTCT
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Mus musculus adult male corpora quadrigemina cDNA, full-length enriched library, clone:B230315G06 product:unclassifiable, full insert sequence.
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
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Submitted (16-JUJ-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIREN), inboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (B-mail:genome-res@gec.riken.go.jp,
WEL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="diencephalon"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .446
/note="unclassifiable"
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                                                                                                                                                                                                                                  The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 4466)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, K., Hayatsu, N., Hiramcko, K., Hiracoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Naya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki, T., Takaki, T., Takaki, T., Takaku, A., Takahashi, F., Takaku, Akahira, S., Muranatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351
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                                      RIKEN Genome Exploration Research Group Phase II Team and
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                                                                                                      Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web site for further details. URL.http://genome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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(db_xref="MGI:339363"
db_xref="taxon:10090"
(clone="9330161A16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.1%; Score 481.397;
.larity 58.6%; Pred. No. 1.2;
Conservative 0; Mismatches 6
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strain="C57BL/6J"
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                                                                                 FANTOM Consortium
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GTOUP Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-langth cDNAs

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
E (bases 1 to 2108)

S Adachi,J., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,I., Kauda,M.,
Hori,F., Imotani,K., Ishii,Y., Itch,M., Kagawa,I., Kauda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Mondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Numazaki,A., Muraca,M.,
Nakamura,M., Nishi,K., Saitoh,H., Sakai,C., Sakai,K., Sakaio,N.,
Okazaki,Y., Saitoh,K., Saitoh,H., Sakai,C., Sakai,K., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shihaqawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Ysunishi,A.,
Muramatsu,M. and Hayashizaki,Y.,
Direct Submission
Submitted (16-201-201) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Subhir.ocho, Tsurumi'ku, Yokohama,
Kanagawa 230-0045, Japan (F-mail:genome-res@gsc.riken.go.jp,
PAKS HTKEN YOKOHAMA Institute of FAKSHIREN YOKOHAMA Institute, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, Yokohama, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST, YOKOHAMA, HTFST,
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                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Skono, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Masumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yamamoto, R., Inoue, K., Tozawa, Y., Isawa, T., Natsuhaki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Taraka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. KIKD integrated sequence analysis (RISA) system-384-format gequencing pipeline with 384 multicapillary sequence.
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Hasloome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL:http://feancom.gsc.riken.go.jp/
URL:http://fancom.gsc.riken.go.jp/.
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/clone="A630048110"
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/clone_lib="RIKEN full-leng
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Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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   CCTTACTGCTTTTAATATTCTGTCTTTTTTAGTGCATTTGTTGTTCTGATTACTATGTG
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1539 TITCCCTGGAAGAGTTTGGTGAATTTGTTGTTGTTTATATTGTTATATTAT	RESULT 14  AK04889  LOCUS  MUS musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230078P05 product:carbonic anhydrase 5a, mitochondrial, full insert sequence.  ACCESSION AK04889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC48889  AKC46889  AKC46889  AKC46889  AKC46889  AKC46889  AKC46889  AKC46889  AKC46889  AKC46ACACACACACACACACACACACACACACACACACACA	REFERENCE 2 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Itch, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes JOURNAL Genome Res. 10 (10), 1617-1630 (2000) MEDLINE 20499374 PUBMED 11042159 REFERENCE 3 AUTHORS Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Query Match Best Local Similarity 62.0%; Pred. No. 3; Matches 1034; Conservative 0; Mismatches 496; Indels 137; Gaps 21; Matches 1034; Conservative 0; Mismatches 496; Indels 137; Gaps 21;  482 INICIATIONATHICGRAGA-GTTCCATCAGGTGTTGAGARGARGATATTCTTTGTTTGTTTTGT	063 AGAATTATCAATGAGGAGTGATTGTTGATTATCTTGCACTTGTGAAGTGTGTT 1122	

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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Bamamoto, R., Matsumoto, H., Sakagurchi, S., Itsegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawi, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3179)
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                                                                                                                                                                                                                                                                      The RIKEN Genome Exploration Research Group Phase II Team and
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59.0%; Pred. No. 2.2;
tive 0; Mismatches 639; Indels 108; Gaps
                                                                                                                                                                                                                                                                                         FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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/clone="C30078P05"
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1321 ATATCTTCATTCTTCCATCATCATGTTATCATTGAGTAGACAG----TGAGTTTCTATG
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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1. .4502
/note="unknown EST (GB|BB455937, evidence: BLASTN,
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URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref="MG1.2396672"
/db_xref="mG1.2396672"
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  GCACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTGGTGTTTTGTATGCTTCTTGTAC 1659
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AKO79106 IG:26098277

HTC: CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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2922 IGTAITITCITIGAITGITGIGICAAIAICITCIAIGGIAICTICAGGGCCTGAGAITCT
                                                                                                                                                                                                                                                                 CTGTT-GAGAAGTCTGTTGTAATTTTTGATAGGTTTGACTTTATATGTTACTT-GACCTTT
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                                                  TCTTTCTTTCTCCAACTATTGTGACAGAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGAC
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ligh-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kornoo, H., Akiyama, J., Nishi, K., Kitsunai, T. Tashiro, H., Itoh, M., Yamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Hatahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., REKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,70 tull-length CDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4502)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The RIKEN Genome Exploration Research Group Phase II Team and
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Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
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                 Email: cgapbs-remail.inh.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland,
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
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Blakesley, R.W., Bockerrom-Sternberg, S.M., Hapighi, P.,
Ransen, N., Ho, S.-L., Karlins, E., Kawong, P., Larid, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency CRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTCCATGGGGATCTGATAGGATGCATGGGATTATTTCAACATTTCTATATCAGTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTGCTTTGTTTTGAAATATGTATTCAATTTTGGAGAGTTTCATAGGGTGCTGACAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGCT-----GATTATATGGTCAATTTTTGGAGAATGT-ACCATGAGGTGCTAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTACAGTCTTTGTGTTTTGGTGAAATAGTCTGTAAATATCTCTAGGTCCACTTGGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACACTICTATITCTIGAITITCTATCTIGGCTCATITITAACTCAGIAGIGAGIIGITIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 GGTTTCCATAAGTTTGTAAGTTTTCTGTTGTTTCTGTTGTTGTTGTTGTTATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1872 AGCTTCCACATGTATGTGGGCTTTGTATTTATGTTGTTATTGAATATC---AGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone has the following problem: retained intron.
Location/Qualifiers
1. .2278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 428.398;
Pred. No. 3.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Mus musculus"
MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Best Local Simi
Matches 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405
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1525	AGCITTACTAAAGTITCTTTAATGAATGTGGATGTGCCCTTGCATTTGGAGCATATATGTTC 1488
764	AGAATTGCAATGTCCTCTTGGTGGATTTT-CCTTTGATGCCTATGTAGTATTCTTCCCAA 822
823	TCTCATCTGCTTAGTTTTGGGTTTAAGTCTATTAGTCAGATATTAAAATGACTGTATCGG 882
	883 CTTGCTTCTTAGGGCCATTTGCTTAG-AATATCTTTTCCATCCTTTTACTCTAAGGTGAT 941
	GTCTATCCATGGTAGGTTGTCTTTTTTGGATGCAGCAGAAGGATGGATCTTGTTTTC 998
999	ATATCCATTCTGTTACCCAGTATCTTTTCTAGAGAATTAAGATCATTGAGTCATTGAT 1058
1059	
1119	
1128	1129
1179	CIGIGICIGIGICITGIGIGICIGGIICICCCCCCCTTITGGIITTTGCCCTGGAATI 1238
1239	ATTATTATTATTCTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTTCTCCTA 1298
1299	GCCTTCTTTAGGTCTGCATTTGAAGATAGATATTCTTTACATCTGATTTTATCTTAGAAT 1358
	GTCTTTCTTTCCCAACTATTGTGACAGAAAGTTTTTCTAAGTGCAGTAGTCTGGCCTGA 1418
1419	CATCIGIAGICCITIGGAGICIGIAGCACATCIGIGCAGGGCCTICITACAITITIGAGIT 1478
1479	TCTATTGGAAAAGTCAGGTGTAATTCTAATACATCTGCCTTTATATGTTAATTGGTCTTT 1538
1539	TITCCCTIGCAICTITIAAIATICTTICTTICTATACTITITAGIGATITGATIAITA 1598
1599	TGCACTGTGGGGAGITICTITICCGGTCCAALCTATITGGTGTTITGTATGCTTCTTGTA 1658 
1659	CCTTGATAGGCALCTCTTTCTCAAGGTTAGGAAAITTTTCTTTTTGGTTTTTTGAAAA 1718 
1719	TATTITICCTGCTITIGACCIGCCTTCTTCCCCTTCCTCTATTCCTTTGGTTTT 1772
1773	TGCATAGTGTCTCTGGCTTCCTGGATGTTTTATGCCTGGATTATTTTAGACTTAACATTT 1832

RESULT 17

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REFERENCE

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Yokohama,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2400 crcriridariracriringerigaaagiciririririranaariraarahagaarigeriacrica 2459
                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      882 GCTTGCTTCTTAGGGCCATTTGCTT-AGAATATCTTTTCCATCCTTTTACTCTAAGGTGA 940
Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1871 Tricicitriariricircécirascéascaricarirasiasasasiricasirice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2340 GAATTCAAATATCAGCTTGGTGTTTTTTTTCCTTTGATGAGTATGAAGTGTCCTTCCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCATCTGCTTAGTTTTGGGTTTAAGTCTA--TTAGTCAGATATTAAAATGACTGTATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTATTTCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGTTTGGTTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCT-TTTATCTGTCGAGACTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1985 GGTGATCTGATAAGATGCAAGGGGTTATTCAATTTTGTATAGTTTTGTTAAGGCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 ATCAGTTAGCTCCAGCATTTCTCT - GTTTCGTTTTTTTTGTTGAGATGACCTAACTGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647 AGAGAATGGGGTATTGAAGTAGCCCACTATCTGTGTGTGAGGTCAATATGTGATTTTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             765 GAATIGCAAIGICCICITIGGIGGA-ITITICCITIGAIGCCIAIGIAGIATICITICCCAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 426; Indels 116;
                                                                                                                                                                                                                                                                                                                 prepare mouse tissues.
Please visit our web site for further details.
URL:http://ganome.gc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 418.399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .3279
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Analysis of the mouse transcriptome based on functional annotation Of 60,770 full-length CDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3279)
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Submitted (16-7UT-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
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High-efficiency full-length cDNA cloning
Heth. Enzymol. 303, 19-44 (1999)
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Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (8-mail:genome-reseger:riken.go.jp, Tel: 181-45-503-9222, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 1922, 
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Analysis of the mouse transcriptome based on functional annotation
6 6,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2535)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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|mol_type="mRNA"
|strain="C57BL/G1"
|db_xref="FANTCM_DB:D030041121"
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Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 99279253
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/translation="MBIETIKKSQRETTLEIENLGRRSGVIDASITNRIQEIKERIPG
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CH230-490E23.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-490E23, genomic survey sequence.
BZ124878 GI:23765825 1670 1802 1610 1922 1430 2041 1310 2063 2123 1862 1GGGTTAGGAGCTTTTTACATTTTGCATTTTCTTTGACTGCTGTGTCAATGTTTTCTAGG 1550 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Chen, D., CTATITICGAGITCICIAGACCTCITGIATATIGATGGGTATCTATITAGGTTATGG icialgacrecagarerecrrecraggrirreraleres TIGITIAITAAITCTAITICCACTITCAGGICCIGAAAIGITITACTCATITITCCTCCA ------GACCTGCC TECTICCCCTTCCTCTATICCTTTGGTTTTTGCATAGTGTCTCTGGCTTCCTGGATGTTT TATGCCTGGATTATTTAGACTTAACATTTTCTTTGACCAAGGTATCCATTTCTTATC TIGICITCACTGCCTGAGATICICITCIATCTCTTGTATTCTGTAGTGAGGCTTGTC TCTGAGGTTCCTG-TTGGGTTCTTAATTTTTTCATTTCCAGATTTCCTTCAGTTTGGGTT rrcrrrarrerricrarrrccarrirragerccresaagecrirarrcaarccerrcac CTATITIGGTGTTTTGTATGCTTCTTGTACCTTGATAGGCATCTCTTTCTCAAGGTTAGGA AAGTTTTCTTCTATAATTTTATTGAAGATATCTACTGGCCCTTTAAGTTGGGAATCTTCT 2042 GTATT----TACATTTTCATAGGTTT 1369 IGTTIGATIGIATITCCTCTTTAAGACTICTACCIGITGACCTGTGTTCTCTCTGTATIT Tacuses 1 to 1151)

S tano, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shac, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Rat sbeyn, A., Gebregeorgis, E., C.M.
Rat BAC End Sequences from Library CHORI-230 Mbol segment
Unpublished (1999)
Other GSSs: CH239, 90523.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208 TAAGGICCTTGCCTTGAGCTATGTTGCATTCTCAGGG 2166

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/clone_lib="CHORI-230 Segment 2"
/notee="Vector: pTARBACI.3; Site_1: MboI; Site_2: MboI;
/CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
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1. 115.
| Corganism="Rattus norvegicus" |
| Mol_type="genomic DNA" |
| Astrain="BN/SahBad/McW" |
| Ab_aref="taxon:10116" |
| Clone="CH230-490E23"
                                                                                                                                                                                                                                    /sex="Female"
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Best Local Similarity
Matches 775; Conserv
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1480   CTATTGRGAAAGTCAGGGTCTGTATGACATCAGGGGTCATCTAATCTAATACATTGTGTAATCTTAATCATTCTAATACATTGTGTGAATTCTAATACATTGTGTGTG	21 0 AAR ION MU er er er Se ON AAR S HTM	ENKATYOLA; Metazoa; Chordata; Cranic Mammalia; Eutheria; Rodentia; Sciurc AUTHORS Carninci, P. and Hayashizaki, Y. CARNIC HIGH-efficiency full-length cDNA CLOURNAL Meth. Enzymol. 303, 19-44 (1999) MEDLINE 99279253 MEDLINE 10349636 2 104000, P. Shibata, Y., Hayatsu, N., REFERENCE 2 AUTHORS (Carninci, P., Shibata, Y., Hayatsu, N., TITLE Normalization and subtraction of prepare full-length cDNA libraries JOURNAL Genome Res. 10 (10), 1617-1630 (2000 MEDLINE 20499374	AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nags Konno,H., Akiyama,J., Nishi,K., Kite Sumi,N., Ishi,Y., Nakamura,S., Haz Yamamoto,R., Matsumoto,H., Sakaguchi Fujiwake,S., Inoue,K., Togawa,Y., IZ Yoneda,Y., Ishikawa,T., Ozawa,K., Towawa,Y., IZ Yoneda,Y., Ishikawa,T., Ozawa,Y., IZ Yoneda,Y., Ishikawa,T., Ozawa,Y., IZ Yoneda,Y., Ishikawa,T., Ozawa,K., Togawa,Y., IZ Yoneda,Y., Ishikawa,T., Ozawa,K., Towawa,Y., IZ ONGRAL Genome Res. 10 (11), 1757-1771 (2000 MEDLINE FURNED 11076861 AUTHORS The RIKEN Genome Exploration Researc FANTOM Consortium JOURNAL NALUE 409, 685-690 (2001) AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS
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Nagaoka,S., Sasaki,N., Carninci,P., Kitsunai,T., Tashiro,H., Itoh,M., Hazama,M., Nishine,T., Harada,A., prchi,S., Ikegami,T., Kashiwagi,K., Tawax,M., Ohara,E., Watahiki,M., Tanaka,T., Matsuura,S., Kawai,J., Y., Kira,A. and Hayashizaki,Y.
Y., Kira,A. and Hayashizaki,Y.
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886 bp DNA linear GSS 11-OCT-2002 CH230-208116.TJB CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-208116, genomic survey sequence.
BZ109340.1 GI:23750219
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Zhao,S., Shetty,J., Gbregeorgis,E., Overton,L., Russell,D., Cl
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="aorta and vein"
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/dev_stage="adult"
1. .2372
/note="unknown EST (GB|BG694861, evidence: BLASTN, 99%,
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Submitted (16-JUL-2001) Yoshihide Hayashizaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 please visit our web site for further details. URL.http://genome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref="MG1:4405827"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Anatrophy, 3. Shatsman, S., Tsegaye, G., Geer, K., Shatswan, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EccRI segment Unpublished (1999)
Other GSSS: (H230-42H13.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: szhaodtigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.thm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
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CH230-42H13.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH330-42H13, genomic survey sequence.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
GITTGATCTCATTGAGICCTGGATTTCCTGTATGTTTTAGGCCAGTAGCTTTTTCCTTTT
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/clone_lib="CHOR1-230 Segment 1"
/clone="Vector: pTARBAC2.1; Site_1: EcoR1; Site_2: E
CHOR1-230 Rat (BN/SsNHsd/MCW) BAC library produced
Pieter de Jong"
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Similarity 67.0%; Pred. No. 17;
77; Conservative 0; Mismatches 261;
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1. .846
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/mol type="genomic DNA"
/strain="BN/SSNHsd/MCW"
                                                                                                                                                                                     CTCTTCTATCTCTTGTATTCTGTCAGTGAGGCT
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/clone="CH230-42H13"
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/cell_type="B
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Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 302 Bmail: szhaoctigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
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CHORI-230 Rat (BN/SSNH8d/MCW) BAC library produced by
Pieter de Jong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
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Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. Rattus. 1 (bases 1 to 825) AUTHORS Zhao,S., Shetty,J., Shatsman,S., Teegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Frascr,C.M. TITLE Rat BAC End Sequences from Library CHORI-230 Mbol segment JONRNAL Unpublished (1999) COMMENT Cortect: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0200 Fax: 301 838 0208 Fmail: Schaogligt.org	Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please context Pieter de Jong (pdejongémail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdobbac_ends/rat/bac_end_intro.html Plate: 361 row: C column: 20 Seq primer: T7 Class: BAC ends. FEATURES  Location/Qualifiers source //organism=Rattus norvegicus"	/mol_type="genomic DNA" /strain="my/ssNesd/mcw" /db.xref="texon:10116" /clone="CH230-361C20" /sex="Female" /cell_type="Brain" /clone lib="CHORI-230 Segment 2" /note="Vector: pTARBAC1.3; Site 1: MboI; Si CHORI-230 Rat (BN/SsNHsd/MCW) BAC library p	Query Ma Best Loc Matches 1	1331 TICTITAGESTITIGGCALATATIAN COLLIGIAGOSCIOGATICA CARACTAGA AND A TICTITACAT CARACTAGA AND A TICTITACAT CARACTAGA AND A TICTITACAT CARACTAGA AND A TICTITACAT CARACTAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND A TICTITAGA AND	0y 151 TGTGCGGGCTTTTTGGGTTTTTTTCCTTGGTGGGGGGGG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone_lib="CHORI-230 Segment 1"
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/strain="mN/SsNHsd/MCW"
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/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: E
CHOR1-230 Rat (BN/SeNHSd/MCW) BAC library produced
Pieter de Jong"
                                                                                                                                                          19;
                                                                                                       Length 900;
                                                                                                                                                        291; Indels
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ACCESSION VERSION	CH230-394F19, genomic survey sequence. BZ132018 BZ132018.1 GI:23772965	ò :	1513 CTGCCTTTATATGTTAATTGGTCTTTTT
NEIWOKUS SOURCE ORGANISM	uss. Rattus norvegicus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;	65 A	CISCOLLIANTE CITACIL CIALACTUTA GARATUTE
REFERENCE AUTHORS	<pre>Rattus. 1 (bases 1 to 1037) Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,</pre>	S a	1633 ATTTGGTGTTTTGTATGCTTCTTGTACC
TITLE JOURNAL COMMENT	Riggs.F., de Jong,P. and Fraser,C.M. Rat BAC End Sequences from Library CHORI-230 MboI segment L. Unpublished (1999) Other_GSSs: CH230_394F19.TJ	Oy QD	1693 ITTITCTTTTTTGGTTTTCTTGAAAAR 
	Contact: Shaying Zhao Contact: Shaying Zhao The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA	λ Q	1741CCTTCTTCCCCTTCCTCTATTCCTTT
	Tel: 301 838 0200 Fax: 301 838 0208 Email: schedeligr.org	ò :	1799 GITTIAIGCCIGGATIAITITAGACITA 
	CIONES ATE WEILVE ITOM THE TAC BAC INDIALY CHARLYSON (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources	G &	
	(http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 394 row: F column: 19	g &	262 TATGGAATCTTCTGCTCCTGAGATTCTC 1919 TGTCTCTGAGGTTCCTGTAGGTTCTTA
FEATURES	<pre>Seq primer: T7 Class: BAC ends.     Location/Qualifiers</pre>	qn (	
source	1. 1037 /organism="Rattus norvegicus" /mol_type="genomic DNA"	දු දු	1978 GGTTTTGTTTATTATTCTATTTCCACT
	/strain="BN/SsNHsd/NCW" /db_xref="taxon:10116" /clone="CH230-394F19"	ò i	CCCA
	/sex="Female" /cell_type="Brain" /clone_lib="CHORI-230 Segment 2" /clone_lib="CHORI-230 Segment 2" /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; CHORI-230 Rat (BN/SSNHsd/MCW) BĀC library produced by Pieter de Jonq"	DB RESULT 27 BZ106508/c LOCUS	01
Query Mat Best Loca Matches	Ouery Match Best Local Similarity 64.5%; Pred. No. 15; Matches 614; Conservative 0; Mismatches 301; Indels 37; Gaps 6;	DEFINITION ACCESSION VERSION	
Oy 11	1155 GIGIGIGIGIGIGIGIGIGIGICIGIGICIGIGICITGIGIGICIGIGICICICCCC 1214 	KEYWORDS SOURCE ORGANISM	S GSS. Sattus norvegicus (Norway rat) ISM Rattus norvegicus Eukaryota; Metazoa; Chordata;
Qy 1215 Db 920	215 TCTTITGATHITIGGCCTGGAATHATHATTATHCATATHITTCTTGAAIGTGGGTAACAT 1274 920 TTCTCTTIGTITGCCAAGAHGATHAGTHTCTTGCTHCTTCTAGGGTATAGCTHGCCT 861	REFERENCE AUTHORS	
Qy 1275 Db 860	275 CTITAGATIGAAGITITICICCIAGCCITCITIAGGICIGCAIITGAAGAIAGAIATI 1332 	TITLE JOURNAL	Shvartsbeyn, A., Gebregeorgis, P. and Frae Riggs, F., de Jong, P. and Frae Rat BAC End Sequences from Lil Unpublished (1999)
Qy .1333 Db 800	333 CTTTÄCATCTGATTTTATCTTAGAATGTCTTTTCTCCAACTATTGTGACAGAAGTT 1392 	COMMENT	Concact: Snaying wing to Department of Eukaryotic Genom The Institute for Genomic Reservation Medical Center Dr., Rocky
Oy 139: Db 74	393 TITCTAAGTGCAGTAGTCTGGCCTGACATCTGTAGTCTCTTGGAGTCTGTAGCACATCTG 1452 		Fax: 301 838 0208 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the re
Oy , 14	1453 TGCAGGCCTTCTTACATTTTGAGTTCTATTGGAAAAGTCAGGTGTAATTCTAATACAT 1512 		(http://www.chori.org/bacpac/ availability, please contact i Clones may be purchased from i (http://www.chori.org/bacpac/

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TATTTTCCCTGCTTTTGACCTG------ 1740
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TTACATTATCTTTGACAGTTGAGTCAATGATTTC 263
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/rat230.htm). For BAC library
Pieter de Jong (pdejong@mail.cho.org).
BACPAC Resources
/or ering_information.htm). BAC end
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,B., Overton,L., Russell,D., Chen,D.,
ser,C.M.
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                                                             TGCACTGTGGGGAGTTTCTTTTCCGGTCCAATCT
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                                                                                                                                                                                                                       /sex="Female"
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/clone lib="CHORI-230 Segment 1"
/note="Vector: PTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SSNH8d/MCW) BĀC library produced by
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page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 204 row: J column: 17
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                             15.5%; Score 353.899; DB 1; Length 914; llarity 66.5%; Pred. No. 17; Conservative 0; Mismatches 271; Indels 19;
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0; Mismatches 271; Indels
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                                                                                                                                                                                  /db_xref="taxon:10116"
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                                                                               Location/Qualifiers
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Email: Szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/tab/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 386 row: A column: 11
Class: BAC ends.
TIC-ATTICCAGATTICCTTCAGTTIGGGTTTTGTTTATTAATTCTATTTCCACTTICAG 2010
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Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Best Local Similarity 64.4%; Pred. No. 15;
Matches 611; Conservative 0; Mismatches
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/clone="CH230-386A11"
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COURNAL Unpublished (1999)  COMMENT COTTACT: Shaying Zhao COTTACT: Shaying Zhao COTTACT: Shaying Zhao COTTACT: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, M Tel: 301 838 0200 Fax: 301 838 0200 Fax: 301 838 0200 Clones are derived from the rat BAC 1. (http://www.ohori.org/Dacpac/rat230.htm) availability, please Contact Pieter di clones may be purchased from BACPAC R.	(http://www.chori.org/bacgac/or ering page: http://www.tigr.org/tdb/bac_end Plate: 240 row: A column: 15 Seg primer: SP6 Class: BAC ends Location/Qualifiers 1. 920 Location/Qualifiers / organism="Rattus norvegicus /mol_type="Genomic DNA" / strain="BaN/SSHYBAG/NCW" / db xref="taxon:10116"	arch cal Similari	Matches 501; Conservative U; Mismatches Qy 1213 CCTCTTTTGATTTTTGCCCTGGAATTATTATTATTAT DB 844 CTTTTGTTTGTTTGTCCCCCAGTGAATTATTTCCCTAGCTTCTTCTTCTTCTTCTTGTTTCTTCTTGTTTCTTCTTGTTTCTTC	Db 784 CTCCTTACATCTGGGCTTTACATTTATCTTTC  Qy 1331 TTCTTACATCTGATTTTATCTTGGAATGTCTTTC  Db 724 TTATGTAAATTTGGTTTTGTGATGGAATATCTTGT  Qy 1391 TTTTCTAAGTGCAGTAGTCTGGCGTGACATCTGT  Db 664 TTTTGTGGATACTGGGCTTGGCTTGT  ON 1451 TGTGCAGGGCTTCTTACATTTGAGTTTCTATTGG		1631 426 1691 366 1741
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AC library CHORI-230
10.htm). For BAC library
2r de Jong (pdejong@mail.cho.org).
AC Resources
ring\_information.htm). BAC end
ends/rat/bac\_end\_intro.html TTCATATTTTCTTGAATGTGGGTAAC 1272 --TAGGTCTGCATTTGAAGATAGATA 1330 GGAAAAGTCAGGTGTAATTCTAATAC 1510 TTGCATCTTTTAATATTCTTTCTTTG 1570 ŝ CCCTGCTTTTGACCTG----- 1740 1741 ----CCTTCTTCCCCTTCCTCTATTCCTTTGGTTTTTGCATAGTGTCTCTGGCTTCCTGG 1796 snt 1"
Site\_1: EcoRI; Site\_2: EcoRI;
CW) BAC library produced by 250; Indels 19; Gaps DB 1; Length 920; MD 20850, USA δ

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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
blute: 218 row: C column: 4
Seg primer: SP6
Class: BAC ends.
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CH230-218C4.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-218C4, genomic survey sequence.
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/clone_lib="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Unpublished Gequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-218C4.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Rattus norvegicus"
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/strain="BN/SsNHsd/MCW"
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/clone="CH230-218C4"
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Rattus norvegicus
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BZ184947
CH230-329122.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-329122, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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1 (bases 1 to 816)
Shao,S. Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
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15.3%; Score 349.699;
67.3%; Pred. No. 17;
cive 0; Mismatches 2
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                                                                                                                                                                                   Email: szhao@tigr.org
Clones are detived from the rat BAC library CHORI-230
(luttp://www.chori.org/bacpac/rat230 htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Seg primer: SP6
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Chen, D.,
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/clone lib="CHORI-230 Segment 2"
/note="Vector: pTARBACI.3; Site 1: MboI; Site 2: MboI;
/note="Vector: pTARBACI.3; Site 1: MboI; Site 2: MboI;
Pieter de Jong"
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Rat BAC End Sequences from Library CHORI-230 Mbol segment Unpublished (1999)
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Pred. No. 19;
0; Mismatches 211; Indels 17;
                                              Unpublished (1999)
Other GSSs: CH230-329122.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Email: szhao@tigr.org
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/db_xref="taxon:10116"
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Sharbeyn, A., Shatsman, S., Tsegaye, G., Geer, K., Shatty, J., Shatsman, S., Tsegaye, G., Geer, K., Shatty, J., Gebregoorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P., and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment
M. Unpublished (1999)
Other GSSs: CH230-22306.TVB
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712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/rat230.htm) Par And Andre And Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre Andre An
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GTTTGACCCCCTCATTGTGTCCTGGATTTTCTGTATGTTTTGGGCCAGTACCTTTTTCTG 245
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/clona_lib="CHORI-230 Segment 1"
/noce="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (EN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                TCTCTCTTCTATCTCTTGTATTCTGTCAGTGAGGCTTGTCTCTGAGGTTCC-TGTTGGGT
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CH230-22306.TJB CHORI-230 Segment 1 Rattus 1
CH230-22306, genomic survey sequence.
BZ097017
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1. 910
/organism="Rattus norvegicus"
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Riggs,F., de Jong,P. and Fraser,C.M.

At BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-41983.TJ
Other GSSs: CH230-41983.TJ
Contact: Shaying Zhao
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
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availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 419 row: B column: 3
Seq primer: T7
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841 TGGATTTGTAGAAAGATATTGTGTAAACTTGGTTTTGTCATGGAATATCTTGGTTTTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mb
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced
Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10116"
/clone="CH230-419B3"
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1. .1061
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BZ244766 1061 bp DNA linear GSS 12-OCT-2002 CH230-419B3.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-419B3, genomic survey sequence.
                                                                                          1270 AACATCTTTAGATTGAAGTTTTTC--TCCTAGCCTTCTTTAGGTCTGCATTTGAAGATAG 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                     ITGTICTATACTTTTAGTGATTTGATTATTATGCACTGTGGGGAGTTTCTTTTCCGGTCC 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAICTAITTGGTGTTTTGTATGCTTCTTGTACCTTGATAGGCATCTCTTTTTCTCAAGGTTA 1687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATCTATTTGGAGTTCTGTAGGCTTCTTGTATGTCTATGGGTATCTCTTTTTTAGGTTA 369
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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                     TCCCCTCTTTTGATTTTTGGCCTGGAATTATTTATTATTCATATTTCTTGAATGTGGGT
                                                                                                                                                                                                                                                                AAGTITITICIAAGIGCAGIAGICIGGCCTGACAICIGIAGICITCITGGAGICIGIAGCAC
                               TICATICITITITITITITITITITICCCCCAAGACGATIAGITITCTGCTTICTTCTAGGGTATAGCT
                                                                                                                                  geereeeritarginegeeritaeearitaataeeerrietaereereearitietaeaae
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Rattus norvegicus (Norway rat.)
Rattus orvegicus
Bukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ244766
BZ244766.1 GI:23905030
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Rat BAC End Sequences from Library CHORI-230 Mbol segment Unpublished (1999)
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Enkryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhoogetigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pateter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 263 row: N column: 19
Seg primer: SP6
Class: BAC ends.
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                                                                                                                          CCAAGGTATCCATTTCTTCTATCTTGTCTTCACTGCCTGAGATTCTCTTCTATCTCTT 1899
                                                                                                                                                                                                                                                         CCAGATTTCCTTCAGTTTTGGGTTTTGTTTATTAATTCTATTTCCACTTTCAGGTCCTGAA 2018
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Sattus norvegicus
Eukaryota: Metaazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
CTICITCCCCTTCCTATICCTTTGGTTTTTGCATAG
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/mol_type="genomic DNA"
/strain="BN/SSNHSd/NCW"
/db_xref="taxon:10116"
/clone="CH230-263N19"
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BZ103057
CH230-228N16.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-238N16, genomic survey sequence.
BZ103057
BZ103057.1 GI:23743936
GSS.
Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224
/sex="Female"
/cell_type="Razin"
/clone lib=CHGRI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: Mbol; Site 2: Mbol;
CHGRI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pierer de Jong"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                             1412 GGCCTGACATCTGTAGTCTCTTGGAGTCT
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Rattus norvegicus
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Contro for Molecular Mechanisms in Disease Wellcome Trust Control Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/.

URL:http://fantom.gsc.riken.go.jp/.
                   The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

In Nature 420, 533-573 (2002)

G (bases I to 2559)

E (dases I to 2559)

E Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukudo, N., Haramata, T., Haranka, T., Hashizuwa, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiramoto, K., Hiracka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, M., Nishi, K., Nomura, T., Miyaziaki, A., Murata, M., Nishi, K., Nomura, K., Mumazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, R., Shibata, K., Shibata, K., Shibata, K., Shibata, Shibata, K., Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shibata, Shi
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

By Submitted (16-APR-2002) Vosihinde Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku; Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9212,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 6.8;
0; Mismatches 277; Indels 21; 0
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|db_xref="MG1:447317"
|db_xref="taxon:10090"
|clone="E430016D20"
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/strain="NOD"
Nature 409, 685-690 (2001)
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Best Local Similarity 66.2%;
Matches 584; Conservative
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CH230-236115.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-236115, genomic survey sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other GSSs: CH230-236115.TJ
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TIGAGITICTATIGGAAAAGICAGGIGTAATICTAATACATCTGCCTTTATATGTTAATT
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237 GACCAGTAGCTITTTCCGCTTTACATTATCTTTGACAGTTGAGTCAATGATTTCTATGGA 178
                                           1865 GICTICACIGCCIGAGAIICICITCIAICICITGIAIICIGICAGIGAGGCIIGICIC
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/db_xref="taxon:10116"
/clone="CH230-228A7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
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1. .833
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                                                          Email: szhaogetigr.org
Clones are derived from the rat BAC library CHORI-230
Clones are derived from the rat BAC library CHORI-230
Clones are derived from the rat BAC library availability please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
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      USA
9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                             Location/Qualifiers
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Best Local Similarity
Matches 559; Conservat
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Fmail: Szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
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(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 228 row: A column: 7
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Unpublished (1999)

Conter, Sass: CH230-228A7.TJ

Conter, Sass: CH230-228A7.TJ

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The Institute for Genomic Research
177 ATCTICTGCTCCTGAGATICTCTTCCATCTCTTGTATTCTGTTGGTGAAGCTTGTATC
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CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced
Pieter de Jong"
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No. 19; Conservative 0; Mismatches 252; Indels
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셤 ò

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Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
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(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 237 row: M column: 16
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/cell type="Brain"
/clone lib="tCORI-230 Segment 1"
/note="Wettor: pTARBAC2.1; Site 1: EcoRI; Site 2: E
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced in Pieter de Jong"
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al Similarity 66.2%; Pred. No. 19;
555; Conservative 0; Mismatches 267; Indels
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/organism="Rattus norvegicus"
/mol type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-237M16"
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CH230-237M16.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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TAACATCITIAGATIGAAGITITIC - TCCIAGCCITCITIAGGICIGCALTIGAAGAIA
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other GSSs: CH230-237M16.TV
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Rattus norvegicus
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Shao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSS: CH230-218G16.TV
Contact: Shaying Zhao
Cotter GSSS: CH230-218G16.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Chttp://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from Research
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 218 row: G column: 16
Seq primer: Sp6
Class: BAC ends.
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GTTTTATGCCTGGATTATTTTAGACTTAACATTTTCTTTGACCAAGGTATCCATTTCTTC, 1858
                                                                     TATCTTGTCTTCACTGCCTGAGATTCTCTTCTATCTCTTGTATTCTGTCAGTGAGGCT 1918
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone_lib="CHORI-230 Segment 1"
/note="Vector: prARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHed/MCW) BAC library produced by
Pieter de Jong"
                      TTCTTCTTGATTGCTTCTATTTCCATTTTTAATTCCTTCAACTGTTTGATTGGTTTTC
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15.2%; Score 345.299; DB 1; Length 854;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 562; Conservative 0; Mismatches 262; Indels 19;
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/mol_type="genomic DNA"
/strain="NN/SaNHsd/NCW"
/db_xref="taxon:10116"
/clone="CH230-218G16"
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Rattus norvegicus
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CH230-232F19.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
BZ091343
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846 CTTTTCTTCTGTGTTTTGTGCCCACGACGATTAGTTTCTTGCTCTTTCTAGGGTATAGC 787
                                                                                                                                                                                                                                                                  667
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                                                                                                                                                                                                          GATATICITIACATCIGATITIATCITAGAATGICITITCITICITCCAACTATIGIGACAG
                                                                                                                                                                                                                                      GATATTGTGTAAAATTTGGTTTTGTCATGAAATATCTTGGTTTCTCCATCTATGTTAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCTGTGCGGGGCCTTCTTACATTTTGAGTTTCTATTGGAAAAGTCAGGTGTAATTCTA
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Rattus norvegicus (Norway rat) Rattus norvegicus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,

1209 CTCCCCTCTTTTGATTTTTGGCCTGGAATTATTTATTATTCATATTTTCTTGAATGTGGG 1268

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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-112118.TV
Contact: Shaying Zhao.
Tother GSSs: CH230-112118.TV
Contact: Shaying Zhao
Contact: Shaying Canomic Research
Figure for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Piecer de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 112 row: I column: 18
Seq primer: Sp6
Class: BAC ends
Class: BAC ends
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BH258120
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1917 CTIGICTCTGAGGTTCCTGTTGGGTTCTTAATTTTTTC-ATTTCCAGATTTCCTTCAGTT 1975
           AATITITICITITITGGTITITCTTGAAATATTTTCCCTGCTTTTGACCTG------ 1740
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                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Brain"
/clone_lib="CHOR1-230 Segment 1"
/note="Wector: pTARBAC2.1; Site_1: BCORI; Site_2: BCORI;
CHORI-230 Rat (BN/SSNH6d/MCW) BAC library produced by
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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CE 1 (bases 1 to 838)

RS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,

Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,

Riggs,F., de Jong,P. and Fraser,C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

AL Upublished (1999)

Other_GSSS: CH230-232F19.TV

Contract: Shaying Zhao

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9712 Medical Center Dr., Rockville, MD 20850, USA

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Fax: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Full: schao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.igr.org/dab/bac_ends/rat/bac_end_intro.html

Plate: 232 row: F column: 19

Seq primmer: SRC

Class: BAC ends.
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"
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/clone="CH230-232F19"
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                                   DB 1; Length 849,
                               Query Match 15.1%; Score 345.099; DB 1; Lengt Best Local Similarity 66.0%; Pred. No. 19; Matches 555; Conservative 0; Mismatches 269; Indels
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GSS 03-DEC-2001

BH327408 821 bp DNA linear GSS 03-DEC-2001 H230-174G8.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-174G8, genomic survey sequence. BH327408

DEFINITION ACCESSION

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Shadus, Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shatsbay, A., Shatsman, S., Tsegaye, G., Geer, K.,
Shatty, J., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Best Local Similarity 67.0
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/CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced ?
                                                                                                                                                                                  831;
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Shorts, Shetty, J. Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-112114.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Email: Sahaodulga.cor
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pleter de Jong (pdelong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 112 row: L column: 14
Seq primer: Spe
Class: BAC ends
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CH230-112L14.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-112L14, genomic survey sequence.
BH258418
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Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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  392 TCTGTAGGCTTCTTGTATGTCTATGGGTATCTCTTTTTTAGGTTAGGAAGTTTTCTTC
                                                                                                                                                                     332 PATGATTITGTIGAAGATATTIACIGGICCTITGAGGIGGGAGGICTICACICTICTIT
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BH258418/c
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DEFINITION
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VERSION
KEYWORDS
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Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shatty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shattsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSS: CH230-163N10.TV
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
Clones are derived from the rat BAC library availability. Please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 163 row: N column: 10
class: BAC ends.
CH230-163N10.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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/note="Wector: pTARBAC2.1; Site 1: EcoR1; Site 2: EcoR1;
CHOR1-230 Rat (BN/SeNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      693 CTTAGTTTCTCCATCAATGTTAATTGGGAGTTTTGCAGGATACAGTAACCTGGGCTGGC
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       CH230-163N10, genomic survey sequence. BH357910 BH357910.1 GI:17288644
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/db_xref="taxon:10116"
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                                                                                                                     Rattus norvegicus (Norway rat)
Rattus norvegicus
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455 TGATGGGGGGGAGTTTCTTTTCTGGTCCAATCTATTTGGAGTTCTGTAGGCTTCTTGTATG 396
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                                                                395 TITAIGGGCATCTCTTTTTTTTTAGGTTAGGGAAGTTTTCTTCTTCATGATTTTGTTGAAGATA
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                                          TIGATAGGCATCTCTTTCTCAAGGTTAGGAAATTTTTCTTT
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Search completed: August 25, 2004, 09:33:44 Job time : 181 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic August 24, 2004, 08:45:30; Search time 14588 Seconds (without alignments) 3.946 Million cell updates/sec Run on:

US-10-664-775-2 3572 1 gtcaggaagggcggcagtga......gcaacaacagcagaaagctt 3572 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

44 segs, 8057215 residues Searched:

88 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

rge2.seq:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ACCESSION: AC1414	ION: AJ42148	SION: AC14500	SION: AC13583	SION: AC13765	31ON: AC09166	:AC13521	N:AC14256	N:AC14185	:AC10888	N: AC14096	AC14488	AC13931	AC14256	256	AC13963	AC09125	AC14688	AC14544	AC14449	CCESSION:AC13521	SSION:AC14719	SION:AC13495	SION: AC14653	SION: AC09975	SION: AC09139	SION: AC10706	SION: AC10991	SION: AC14759	SSION: AC13765	ESSION: AC09272	CESSION:AC09241	07E
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing: In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence

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53.5 216698 53.4 171875 52.9 2183747 52.9 1537474 52.9 154440 52.8 165992 52.8 165992 52.3 154577 52.2 154577 52.2 154577 52.2 154577 52.1 151609	
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115101 GTCAGGAAGGFGGCGGTGAGGAGA-----TACCCCTCGTCCAAGGFAAGGATCAGCAGC 115047

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114926 GAAAACTAGTCAGTCTAATCACACTAGGCCACAGCCTTGTCTAACTCAATGAAACTAAG 114867 114866 CCATGCCTGTGGGGCAACCCATGATGGGGGGTCATGGTGGAGAGTCTGACAGAATGTG 114807 114806 GTCCACTGGAGAGAGAGATGGCAAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAAC 114747 114986 TAAGACGGTAGGTGTTGCAAGAGGGCATCAGAGGGCAGACACACTGAAACCATACTCACA 114927 114687 114567 114507 114506 GTCGTCAAACAAGAGAGATGGCAAGAGTGAATGTCGACATTTCTAGGAATTCAGCAAACTAAAA 114447 114446 TGGACTGGAATGGGTGAATTTAACTCAGATGTCCATTATATCTACTACTGCGGGCAGGAA 114387 114327 114147 CTGGTCATAACAACACCCTCTTCCAACAACAACAACAACATCTATACATGGACATCA 113967 114267 114207 114087 114027 1020 1140 180 240 420 540 1141 CCAGATGGTCAACACCGAAATCAGATTGATTATATTTTGCAGCCAAAGATGGAGAAGC 1200 TGCGCTTTGCTGGAGCAGCCGTAAAGAGATACCCCACGCCCAAGGTAAGAGAAACCCAAG 120 600 099 840 780 096 115046 TGCCCTTTGCTGGAGCAGCCATGAAGAGATACCCCATGCCCAAGGTAAGAGAAAACCCAAG CCATGCCCGTGGGGAACCCAAGATGGCAAGGTCATGGTGGAGAGATCTGACAGAATGTG GTCCACTGGAGAAGGGAATGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAAC 114626 AAGCAAAAAGAATACCCAGCTGTGGATGTGACTGGTGATAGAAGCAAGGTCCAATGCTGT 114566 AAAGTGCACTATTGCATAGGAACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGGAA TAAGATGGTAGGTTTGTGAGGGCATCAGAGGCCAGACATACTGAAACCATACACGCA GAAAACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAG 601 GTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGGAATCAGCGAACTAAAA 114386 TCCCGCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAAGAGTTGGAAAATGTAGCACTT 114326 GGATGCAATCTCAAAAACAACAGAATGATCTCTGTTTCGTTTCCAAGGCAAACCATTCAAT 114086 GGCCTTGGAATACGGAATGAAGTAGGGCAAAGACTAATAGACTTTTGCCAAGGAAATGCA 481 AAGCAAAAAGAATACCCAGCTGTGGATGTGACTGGTGATATAAGCAAGGTCCGATGCTGT 541 AAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGGAA 661 TGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATCTACTACTGCGGGCAGGAA TCCCTCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAAGAGTCCGAAATGCAGTACTT TCCTATGAAGACCTACAAGACCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCATT 961 ATAGGGGACTGGAATGCAAAAGTAGGAAGCAAAGAAACACCTGGAGTAACAGGCAAATTT 114146 ATAGGGGACTGGAAATGCAAAAGTAGGAAGTTAAAGAAACACCTGGAGTAACAGGCAAATTT 1021 GGCCTTGGAATACGGAATGAAGCAGGCAAAGACTAATAGAGTTTTGCCAAGAAATGCA 841 ATCACAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGAAGTTGAACGG CTGGTCATAGCAACACCCTCTTCCAACAACAACAAGAGACTCTACACATGGACATCA 1081 114026 à g

TIGAGICIGGGIGAACICCIGG 2704 GAAGACTCTTGAGAGTCCCTT 2464 TCAGCCCTGGGATTTCTTTGG 2524 AICACTICAIGGGAATAGAT 2166 TTGGAAGAAAGTTA--ACCA 2284 |||||||||||||| TTGGAAGAAAGTTATGACCA 112227 ACCTGATCAGAAGACTGACT 2584 ACCCTTAIGGCAGAAAGIGAA 2046 |||||||||||||||||||||||| ACCCTTAIGGCAGAAAGIGAA 112467 CAACAAAGCCCCATCTAGTCA 2344 TTGATTGTGGATCACAAT 112767 BAAAAAGCAAGAGAGTTCCAG 112827 GGAGGAGAAGGGGACGACAGA 2644 TIGACIGIGGGGGTCACAAT 1747

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3323. .8443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (16585, .16726)

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complement (16834, .16994)

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1974. 9118
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164. 9391
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1598. .21898
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4072. .14450
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:omplement (20011. .20113)

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complement(16585..16726)
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                                                                                                               AJ421481 233345 bp DNA linear MAM 12-JUN-2002
Bos taurus X-inactivation center region, Jpx and Xist genes.
AJ421481
                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                  Chureau, C., Prissette, M., Bourdet, A., Barbe, V., Cattolico, L., Jones, L., Eggen, A., Avner, P. and Duret, L. Comparative sequence analysis of the X-inactivation center region in mouse, human, and bovine Genome Res. 12 (6), 894-908 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (27-NOV-2001) Duret L., Biologie et Biologie Evolutive,
Submitted (27-NOV-2001) L., i., rue Raphael Dubois, 69622
Villeurbanne cedex, FRANCE
Sequenced by the Genoscope. Contact: Philip Avner, Institut
Pasteur, 25, rue du Docteur Roux, 75015 Paris, France.
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Jpx gene, Xist gene.
Bos taurus (cow)
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> 14; 1 GTCAGGAAGGGCGCCAGTGAGGAGGTACCTACCTCGTCCAAGGTAAGGAGCAGTAGC Query Match 60.4%; Score 2158.67; DB 1; Length 233345; Best Local Similarity 72.0%; Pred. No. 0; Matches 2910; Conservative 0; Mismatches 468; Indels 661; Gaps

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TGCGCTTTGCTGGAGCAGCCGTAAAGAGATACCCCACGCCCAAGGTAAGAGAAACCCAAG 120 223975 erchegahadededegredrehdahah----rheceeeregrechadedahadahadedede 61

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223141 223261 223201 222901 222841 223440 TAAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGGA 223381 223081 223021 223561 223920 TGTGCTTTGCTGGAGCAGCCGTGAAGAGAAACCCCACACCCAAGGTAAGAGAAACCCAAG 223861 223741 1019 TGGCCTTGGAATACGGAATGAAGCAGGGCAAAGACTAATAGAGTTTTGCCAAGAAAATGC 1079 719 839 899 ACTGGTCATAACAAACGCCCTGTCTTCCAACACACAGAGAAGAGACTCTATACATGGACA 223140.TACCACAGTAATCCAAGTCTATGCCCGACCAGTAATGCTGAAGAAGCTGAAGTTGAACG 223320 Arggacriggaardggrigaartraacricagargaccarrigrarcrigcraccgcgggaga TAAGATGGTAGGTGTTGCCAAGAGGGCATCAGAGGGGCAGACACACTGAAACCATACTCACA GECCACTGGAGAAAGGGAATGGCAATGCTTGAGTATTCTTGCCTTGAGAACCCCATGAA AAAGCAAAAAAAATACCCAGCTGTGGATGTGACTGGTGATATAAGCAAGGTCCGATGCTG TAAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGGA 660 ATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATCTACTACTGCGGGCAGGA TGGATGCAGTCTCAAAAACGACAGAATGATCTCTCTGTTTCCAAGGCAAAACCATTCAA TATCACAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACG GTCCTATGAAGACCTATTTAGAACTAACACCCAAAAAAGATGTCCTTCTCAT GTCCACTGGAGAAGGGAAT-GCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAA 600 AGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGGAATCAACTAAA CAGTATGAAAAGGCAAAATGATAGAATACTGAAAGAGGAACTCCCCAGGTCAGTAGGTGC GAAAACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAG TAAGATGGTAGGTGTTGTGAGAGGGCATCAGAGGGCCAGACATACTGAAACCATACACGCA 840 096 540 720 780 900 1020 223080 360 480 181 223740 121 223860 241 223680 223800 301

GACCACCIGATCTGCCTCTTGAGAAAT 221597 TCACCCGGCTTGTTTAACTTCTATGCA 1930 ACCACCTTATGGCAGAAGTGAAGAG 2049 221537 GAGAGTGAAAAGTTGGCTTAAAGCTC 2109 CCTTGGAAGAAAGTTA--ACCAACC 2287 TGCCAACAAAGCCCCATCTAGTCAAGG 2347 AGATCAGCCCTGGGATTTCTTTGGAAG 2527 CCCATCACTTCATGGGAATAGATGGG 221237 GCCACCTCATGCAAGAGTTGACTCAT 220818 1810 1870 1989 2169 2647 recegegerccaaaarcacrecagare 2229 CGTGAGTCTGGGTGAACTCCTGGAGT 2707 CCACCTGATCAGAGAGCTGACTCAC 2587 TCATGGGGTCACAAGAGTTGGACAC 2767 GACCACCTGACCTGACTCTTGAAAAT GCACAAGCTGGAATCAAGATTGCCGGG CCCATCACTTCATGGGAAATAGATGGG CAGGAGGAGAGGGACGACAGAGGA

AACCTTAGTAGTTTATATTACT---- 2823

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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in O20 bases and has been reviewed to rule out gross misssemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
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* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 19089 21334 contig of 19088 bp in length 19189 21334: contig of 19088 bp in length 21435 37376: contig of 15942 bp in length 37377 37476: gap of unknown length 109938 1100937; contig of 47942 bp in length 15998 159093 contig of 47942 bp in length 15909 160129: contig of 2050 bp in length 15909 160129: contig of 2050 bp in length 160130 170532: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 170533 1908916: contig of 2050 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 160500 bp in length 16050
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Submitted (03-OCT-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Galthersburg, MD 20877, USA
On Oct 3, 2003 this sequence version replaced gi:32964885.
                                                                                                                                                                                       Sequencing Center, 8717
77, USA
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Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-treminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197401 bases at least Q40
Consensus quality: 198094 bases at least Q20
Consensus quality: 198094 bases at least Q20
Insert size: 153000; agarose-fp
Insert size: 19816; sum-of-contigs
Quality coverage: 15.52x in Q20 bases; sum-of-contigs
Quality coverage: 11.98x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: NIH Intramural Sequencing Center
                                                           Green, B.D.

Direct Submission

Submitted (30-MAY-2003) NIH Intramural Seq
Grovemont Gircle, Gaithersburg, MD 20877,

3 (bases 1 to 198916)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc zoo@nhgri.nih.gov
    Comparative Sequencing Initiative
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Center clone name: 385L09
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        220637 GACTGAGCGACTGAACTGAACTGAATTCGGTTGTTCATAATTTCAATTTCTTCT 220578
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Bos taurus clone RP42-385L9, WORKING DRAFT SEQUENCE, 8 ordered
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Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
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Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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	197901	DD 19781 AIGGACIGGAAIGGGIGAAITIRACIGAGAIGACAITATAICTACTACTACTGIGGGCAGGA 1977.  QY 720 AICCCTCAGAAGAAAIGGAGTAGCCATCAIGGTCAACAAAAGAGTCCGAAATGCAGTACT 779  DD 197781 AICCCTCAGAAGAAGAGGCCATCATGGTCAACAAAAGAGTCTGAAAIGCAGTACT 1977.		Oy B40 TATCACAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACG  DD 197661 TATCACAGCAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACG	QY 900 GICCIAIGAAGACCIACAAGACCITITAGAACIAAACACCCAAAAAAGATGICCITICTAT 959  DD 197601 GITCIAIGAAGACCIACAAGACCITITAGAACIAACACCAAAAAAAGAIGICCITITCAT 197	Oy 960 TATAGGGGACTGGAATGCAAAAGTAGGAAGGAAAGAAAGA	OY 1020 TGGCCTTGGAATACGGAATGAGGCGAAGACTAATAGAGTTTTGCCAAGAAATGC 1079	OY 1080 ACTGGTCATAGCAAACACCCTCTTCCAACAACAAGAAGAAGACTCTACACATGGACATC 113  Db 197421 ACTGGTCATAGCAAACACCTCTTCCAACAACAAAGAAAGA		N	Oy 1260 TATTGCCAAATTCAGACTTAAATTGAAGAAAGTAGGAAAACCACTAGATCACGGTA 1319 . 197241 TATTGCCAAATTCAGACTTAAATTGAAGAAAGTAGGGAAAACCACTAGACCATTCAGGTA 197182	CY 1320 AGACCTAAATCCAATCCCTTATGATTATACAGTGGAAGTGAGAAATAGATTTAAGGGCCT 1379	QY         1380 AGATCTGATAGACAGAGTACCTAATGAACTATGGACAGAGGTTCATGACATTGTACAGGA 1439           DD         197121 AGATCTGATAGATAGATAGATGCCTGATGAACTATGGACTTGTGACATTGTACAGCA 19706	00	QY         1500 GGAGGCCTTACAAATAGCTGTAAAAGAAAGAAAGGAAAAGGAAAAGGAAAAGGAAAAG 1559           DD         197002 GGAGGCCTTACAAATAGCTGTGAAAAGAAAGAAAGAAAAGAAAAGAAAAAGAAAAGGAAAA	OY 1560 ATAAAAGCATCTGAATGCAGAGTTCCAAA	Qy Db 19	OV 1589
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OY 2226 GATGGTGACTGCAGCCATGAAATTAAAAGACACTTACTGCTTGGAAGAAAGTTAACC 2283	19	195505 GAGGCCCAAAGAATTGATTTGATTTGAAGGAGATCAAAGAAGAATTGATTG	Db 195325 TCATTGGAAAAGACTCTGATGCTGGAGGGGATTGGGGGGAGGAGAAAAGGGCATGACAC 195200  Qy 2644 AGGATGAGTGGCTGGATGGCTGCTGGTGGAGGTGACTCTGGTGACTCTG 2703  Db 195265 AGGATGAGTGGATGGCTGCTCGATGGACTCAGTGAGTCTGGTGAACTCTG 2703  Qy 2704 GAGTTGGTGATGGACGGGGGCTGTCCTGCGGGCATTCATGGGGTCAAAGAGTTGG 195206  Db 195205 GAGTTGGTGATGGACGGAGGCTGTCCTGCGGCGATTCATGGGGTCAAAGAGTTGG 2763  Db 195205 GAGTTGGTGATGGACGGAGGCTGCTGCTGCTGCTGCTGATTCATGGGGTCGCAAAGAGTTGG 195146  Dy 2764 ACACGACTGAGCAACTGAACTGAACTGAACTG 2795  Db 195145 ACACGACTGAGCAACTGAACTGAACTGATCTG 195114	RESULT 4 AC135839/C LOCUS AC135839 LOCUS DEFINITION Bos taurus clone RP42-2H17, WORKING DRAFT SEQUENCE, 6 ordered ACCESSION AC135839.2 AC135839.2 AC135839.2 AC135839.2 AC135839.2 AC135839.2 AC135839.2 Bos taurus CORGANISM EDVIGUE Bos taurus CORGANISM EDVIGUE; Bos taurus CORGANISM EDVIGUE; Bovine; Bos taurus CORGANISM EDVIGUE; Bovine; Bos taurus ACCESSION AC135839.2 Bovine; Bos taurus Bovine; Bos taurus Bovine; Bos taurus Bovine; Bos taurus Bovine; Bos taurus Bovine; Bos taurus Borides; Bos taurus Borides; Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Bovines; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Borides; Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taurus Bos taur	Cariaga, K., Coleman, B., Engle, J., Granite, S., Gupta, J., Haghighi, P., Hansen, N., Ho, SL., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, SO., Legapsi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Pagnirian, C., Pearson, R., Portroy, M.E., Presad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D. JOURNAL Unpublished REFERENCE 2 (bases 1 to 179015) AUTHORS Green, E.D. TITLE Direct Submission JOURNAL Schwhission Growemont Circle, Gaithersburg, MD 20877, USA
196822 CAAGAAATTAGAGGTACCAAAGGAACATTTCATGCAAAGATGAGCTCGATAAAGGACAG 196763 1589 1588 196762 AAATGGTATGGACCTAACAGAAGCAAAGATATTAAGAAGAGTGGCAAGAATACACAGA 196703	1589 1588  196702 AGAACTGTACAAAAAGATCTTCACGACCCAGATAATCACGATGGTGTGATCACTGACCT 196643  1589	196582 AGCTAGTAGAGGTGATGGAATTCCAGTTGAGCTATTCCAAATCCTGAAAGATGATGCTGT 196523 1589	196402 CCGCACAATTGCACTCATCTCACGCTAGTAATGCTCAAAATTCTCCAAGCCAG 196343   1589GAACTTCACGTTTTAGAAAATTCTCCAAGCCAG 196343   196342   196342   196342   196342   196342   196342   196342   196343   196342   196342   196383   196382   196383   196382   196383   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382   196382	1747 TAAACTGTGGAAAATTCTGAAAGGGATACCAGACCACCTGACCTGACTTGAA 1806	1986 CGGGGGAAATAGCAATAACCTCAGATATGCAGATATACCACCTTATGGCAGAAGTGA 2045

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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-darived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 194999 contig of 94999 bp in length 94999 contig of 5636 bp in length 94999 contig of 5636 bp in length 100735 100834; contig of 5636 bp in length 100835 108201; contig of 7367 bp in length 108202 108301; gap of unknown length 108202 108301; gap of unknown length 13524 136023; gap of unknown length 13524 136023; gap of unknown length 16623 contig of 27622 bp in length 16623 is contig of 12192 bp in length 16623 is contig of 12192 bp in length 16624 179018; contig of 12192 bp in length 16624 179018; contig of 12192 bp in length
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AC136201 clone RP42-131B20 (center project name cjz)"
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Chemistry Charlestics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177630 bases at least Q40
Consensus quality: 17830 bases at least Q20
Consensus quality: 17830 bases at least Q20
Insert size: 158000; agarose-fp
Insert size: 178515; sum-of-contigs
Quality coverage: 10.16x in Q20 bases; sum-of-contigs
                                                                                               Submitted (13-NOV-2002) NIH Intramural Sequencing Center, Efforvement Circle, Gatthersburg, MD 20877, USA On Nov 13, 2002 this sequence version replaced gi:24270702.
                                                                                                                                                                                                                                  Center: NIH Intramural Sequencing Center
Center code: NISC
                                                                                                                                                                                                                                                                                              Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .179015
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Center clone name: 002H17
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vector side:
                                   Green, E.D.
Direct Submission
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146496 AGAAAGCTAGTCAATCTAATCACACTAGGACCACACGGCGTATCTAACTCAATGAAACTAA 146437
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237141: contig of 5199 bp in length
237241: gap of unknown length
241923: contig of 4682 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="texcn:9913"
/clone="RP42-75B10"
/clone_lib="RP42"
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                                                                                                                                                                                                                                        143682 AGCGCTGAAGAATTGATGCTTTTGAACTGTGGTGTTGGAGAAGACTCTTAAGAGTCCCTT 143623
                                                                                                                                                                           143503
                                                                                                                                                                                                                                                                                                                            143382 Adridgigargdacadgdgccroccroccartrorogdgrucchaadagrodda 143323
                                                                                                                          2525 AAGGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGACT 2584
                                                                                                                                                                                                                                                                                                        2704
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Bos taurus clone RP42-75B10, WORKING DRAFT SEQUENCE, 13 ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                              143562 AAGGAATGATGCTGAAGCTGAAACTCCAGTACTTTGGCCACCTGATGCGAAGAGTTGACT
                                                                                 143622 GGACTGCAAGGAGATCCAACCACTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTTTGG
                                                                                                                                                                                                                CACTGGAAAAGACCCTGATGCTGGGAGGATTGGGGGCAGGAGGAGGAGGACGACAGA
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Submitted (27-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 241923)
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OM Mar 11, 2003 His sequence version replaced gi:27764650.
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Center code: NISC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: nisc_zoo@nhgri.nih.gov
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Center clone name: 075B10
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HTG; HTGS PHASE2; HTGS_DRAFT..
Bos taurus (Cow)
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AC137656/c
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The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by Por testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contiss have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap, version 0.990319

Consensus quality: 240096 bases at least Q30

Consensus quality: 240096 bases at least Q30

Insert size: 187000; agarose-fp

Quality coverage: 10.42x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**John History and the submittor of 13063 bp in length 13164 20877: contig of 7714 bp in length 20878 20877 gap of unknown length 20878 20877 gap of unknown length 20878 20877 gap of unknown length 20878 20877 gap of unknown length 20878 20879 contig of 25039 bp in length 55042 56041; gap of unknown length 123881 123880; contig of 30857 bp in length 123881 123880; contig of 33520 bp in length 159001 171557; contig of 13550 bp in length 159001 171557; contig of 12357 bp in length 17818 17818; gap of unknown length 17818 17818; gap of unknown length 17819 183813; contig of 6661 bp in length 17819 183813; contig of 6650 bp in length 17819 183813; gap of unknown length 183814 231842; contig of 48029 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length 183814 231842; contig of 661 bp in length
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CCAAAATCACTGCAG 64036 CTCTTAAGAGTCCCTT 63796 CCTGGGATTTCTTTGG 2524 CTGGGTGAACTCCTGG 2704 GTCACAAAGAGTTGGA 2764 || || || || || || || STTGCAAGAGTCGGA 63496 AAGCCCCATCTAGTCA 2344 CTCTTGAGAGTCCCTT 2464 ear MAM 10-OCT-2002 rata; Euteleostomi; a; Pecora; Bovoidea; B., Blakesley,R.W., S., Dietzich,N.L., J.R., Karlins,E., cDowell,J., Maduro,V.B., s. Stantripop,S., B., Stantripop,S., reen,E.D.

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                                                                                                                                                                                                            all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                      otherwise noted
                                                                                                                                                                                                                                                                                                     CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlapp are noted in the beginning and end of the Peatures section.
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  Direct Submission
Submitted (25-UD1-2001) NIH Intramural Sequencing
Grovemont Circle, Gaithersburg, MD 20877, USA
4 (bases 1 to 173068)
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Best Local Similarity 76.6%; Pred. No. 0;
Matches 2628; Conservative 0; Mismatches 165;
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/mol type="genomic DNA"
/db_xref="taxon:9913"
/clone="RP42-354B6"
/clone_lib="RP42"
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ATATACAGGACTECTACAAATAGCTGTGAAAAGGAAAGCAAAAAGCAAAAAGCAAAAAGGAAAAGAAAGGAAAAGAAAAGGAAAAGGAAAAGGAAAA	1718 GCAAAAGCCTTTGACTGTGGGGCTCAATAAACTGTGGAAATTCTGAAGGGGGGGG

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Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.W., Barlamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S. Garlaga, K., Coleman, B., Engle, J., Granite, S., Gunta, J., Haphghi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Paguirigan, C., Pearson, R., Pertnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Wetherby, K.D., Wiggins, L., Yhomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassembles, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid, n/a; 100% of reads Assembly program: Phrap, derived quality: 170812 bases at least Q40 consensus quality: 170812 bases at least Q30 consensus quality: 170812 bases at least Q30 lnsert size: 17500; agarose-fp lnsert size: 17500; agarose-fp Quality coverage: 12.55x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs.

* are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 88373 88472: contig of 88372 bp in length

* 88473 91627: contig of 3155 bp in length

* 91628 91727: gap of unknown length

* 91728 171153: contig of 79426 bp in length.
                                                                                                                                                                                                                                                                                                                                             Submitted (09-OCT-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 171153)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-NOV-2002) NIH Intramural Sequencing Center, 8717 Grovement Circle, Gaithersburg, MD 20877, USA.
On Nov 27, 2002 Lits sequence version replaced gi:23622185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------- Project Information
Center project name: djy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: 243A04
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/organism="Bos taurus<sup>|</sup>

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                                                                                                                                                                                                                                                                                                                    59.5%; Score 2125.5; DB 1; Length 77.3%; Pred. No. 0; tive 0; Mismatches 165; Indels
                                                                                                                        1. .88372
/note="assembly_fragment
/mol_type="genomic DN:
/db_xref="taxon:9913"
/clone="RP42-243A4"
/clone_lib="RP42"
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Bos taurus clone RP42-56B14, WORKING DRAFT SEQUENCE, 2 ordered
pieces.
2466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (04-APR-2003) NIH Intramural Sequencing Center, 8717
Grovenont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 145088)
Green, B.D.
                                                                                                                                                                                                 88501 GGAATGATGCTAAAGGTGAAACTCCAGTACTTTGGCCACCTCATGGAAGAGTTGACTCA
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  2407 CACTGAAGAATTGATGCTTTTGAACTGTGTGTTGGAGAAGACTCTTGAGAGTCCCTTGG
                                      18382 ceccaagaarrearecrirrreaacreregierrregaagaagacrerreagaerecrieg
                                                                                                     2587 CTGGAAAAGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGGAAGGGGACGACAGAG
                                                                                 2467 ACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTTTGGAA
                                                                                                                                                             GGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGCCCACCTGATCAGAAGAGCTGACTCA
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Center code: NISC
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AC142564.2 GI:30315712
HTG; HTGS_PHASE2; HTGS_DRAFT.
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Green, E.D.
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DEFINITION
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## Center clone name: 056B14

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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are prepared as two of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced.

* This sequence will be replaced.

* This sequence will be preserved.

* The accession number will be preserved.

* The accession number will be under the sizes.

* The accession number will be preserved.

* The accession number will be under the sizes.

* This sequence is soon as it is available and by the finished sequence as soon as it is available and the accession number will be unserved.

* This sequence is soon as it is available and the accession number will be unknown length.

* 32952 145088: contig of 112037 bp in length.

* Jorganism="Bost taurus".

* Accession as a contigue of 112037 bp in length.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

24497 24596: contig of 24496 bp in length 24597 47666: contig of 22970 bp in length 47567 47666: gap of unknown length 4757 192431: contig of 144765 bp in length 4767 192431::contig of 144765 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29026 GTCAGGAAGGGGGGGGGGAGAGA----TACCCCTCATCCAGGAGGAAGGAGCAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29201 GAAAACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTCAGGAAGGCGGCAGTGAGGAGGTACCTACCTCGTCCAAGGTAAGGAGCAGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TAAGATGGTAGGTGTTGTGAGAGGCATCAGAGGCCAGACATACTGAAACCATACACGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /noce="clone overlaps with GenBank Accession Number AC141852 clone RP42-269D20 (center project name djg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.4%; Score 2123.49; DB 1; Length 192431; larity 75.1%; Pred. No. 0; Conservative 0; Mismatches 280: Indela 215.
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Consensus quality: 192184 bases at least
Consensus quality: 192227 bases at least
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/organism=Bos taurus"
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/clone lib="RP42"
1. .24496
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29500 29620 29732 29560 29672 29792 29912 30032 30092 30093 ACTGGTCATAGCAAACACCCTCTTCCAAGAACACAAGAGAAGACTCTATACATGGACATC 30152 29972 30212 30332 30392 30452 30512 1019 1079 1139 1259 1319 1379 1439 1199 719 899 29501 AAAGCAAAAAGAATACCCAGCAGTGGATGTGACTGGTGATAGAAGCAAGGTCCGATGCTG 29561 TAAAGAGCAATATTGCATAGGGACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGGA ACCAGATGGTCAACACCGAAATCAGATTTATTTTTTTTCACAGCCAAAGATGGAGAAG <u>AAAGCAAAAAGAATACCCAGCTGTGGATGTGACTGGTGATATAAGCAAGGTCCGATGCTG</u> 540 TAAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGGA AGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGGAATCAGCGAACTAAA 29621 AGTGGTCAAACAAGACATGGCAAGAGTGA-----ATTCTAGGAATCAGCAAACTGAA ATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATCTACTACTGCGGGCAGGA 29673 ATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATCTACTACTGTGGGCCAGGA **ATCCCTCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAGAGTCCGAAATGCAGTACT** 29793 IGGATGCAATCTCAAAAACGACAGAATGATCTCTGTTCGTTTCCAAGGCAAACCATTCAA 840 TATCACAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACG 29853 TATCACAGTAATCCAAGTCTATGCCCCAACCAGTAACACTGAAGAAGCTGAAGTTGAACG TGGCCTTGGAATACGGAATGAAGCAGGCCAAAGACTAATAGAGTTTTGCCAAGAAAATGC 30033 TGGCCTTGGAATACGGAATGAAGCAGGTAAAGACTAACAGAATTTTGCCAAGAAAATGC 1080 ACTGGTCATAGCAACCCCCTCTTCCAACAACAAGAAGAAGAAGACTCTACACATGGACATC ACCAGATGGTCAACACCGAAATCAGATTGATTATATTCTTTGCAGCCAAAGATGGAGAAG CTCTATACAGTCAGCAAAAACAAGAACCAGGAGCTGACTGTGTGCTGCAGACCATGAACTCCCT AGATCTGCTAGATAGACTGCCTGATGAACTATGGAATGAGGTTCCTGACATTGTACAGGA GTCCTATGAAGACCTACAAGACCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCAT TATAGGGGACTGGAATGCAAAGTAGGAAGCAAAGAACACCTGGAGTAACAGGCAAATT TATTGCCAAATTCAGACTTAAATTGAAGAAAGTAGGGAAAACCACTAGATCACTCAGGTA 30333 TGACCTAAATCCCTTATGATTATACAGTGGAAGTGAGAAATAGATTAAGGGCCT CTCTATACAGTCAGCAAAAACAAGACCAGGAGCTTACTGTGGCTCAGATCATGAACTCCT 30273 TATTGCCAAATTCAGACTTAAATTGAAGAAAGTAGGGAAAACCACCACCAGACCATTCAGGTA AGATCTGATAGACAGAGTACCTAATGAACTATGGACAGAGGTTCATGACATTGTACAGGA 1320 AGACCTAAATCCAATCCCTTATGATTATAGAGTGGAAGTGAGAATAGATTTAAGGGCCT

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                                                                                                                                   Athter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, M., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Teurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D., MILL, L., L., L., L., Zhang, L.-H. and Green, E.D.
                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
1 (bases 1 to 173207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-FEB-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 173207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
                AC108887.2 GI:22262483
HTG; HTGS_PHASE2; HTGS_DRAFT.
Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 173207)
Green, E.D.
                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                Green, E.D
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                          REFERENCE
AUTHORS
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
TITLE
JOURNAL
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30890 GTCAGGAAGGCCGGCGGTGAGGAGA----TAACCCTCATCAAGGTAAGGAATGGC 30944
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| . .2422
/note="clone everlaps with GenBank Accession Number
/note="clone everlaps with GenBank Accession Number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31065 GAAAACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TGCGCTTTGCTGGAGCAGCCGTAAAGAGATACCCCCACGCCCAAGGTAAGAGAAACCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31185 AGTCCACTGGAGAAGGGAATGGCAAACCACTTCAGTATTCTTGCCTTGAAAACCCCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31245 ACAGTATGAAAAAGGCAAAATGATAAGGATACTGAAAGAGAAACTCCCCAGGTCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTCAGGAAGGCCGCCAGTGAGGAGAGGTACCTACCCTCGTCCAAGGTAAGGAGCAGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TAAGATGGTAGGTGTTGTGAGAGGGCATCAGAGGGCAGCATACTGAAACCATACACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GAAAACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31125 CCATGCTGTGTGGGGCAACCCAAGATGGGCGGGTCATGGTGGAGAGATCTGACAGAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 ACAGTATGAAAAGGCAAAATGATAGGATACTGAAAGAGGAACTCCCCAGGTCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="clone overlaps with GenBank Accession Number
AC108891 clone RP42-252K20 (center project name cbb)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.0%; Score 2108.1; DB 1; Length 173207;
the accession number will be preserved.

1 42204: contig of 42204 bp in length
42305 42304: gap of unknown length
42305 46414: contrig of 4110 bp in length
46415 46514: gap of unknown length
46515 109660: contig of 63146 bp in length
109661 109760: gap of unknown length
109661 103760: gap of unknown length
109661 103760: gap of unknown length
109661 103760: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.1%; Pred. No. 0;
ive 0; Mismatches
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46515. .109660
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Best Local Similarity 77.1
Matches 2613; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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	- yo	1589 1588
539 GTAAAGAGCAATATTGCATAGGAACCTCGAATGTCAGGTCCATGAATCAAGGGAATTGG 598	35°	32496 TCAGCAATCAATGCAAAGAAATAGAGGAAAACAACAGAATGGGAAAAACTAGGGATCTCT 32555
9 GIAAAGAGCAATATGCATAGGAACCIGGAATGICAGGICCATGAATICAGGICCAGGCAAATTGG	Oy 11	1589 1588
AAGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGSAATCAGCGAACLAA	Db 32	32556 TCAAAAATCAGAGATACCAAAGGAACATTTCATGCAAAGATGGGCTCGATAAAGGACAGA 32615
9 AAGTGGTCAAACAGGAGATGGCAAGAGTGAATGTCGACATTCTAGGAATCAGCGAACTGA	Qy 11	1589 1588
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AATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATCTACTACTGTGGGGCAGG	Qy	1589 1588
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AATCCCTCAGAAAGAAATGGGGCGGCCATCATGATCAACAAAAGAGCCCAAGAAGGGGGCCATCATGATGATGAAGAGTGCAAGAAGAGAGAG	۵۷ 1	1589 1588
779 TTGGATGCAGTCTCAAAACGACAGAATGATCTCTTGTTTGT	Db 32	GATCCAGACATCCTGGAATGTGAAGTCAAGTGGGCCTTAGAAAGCATCACTACGAACAAA
ATATCACAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAAC		
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	Oy 1	1289
TTTCA	0y	1589 1588
9 TTATAGGGGACTGGAATGCAAAGTAGGAAGCAAGAAAGAA		32916 AAAAGGTCCGTTTTCATTCCAAATCCCAAAGAAAGGCAATGCCAAAGAATGCTCAAACTAC 32975
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GACAT	,	1589
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AGGT	, ç	1808 AAITIGIAUGCAGGICAGGAAGCAACAGITAGAACTGGACATGGACAACAACAGTTC 1867
1319 AAGACCTAAATCCAATCCCTTATGATTATACAGTGGAAAGTGAGAAATAGATTTAAGGGCC 1378	. Db 33	m
ALGACTICHGICHGICCCIIAIGAIIAICAGA GGAGGGGGGGGGGGGGGGGG	oy .	CAAGTAGGAAAAGGAGTATGTCAAGGCTGTATATTGTCACCCGGCTTGTTAACTTCTAT 1927
TAGATCTGATAGATAGAGTGCCTGATGAACTATGGAATGAGGTTCATGACATTGTACGG		
STCTG	70 AQ	
AGACAGGGATCAAGACTATCCCCATGGAAAAGAAATGCAAAAAAGCAAAATGGCTC	, ço	1987 GGGAQAAATAGCAATAACCTCAGATATGCAGATGATAACCACCCTTATGGCAGAAAGTGAA 2046
1499 GGGAGGCCTTACAAITAGCTGTGAAAAGAAAAAAAAAAAA	m	AGGAGAAATATCAATAACCTCAGATATGCAGATGGACCCACCACCGTTATGGCAGAAA
	% 4d	2047 GAGGAACTAAAAAGCCTCTTGATGAAGGTGAAAGGAGGGGGAGAGTGAAAAAGTTGCTTAAAG 2200 
32436 GATATAAACATCTGAATGCAGAGTTCCAAAGAATAGCAAGAAGAGATAAGAAAGCCTTCT 32495	1	

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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence configs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid, n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Assembly program: Phrap; version 0.990319

Consensus quality: 212561 bases at least Q30

Consensus quality: 212813 bases at least Q30

Consensus quality: 212927 bases at least Q20

Insert size: 155000; agarose-fp

Insert size: 155000; agarose-fp

Cuality coverage: 9.17x in Q20 bases; sum-of-contigs
                                                             Green, B.D.
Direct Submission
Submitted (06-MAR-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 213549)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 1801: 0001: Gap of unknown length
                                                                                                                                                                                                                              Direct Submission
Submitted (28-MAR-2003) NIH Intramural Sequencing Center, 8
Grovemont Circle, Gaithersburg, MD 20877, USA
On Mar 28, 2003 this sequence version replaced gi:28866995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of unknown length
contig of 39776 bp in length
gap of unknown length
contig of 39921 bp in length
gap of unknown length
contig of 13387 bp in length
contig of 11417 bp in length
gap of unknown length
contig of 145689 bp in length
gap of unknown length
contig of 45689 bp in length
gap of unknown length
contig of 45689 bp in length
gap of unknown length
contig of 60958 bp in length
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
Center: project Information
Center project name: djt
Center zlone name: 525L10
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                                       (bases 1 to 213549)
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41648
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                                                                                                                                                                                                                                                                                                                                COMMENT
CTCAACATTCAGAAATGAAGATTATGGCATCCGGTCCCATCACTTCATGGGAAATAGAT 33635
                                                                                                                                                                                                                                                                33694 ATGTTGACTGCAGCCATGAAATTAAAAGACGCTTACTCCTTGAAAGGAAAGTTATGACCA 33753
                                                                                                                                                                                                                                                                                                                                                         33754 ACCTAGATAGCATATIGAAAAGCAGAGACATTACTTIGCCAACAAAAGGTTCATCTAGTCA 33813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34174 AGTIGGITATGGACAGGGAGGCCTGGCATGCTGTGATTCAT-GGGTAGCAAAGAGTCGGA 34232
                                                                                                                                                                                                               2284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33934 GGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTTTGG 33993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34114 GGANGAGANGGCNGGANGGCANCACNGANGGAGGNGGAGGNGTGAGTGAACNCCGGG 34173
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                                                                                           GGGGGAAACAGTGGAAACAGTGTCAGACTTTATTTTTGGGGGGCTCCAAAATCACTGCAG 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                        2345 AGGCTATGGTTTTTCCAGTGGTCATGTATGGATGTGAGAGTTGGACTGTGAAGAAGCTG 2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2585 CACTGGAAAAGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGGAGAAGGGGACGACAGA 2644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTIGGIGATGGACAGGGAGGCCIGICCIGCGGCATICAIGGGGICACAAAGAGIIGGA 2764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC140963 213549 bp DNA linear HTG 28-MAR-2003
Bos taurus clone RP42-525110, WORKING DRAFT SEQUENCE, 7 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATGAGATGGCTGGATGGCATCACTGGATGGACGTGAGTCTGGGTGAACTCCTGG 2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mamalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos 1 to 213549)
                                                                                                                                33636 GGAGAAACAGTGGAAACAGTGTCAGATTTTTATTTTT--CTGGGGTCCAAAATCACTACAG
                                                                                                                                                                                                         ATGGTGACTGCAGCCATGAAATTAAAAGACACTTACTCCTTGGAAGAAAGTTA--ACCA
                                                                                                                                                                                                                                                                                                                       2285 ACCTAGATAGCATATTGAAAAGCAGAGACATTACCTTGCCAACAAAGCCCCCATCTAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2405 AGCACTGAAGAATTGATGCTTTTGAACTGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTT
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HTG; HTGS PHASE2; HTGS_DRAFT.
Bos taurus (cow)
Bos taurus
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Antonellis, A., Ayole, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeeley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Culu, G., Coleman, H., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, V.B., Marghiles, E.H., Masiello, C., Maskeri, B., McDowell, J., Paquirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sion, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Wogt, J.L., Wetherby, K.D., Wagins, L., Young, A. and Green, E.D., NISC, Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
1 (bases 1 to 196994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence control has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or compirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                     AC144887 196994 bp DNA linear HTG 18-JUN
Bos taurus clone RP42-433E9, WORKING DRAFT SEQUENCE, 8 ordered
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Submitted (18-JUN-2003) NIH Intramural Sequencing Center, 8717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grovemont Circle, Gaithersburg, MD 20877, USA
On Jun 18, 2003 this sequence version replaced gi:31044307.
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Consensus quality: 195487 bases at least Q40
Consensus quality: 195527 bases at least Q30
Consensus quality: 1957000, agarose-fp
Insert size: 167000, agarose-fp
Insert size: 167001, sun-of-contigs
Quality coverage: 12.61x in Q20 bases; agarose-fp
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgril.nih.gov
Centact: project Information
Center project name: eeg
Center clone name: 433E09
AC144887.2 GI:31880107
HTG; HTGS_PHASE2; HTGS_DRAFT.
Bos taurus (cow)
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                                              GAGTACATCATGAGAAACGCTGGACTGGAAGAACACACAAGCTGGAATTGCCGGG
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                       AACATCTATTTCTGCTTTATTGACTATGCAAAAGCCTTTGACTGTGGGGGTCACAATAAA
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                                                                                                                                                                                                                                                                               1871 GTAGGAAAAGGAGTATGTCAAGGCTGTATATTGTCACCCGGCTTGTTAACTTCTATGCA
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51811 GCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAACAGTATGAAAAGGCAAAATG 51752
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                            261 AAGATGGGCAGGTCATGGTGGAGAGATCTGACAGAATGTGGTCCACTGGAGAAGGGAAT- 319
                                                                                                                                                                                                                            51751 ATAGGATACTGAAAGAGAACTCCCCAGGTCGGTAGGTGCCCAATATGCTACTGGAGATC
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                       **NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced the sequence as soon as it is available and the accession number will be preserved.

**A6248 68108 contig of 46247 bp in length 46348 68108 contig of 46247 bp in length 46348 68108 contig of 21761 bp in length 68108 contig of 28412 bp in length 68209 96680 contig of 26698 bp in length 96780; gap of unknown length 123479 123579; gap of unknown length 123579 135607; contig of 26698 bp in length 123579 135607; contig of 12029 bp in length 142953 145991; contig of 2639 bp in length 142953 145991; contig of 2639 bp in length 142953 145591; contig of 2639 bp in length 142953 145591; contig of 2639 bp in length 142953 145591; contig of 2639 bp in length 142953 145591; contig of 51303 bp in length.

**Location/Qualifiers**
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 59.0%; Score 2106.5; DB 1; Length 196994; Best Local Similarity 77.5%; Pred. No. 0; Matches 2609; Conservative 0; Mismatches 145; Indels 611; Gaps
Quality coverage: 10.73x in Q20 bases; sum-of-contigs
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/note="assembly_fragment"
68209._96680
/note="assembly_fragment"
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145692. .196994
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/clone_lib="RP42"
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/note="assembly_fragment
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/db_xref="taxon:9913"
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vector_side:right"
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AC139312 192199 bp DNA linear HTG 21-FEB-2003 Bos taurus clone RP42-482K4, WORKING DRAFT SEQUENCE, 10 ordered pieces.

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AC139312.

AC139312.

AC139312.2 GI:28460773

HTG; HTGS_PHASE2; HTGS_DRAFT.

BOS taurus

BOS taurus

BOS taurus

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Bovidea; Pecorai Bovidea;

Satheria; Cetartiodactyla; Ruminantia; Pecorai Bovidea;

Bovidea; Bovinea; Bos.

1 (bases 1 to 192199)

E Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.W.,

Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,

Cariaga,K., Coleman,B., Engle,J., Granite,S., Guna,X., Gupta,J.,

Haghighi,P., Lee-Lin,S.-O., Legaspi,R., Maduro,Q.L., Maduro,V.B.,

Reddix-Dugue,N., Schanler,M., Schueler,M.G. Sison,C.,

Stantripop,S., Thomas,J.W., Thomas,P.Y., Touchman,J.W., Vogt,J.L.,

NECComparative Sequencing Initiative

NINC Comparative Sequencing Initiative

Schools S. Thomas,D.,

Stantribop,S. Thomas,D.,

Stantribop,S. Thomas,D.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,

Netherby,K.D., Wiggins,L., Young,A. and Green,E.D.

Stantribop,S. Thomas,D.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,

Netherby,K.D., Wiggins,L., Young,A. and Green,E.D.

Stantribop,S. Thomas,D.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,

Netherby,K.D., Wiggins,L., Young,A. and Green,E.D.

Stantribop,S. Thomas,D.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,

Netherby,K.D., Wiggins,L., Young,A. and Green,E.D.

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Submitted (30-JAN-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 192199)
Green, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-FEB-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA. On Feb 21, 2003 this sequence version replaced gi:28144407.
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Center code: NISC
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least BX average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Chemistry: Dye-terminator Big Dye; 100% of reads assembly program: Planeaud; n/a; 100% of reads Assembly program: Phrap, else is 090319

Consensus quality: 190839 bases at least Q40

Consensus quality: 190839 bases at least Q20

Insert size: 160000; agarose-fp

Quality coverage: 0.93x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and

1310 150454 1370 150394 1430 150338		150158 AAGCCTTCTTCTGCGATCAATGCAAAGAAATAGAGGAAAACAACAAGAATGGGAAAGACTA 150099 1589 1588 150098 GGGATCTCTTCAAGAAAATCAGAGATACCAAAGGAACATTTCATGCAAAGATGGGCTCGA 150039	B TAAAGGACAGAAATGGTATGGACCTAACAGAAGCAGAAGATATTAAGAAGAGATGGCAAG  9	B TCACTGACCTAGAGCCAGACATCCTGGAATGTGAAGTCAAGTGGGGCCTTAGAAAGCATCA 9	1589	149678   GCTCAAACTACCGTACAATTGCACTCATCTCCACCACCACTAAAGTTATGCTCAAATTC   149619     1589	1677 GAGAGTTCCAGAAAACATCTATTTCTGCTTTATTGACTATGCAAAAGCCTTTGACTGTG 1736
6 8 6 8 6 8 6	8 8 8 8	4 6 6	6 6 6 6	6 6 6 6	8 8 8 8 8	8 8 8 8	8 8 8 8 8
231 TGAAACTAAGCCATGCGGCAACCCAAGATGGGCAGGTCATGGTGGAGAGATCTG [	410 CAGTAGGTGCCCATATGCTACTGGAGATCAGTGGAGAAATAACTCCAGAAAGAA	530 TCGATGCTGTAAAGAGCAATATTGCATAGGAACCTGGAATGTGAGGTCCATGAATCAG 589   151233 TCCGATGCTATAAAGAGCAATATTGCATGGAACCTGGAATGAGGTCCAGGAATCAG 151174   151233 TCCGATGCTATAAAGAGCATATTGCAAACCTGGAATGCAGGATGCAGATCAGATCAG 151174   590 GCAAATTGGAAGTGGTCAACCAAGAGGGCAAGAGTGAAATGTAAGAATCA 649	650 GCGAACTAAAATGGACTGGAATTAACTCAGATGACCATTATATCTACTACT 709	770 ATGCAGTACTTGGATGCAGTCTCAAAACGACAGATGATCTCTGTTTGCAAGGCA 829	890 150873 950 150813	150753 CAGGAAATTGGCCTTGGAATATGGAATAAGCAGGCAAAGACTAATAGAGCTTGAC  1070 AAGAAAATGCACTGGTCATAGCAAACACCCTCTTCCAACAAGACTAATAGAGTCTTGAC  150693 AAGAAAATGCACTGGTCATAACAAACACCCTCTTCCAACAACACAAAAGAGACTCTACAA  1130 CATGGACATCACCAGATGGTCATAACAAACACCCTCTTCCAACAACACACAAAAGAAGACTCTACAA  1130 CATGGACATCACCAGATGGTCAAACACACACAAATGATTATATTCTTTGCAGCCAAA	150633 CATGGACATCACCAGATGGTCAACACCGAAATGATTATATTCTTTGCAGCCAAA 150574   1190 GATGGAGAAGCTCTATACAGTCAGCAAAAACAAGAACCAGAGGCTTACTTGTGGCTCAGATC 1249   150573 GATGGAGAAGCTCTATACAGTCAGCAAAAACAAGACCAGAAGCTGACTGTGGCTCAGATC 150514
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                                                             149258 TTAACTTATATGCAGAGTACATCATGAGAAATGCTGGACTGGAAGAAGCACAAGCTGGAA 149199
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                                         CAGACTGGTTCCAAGTAGGAAAAAGGAGTATGTCAAGGCTGTATATTGTCACCCGGCTTGT 1916
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                                                                                                 GAAGAAAGCTGAGCACTGAAGAATTGATGCTTTTGAACTGTGGTGTTGGAGAGACTCTT
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AC142564 145088 bp DNA linear HTG 02-MAY-2003 Bos taurus clone RP42-56B14, WORKING DRAFT SEQUENCE, 2 ordered pieces.

RESULT 14 AC142564/c LOCUS DEFINITION

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8587 ATGGACTGGAATGGGTGAATTTA	Qy 720 ATCCTCAGAAGAAATGGAGTAGCC 	Qy 780 TGGATGCAGTCTCAAAAAGGACAGA 	Qy 840 TATCACAGTAATCCAAGTCTATGCC	8407	OY 900 GTCCTATGAAGACCTTACAAGACCTT D	096	Db 8287 TATAGGGGAC-AGAATGCAAAAGTA	Qy 1020 TGGCCTTGGAATACGGAATGAAGCACACACACACACACAC	1080	8168 ACTGGTCATAGCAAACAC	1140	8108 ACCAGATGGTCAACACCGAA	QY 1200 CTCTATACAGTCAGCAAAACAAGA	1260	7988	Db 7928 TGACCTAAATCAAATCCTTATGATCAATCAATCAATCAAT	1380	Db 7868 AGATCTGATAGATAGAGTGCCTGATA	7808		7748	OY 1560 ATAAAGCATCTGAATGCAGATTC  -  -	1589		1589	DD /568 CAGGAAATTAGAGAIACCAAAGGC
accession number will 32951: contig	<ul> <li>\$ 32952 33051: gap of unknown length</li> <li>\$ 33052 145088: contig of 112037 bp in Location/Qualifiers</li> </ul>	source 1. 145088   organism=Bos taurus"   mol_type="genomic DNA"   db_xref="taxon:9913"	/clone="RP42-56B14" /clone_li="RP42" misc feature 132951		vector side:left" misc_feature 33052.~14508 /note="massembly fragment	clone_end:SP6 '	) 4 5 9 9 9	; DB 1; Length	st notal Similarity 76.3%; Fred. No. 0; tches 2613; Conservative 0; Mismatches 168; Indels 618; Gaps 10;	1 GTCAGGAAGGGCGCAGTGAGGAGAGGTACCTACCCTCGTCCAAGGTAAGGAGCAGTAGC 60 9242	TGCGCTTTGCTGGAGCAGCGGTAAAGAGATACCCCACGCCCAAGGTAAGAGAAACCCCAAG		121 TAAGATGGTAGGTGTTGTGAGAGGCATCAGAGGCAGACATACTGAAACCATACAGGCA 180	INNON TOGITAGOILO ILGENNON COOLOGIA CHARACACACACACACACACACACACACACACACACACAC	9067 GAAAACTAGTCAATCTAATCACCTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAG 9008	241 CCATGCCCGTGGGGCAACCCAAGATGGGCAGGTCATGGTGGAGATCTGACAGAATGTG 300	GTCCACTGGAGAAGGGGAAT-GCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAA 359	8947 GTCCACTGGAGAAGGGAATGGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAA 8888	360 CAGTATGAAAAGGCAAAATGATAGATACTGAAAGAGGAACTCCCCAGGTCAGTAGGTGC 419	CCCATATGCTACTGGAGATCAGTGGAGAATAACTCCAGAAAGAA	8827 CCAATAIGCTACTGGAGATCAGTGGAGAATAACTCCAGAAAGAATGAAGGAIGGAGCC 8768	480 AAAGCAAAAAGAATACCCAGCTGTGGATGTGACTGGTGATATAAGCAAGGTCCGATGCTG 539	8767 AAAGCAAAAAGAATACCCAGCTGTGGATGTGACTGGTGATAGAAGCAAGGTCCGATGCCT 8708	540 TAAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGGA 599 8707 CAAAGAGCAATATTTGCATAGGAACCTGGAATGTCAAGTCCATGAATCAAAGAGAAATGAAAAAAAA	ATTGCTCAACAGGGCAGGCGAGGGGGGGGGGGGGGGGGG	8647 AGTGGTCAAAGAGAGGCAAGAGTGAATGTCCACATTGTAGGAAACAGCGAACTGAA 8588

8468 8408 8348 8288 1019 8229 8109 1199 AGGGCAAAGACTAATAGAGTTTTGCCAAGAAATGC 1079 AGGCCAAAGACTAATAGAGTTTTGCCAAGAAAATGC 8169 CCAACAACAAGAGAGACTCTACACATGGACATC 1139 8049 1259 1319 7929 1379 7869 1439 7809 1499 7749 CTCAGATAACCATTATATCTACTACTGTGGGCAGGA 8528 7989 7689 7629 839 899 AGAAGATATTAAGAAGAGATGGCAAGAATACACAGA 7449 959 AAGAAGAGGAAAGCAAAGGAAAAAGGAAAG 1559 GAAAACAACAGAATGGGAAAGACTAGGGATCTCTT 7569 CACATTICATGCAAAGATGGGCTCGATAAAGGACAG 7509 ACCAGGAGCTTACTGTGGCTCAGATCATGAACTCCT AATGATCTCTGTTTGCAAGGAAACCATTCAA CCCAACCAGTAACACTGAAGAGCTGAAGTTGAACG AGGAAGCAAGAACACCTGGAGTAACAGGCAAATT CTAACAACACAAGAGAAGACTCTATACATGGACATC TGAACTATGGACAGAGGTTCATGACATTGTACAGGA CCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACG TTTAGAACTAACACCCAAAAAAGATGTCCTTCTCAT AGGAAGTCAAGAACACCTGGAGTAACGGGCAAATT GAAGAAAGTAGGGAAAATCACTAGACCATTCAGGTA GAAGAAAGTAGGGAAAACCACTAGATCACTCAGGTA TTATACAGTGGAAGTGAGAATAGATTTAAGGGCCT TGATACAGTGGAAGTGAGAATAGATTTAAGGGCCT CCAAAGAATAGCAAGAAGAGATAAGAAAGCCTTCTT

2285 ACCTAGATAGCATATTGAAAAGCAGAGACATTACCTTGCCAACAAAGCCCCCATCTAGTCA 2344 6382 ACCTAGATAGTGTATTCAAAAGCAGAGACATTACTTTGCCAACAAAGGTCCGTCTAGTCA 6323 2345 AGGCTATGGTTTTTCTGTGGTCATGTATGGAGTTGGACATTGCACAAAAGCTC 2404 6322 AGGCTATGGTTTTTCTTGTGGTCATGTATGGAGTTGGACTTGGACAAAAGCTC 6263 2405 AGCACTGGAAAAAGTTTTTTTTTTTTTTTTTTTTTTTTT	AC142562  AC142562  Bos taurus clone RP42-371H23, WORKING DRAFT SEQUENCE, 3 unordered pleces.  Bos taurus clone RP42-371H23, WORKING DRAFT SEQUENCE, 3 unordered pleces.  AC142562.  AC142562.  AC142562.  AC142562.  GUI: 11044306  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                              Consensus quality: 188774 bases; sum-of-contigs

Sequencing vector: plasmid; n/a; 100% of reads

Sequencing vector: plasmid; n/a; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 188607 bases at least Q40

Consensus quality: 188774 bases at least Q30

Consensus quality: 188774 bases at least Q30

Consensus quality: agarose-fp

Insert size: 108000; agarose-fp

Quality coverage: 18.32x in Q20 bases; agarose-fp

Quality coverage: 18.32x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
    May 23, 2003 this sequence version replaced gi:29540597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.8%; Score 2100; DB 1; Length 189278; 77.0%; Pred. No. 0; 77.0%; ive 0; Mismatches 170; Indels 610;
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                                                                                                                                                               Akther, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariania, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariania, S., Guan, K., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Iddl, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Witcherby, K.D., Wiggins, L., Young, A. and Green, B.D.
                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in 020 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (07-FEB-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 224721)
Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (122-MAR-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA ON MAR 22, 2003 this Sequence version replaced gi:28269383.
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* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* is believed to be correct as given, however the sizes

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 2461: contig of 2461 bp in length
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Insert size: 223921; sum-of-contigs
Quality coverage: 11, 7x in Q20 bases; agarose-fp
Quality coverage: 10.04x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 222839 bases at least Q30 Consensus quality: 223479 bases at least Q30 Consensus quality: 223749 bases at least Q20
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  HTGS PHASE2; HTGS DRAFT
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SOURCE
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COMMENT

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46939 TGAAACTAAGCCATGCCCATGGGGAACCTAAGACGGGCAGGTCATGGTGGAGAGATTTG 46880
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/note="clone overlaps with GenBank Accession Number
AC139312 clone RP42-482K4 (center project name ddk)"
2561: gap of unknown length 44437: contig of 39876 bp in length 45337: gap of unknown length 145666: contig of 103129 bp in length 145666: gap of unknown length 147122: gap of unknown length 147212: gap of unknown length 180593: contig of 1346 bp in length 180593: gap of unknown length 185471: contig of 3381 bp in length 185471: gap of unknown length 185471: gap of unknown length 187940: gap of unknown length 187940: gap of unknown length 187940: gap of unknown length 215756: gap of unknown length 215756: gap of unknown length 215756: gap of unknown length 215756: gap of unknown length 215756: gap of unknown length 215756: gap of unknown length
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Green, E.D.
Direct Submission
Submitted (06-OCT-2001) NIH Intramural Sequencing Center, 8717
Submitted (06-OCT-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
ON Oct 6, 2001 this sequence version replaced gi:14192894.
On Oct 6, Zong this sequence conter
                                                                                                                                                                                                                                                                                                                                                                                                    Green E.D.

Direct Submission
Submitted (11-APR-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 183383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlapping are noted in the beginning and end of the Features section.

Location/Qualifiers
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/note="single clone coverage"
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135741. .135747
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Web site: http://www.nisc.nih.gov
Contact: nisc mouse@hhgri.nih.gov
Center project Information
Center project name: axx
Center clone name: 324C24
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                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                 TTAACTICTATGCAGAG-ACATCATGAGAAACGCTGGGAGGAAGAAGAAGCACAAGCTGGAA 1975
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                                                             AGTTA--ACCAACCTAGATAGCATATTGAAAAGCAGAGACATTACCTTGCCAACAAAAGCC
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Score 2081.09; DB 1; Length 183383; Pred. No. 0;

58.3%; 75.5%;

Query Match Best Local Similarity

Bos taurus (cow) Bos taurus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS

/note="single clone coverage" 160866. 160900 /note="single clone coverage"

misc\_feature

1084 GTCATAGCAAACACCTCTTCCAACAAAGAAGACTCTACACATGGACATCACCA 1143	1264 GCCAAATTCAGACTTAAATTGAAGAAAGTAGGGAAAACCACTAGATCACTCAGGTAAGAC 1323	1444 GGGATCGAGACCATCCCCATGGAAAAGAAATGCAAAAAGCAAAATGGCTGTCTGGGGAG 1503	1589	CTGTACAGAAAGATCTTCATGACCCAGATAATCACAATGGTGTGATCACTGACCTAGAG	71798 AGTGGAGGTGATTCCAGTTGAGCTATTCCAAATCCTGAAAGATGATGTGTGAAA 71857 1589
8 6 8 6 8 6	868686	8 8 8 8 8	868686	8888	8 8 8 8 8 8
Matches 2669; Conservative 0; Mismatches 244; Indels 623; Gaps   Gaaggaggaggaggaggaggaggaggaggaggaggaggag	70003 CGGTAGGTGTTGCAAGAGGGCATCAGAGGCCAAACCACTGAAACCATACTCACAG-AAA  186 CTAGTCAATCTAATCACACTAGGACCACGCCTTGTCTAACTCAATGAAACTAAGCCATG	DD   70182 CTGGAGAAGGAATGGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAACAGTA 70241	545 AGCAATATTGCATAGGAACCTGGAATGCAGGAATGAAGGCAAATTGGAAGTGG	Db 70542 CTGG-AIGGGIGACTITAACTCAGAIGACCATTATATCTACTACTGCGGCAGGAATCCC 70600  Qy 725 ICAGAAGAAAIGGAGTAGCCATCATGGTCAACAAAAGAGTCCGAAATGCAGTACTTGGAT 784	

	z E	Mammalla: butnerla; Bovidae; Bovinae; Bo 1 (bases 1 to 1396; Antonellis,A., Ayele Bouffand,G.G. Brinh Coleman,H., Engle,U Han,J., Hansen,N., Karlins,E., Kwonel, Legaspi,R., Maduro,, Maskeri,B., McDowell Portnoy,M.E., Prasac		Green, B.D.  Direct Submission  Submitted (04-NOV-2003) NIH Intramural Sequencing Center, 8717  Submitted (04-NOV-2003) NIH Intramural Sequencing Center, 8717  Grovemont Circle, Galthersburg, MD 20877, USA  ON Nov 4, 2003 this sequence version replaced gi:37693553.	Center project name: eyr  Center clone name: 509J20  The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g.,
8 6 8 6 8 6 8	RESULT 18 AC146889 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE	AUTHORS TITHE JOURNAL COMMENT	
	1871 GTAGGAAAAGGAGTATGTCAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTATGCA 1930 72337 ATAGGAAAAGGAGTTCATCAAGGCTGTCTATTGTCACCCTGTTTTATTTA	2050 GAACTAAAAAGCCTCTTGATGAAGGGGAAGGGGAGGGAAAAGGTTGGCTTAAAGCTC 2109	GTGACTGCAGCCATGAAATTAAAAGACACTTACTCCTTGGAAGAAAGTTAAC 	0 0 0 0 0	2528 GAATGATGATGAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGTGACTCACTC

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30076 AGGGCAAAACAATACCCAGCTGTGGATGTGACTGGTGATAGAAGCAAGGTCCGATGCTG 30135
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TAAGATAGGTATTGCAAGAGGGCATCAGACGGCAAACAACACTGAAACCATACTCACA
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**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**S9778** 114249: contig of $9777 bp in length 114250 114349: contig of $4372 bp in length 114350 113549: contig of $1003 bp in length 113552: contig of $1003 bp in length 113553 135617: contig of 4165 bp in length 115450 115452: gap of unknown length 115553 135617: contig of 4165 bp in length 115553 135617: contig of 4165 bp in length 115551 contig of 4165 bp in length 115551 contig of 4165 bp in length 115551 contig of 4165 bp in length 115551 contig of 4165 bp in length 115551 contig of 4165 bp in length 115551 contig of 4165 bp in length
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31992 AAATCTGTATGCAGGTCAGGAAGCAACAATTAGAACTGGACATGGAGCAACAGACTGGTT 32051	1867 CCAAGTAGGAAAAGGAGTATGTCAAGGCTGTATATTGTCACCGGGCTTGTTTAACTTCTA 1926 	1927 TGCAGAG-ACATCATGAGAAACGCTGGGAAGAAGAAGCACAAGCTGGAATCAAGATTGC 1985 	1986 CGGGAGAAATAGCAATAACCTCAGATATGCAGATGATAACCACCCTTATGGCAGAAAGTGA 2045 	2046 AGAGGAACTAAAAAGCCTCTTGATGAAGGTGAAAGAGGAGAGTGAAAAAGTTGGCTTAAA 2105 	2106 GCTCAACATTCAGAAAACGAAGATCATGGCATCTGGTCCCATCACTTCATGGGAAATAGA 2165	2166 IGGGGAAACAGTGGAAACAGTGTCAGACTTTATTTTTGGGGGGCTCCAAAATCACTGCA 2225 	2226 GAIGGIGACTGCAGCCAIGAAATIAAAAGACACTIACTCCTIGGAAGAAAGTIAACC 2283	2284 AACCTAGATACCATATTGAAAAGCAGAGACATTACCTTGCCAACAAAGCCCCATCTAGTC 2343 	2344 AAGGCTATGTTTTCCAGTGGTCATGTATGGATGTGAGAGTTGGACTGTGAAGAAGCT 2403 	GAGCACTGAAGAATTGATGCTTTTGAACTGTGTGTTGGAGAAGACTCTTGGAGAGTCCCT 24	GAGIGGCCARAGARIIGANIGGIIIIGANG CIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAAGGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGAC	TCATTGGAAAAAGCCTGATGCTGGGGGGATTGGGGGCAGGAGAGAGGGGACGACGCTCTGATGCAAAAAAAA	2644 AGGATGAGATGGCTCGGTGGCATCACTGACTCGATGGGTGAGTCTGGGTGAACTCCTG 2703 	2704 GAGTIGGIGALGGAGGGAGGCCTGICCTGCGGGGATTCATGGGGTCACAAAGAGTTGG 2763 32890 GAGTIGGTGALGGACAGGGAGCCCTGCGGCGATTCATGGGGTCGCAAAGAGTTGG 2763 2764 ACACGACTGAGCAAGTGAACTGAACTGAACTGAACTGAA	ACATGACTGAGTGACTGAACTGAACT 329	RESULT 19 AC145440/c LOCUS AC145440 DEFINITION BOS taurus clone RP42-116J2, WORKING DRAFT SEQUENCE, 5 ordered  , so taurus clone RP42-116J2, WORKING DRAFT SEQUENCE, 5 ordered  , so taurus clone RP42-116J2, WORKING DRAFT SEQUENCE, 5 ordered
1320 AGACCTAAATCCATATGATTATACAGTGGAAGTGAGAAATAGATTTAAGGGCCT 1379	AGATCTGATAGACAGAGTACCTAATGAACTATGGACGAGGTTCATGACATTGTACAGGA 	GACAGGGATCGAGACCATCCCCATGGAAAAGAAATGCAAAAAAGCAAAAAGGCTGTCTGG	GGAGGCCTTACAATACCTGCAAAAAAAGAAGAAGAAGAAGAAACAAAAAAAA			31212 CAGTGAICAANAGAAAIAGAAAIAAGAAAIAAGAAIGAGAAAGACIAGAAAGACIAGAGAAIGAGAAIAGAGAAIACICICII 312/1  1589		ANA I GGA A I GGARCC I ANCAGANGA I AN I ANGANGAG I GGCANGAN I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGARA I ANGA	31392 AGAACTGCACAAAAAGGCTTCACGACACAGATAATCACGATGGTGTGATCACTGACCT 31451 Qy 1589	31452 AGAGCCAGACATCCTGGAATGTGAAGTCAAGTGGGCCTTAGAAAGCATCACTACGAACAA 31511 Qy 1589 1588	31512 AGCTAGIGGAGGIGAATTCCAGTTGAGCTATTTCAAATCCTGAAAGATGATGCTGT 31571 UD  QY 1589 1588	31572 GAAAGTGCTGCACTCAATATGCCAGCAAATTTGGAAAACTCAGCGGTGGCCACAGGACTG 31631 QY 1589 1588	31691 1588	31692 CTGCACAATTGCACTCACACACTAGTAAAGTAATGCTCCAAAATGCTCCAAGCCAG 31751  1589	aggaaccagagaccaanttgccaacatctctgtatcatggaaaagcaagagttcca 	1687 GARARGATCTATTCTGCTTTATTGACTATGCAAAGCCTTTGACTGTGGGGGTCACAA 1746	1747 TAAACTGTGGAAAATTCTGAAAGGGATGGGAATACCAGACCACCTGACCTGACTCTTGAA 1806 31932 TAAACTGTGGAAAATTCTCAAAGAGATGGGAATACCAGACCACCTGACCTGCTCTTGAG 31991 D5 1807 AAATTGTATGCAGGAAGAAGATGAAACTGGAACAGACGACAACAGAACAGACTGGTT 1866

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                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Eutheria, Cetartiodactyla, Ruminantia; Becora, Bovoidea,
Bovidea; Bovinae; Bos.

1 (bases 1 to 17202)
S Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K.,
Chu, G., Coleman, B., Coleman, H., Engle, J., Ho, S.-L., Hu, P.,
Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-O.,
Legaspi, R., Maduro, O.L., Maduro, V.B., Margulies, E.H., Masiello, C.,
Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M. E.,
Praaad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K.,
Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V.,
Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-JUL-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 172022)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 700.000.

Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 717103 bases at least Q40
Consensus quality: 717106 bases at least Q30
Consensus quality: 177567 bases at least Q20
Insert size: 164000; agarose-fp
Insert size: 1162; sum-of-contigs
Quality coverage: 11.81x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and
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AC145440.2 GI:33413342
HTG, HTGS_PHASE2; HTGS_DRAFT.
Bos taurus (cow)
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Green, B.D.
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ACCESSION
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KEYWORDS
SOURCE
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TITLE
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/note="clone overlaps with GenBank Accession Number AC140094 clone RP42-36903 (center project name edy)"

61598. 1100735

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61498 61597; contig of 61497 bp in length 61598 61597; gap of unknown length 100735; contig of 51313 bp in length 100736 100835; gap of unknown length 114149 114248; contig of 13313 bp in length 114149 114248; gap of unknown length 11429 114248; gap of unknown length 11429 1147871; contig of 33623 bp in length 47972 172022; contig of 24051 bp in length. Location/Qualifiers
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114249. .147871
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1017   AGADAMATTGCCCTTCGAAAACACACAAACACTCCTCCAAAACCTCCAAAACTTCCAAAACACTCCAAAACTTCCACCA	ò			45723 CTCAAACTACGGCACP
10.11   AGAMANICCACCIOCATAGACACCACAGAGAGAGAGACTICACA   146684   146743   AGAMANICCACCIOTATACATACACAGAGAGAGAGAGACTICACA   146684   09   146693   146743   AGAMANICCACTOGTCATACACACACAGAGAGAGAGAGAGACTICACACAGAGAGAGAGACTICACACAGAGAGAGAGACTICACACAGAGAGACTICATACATACATACATACACACAGAGACTICATACATACAGACACCACAGACTICACAGAGACACACAGACACACAGACACACAGATACAGACACAGAGACACACAGACACACAGACACACAGACACACACAGACACACAGACACACAGACACACACACACACACACACACACACACACACACACACAC	q <sub>Q</sub>			
1131   ATGACATCATCATCACAAAACACCAAAACACAAAACATCACAAAACATCACAAAACATCACAAAAACATCACAAAAACACCAAAACACCAAAACACCAAAACACCAAAA	à			.45663 CCAGGCCAGGCTTCAG
1131   ATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Q C		ò	1618 AAAAGTCAGAGGAACC
1191   ATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	& &			
146523 ATGAGGGCTAATTACCAAAACAAAACAAAACAAAACAAA	ì à		δ	
1251   TGAACTCCTTATTCCCAAATTCAACTAAATTGAACGGAAAACCACTAGATC   1310   Db   145488   146563   TAAACTCCTTATTACCAAATTCAACAAAAACTAACGGAAAACCACTAGACC   146504   Oy   1738   1311   TAACGGCTAACATCCAAATTCAACAATTAAATTACAGTGGAAAACACAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTCAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAAA	ž <u>£</u>		Dp 7	
146563   TAACTCCTTATTACCAATTCAACCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAAAAA	ò		yo t	
1311   ACTCAGGTAAGACCTAAATCCAATCCTTATGATTATCAGTGGAAGTGAGAATAGATT   1370   DE   145423     146503   ATTCAGGTATGACCTAAATCCCTTATGATTATCAGTGGAAGTGAGATAGAT	qq	TAAACTCCTTATTACCAAATTCAGACTGAAATTGAAGAAAGTAGGGAAAAACCACTAGACC	g è	
146503 ATTCAGGTATGACCTAAATCAAATCAAATCAAATCAAAT	ò			45423 CCTCTTGAGAAACCTA
1371   TAAGGGCCTAGATGATGACTAATGACTATGACGAGAGTTCATGACT   146143   TAAGGGCCTAGATGATGACTAATGACTATGACATAGATTCATGACT   145364   1918     146143   TAAGGGCCTAGATGATGACTACTGAAAACTATGAAAAATG   146384   09   145363     146143   TGTACAGGAGACCAGGAACCATCCCCATGGAAAAGGAAAAAGGAAATG   1490   Db   145303     146143   TGTACAGGAGACAGGGATCAGAAAAGGAAAAGGAAAAATG   1490   Db   145303     146143   TGTACAGGAGACAGGGATCAGAAAAGAAAAAGAAAAAAAA	QQ			1858 AGACTGGTTCCAAGTA
1431   TGTACAGGGACCTAGGAAACTATGGAAACTATGACATTCATGACATTCATGACATTCATGACATTCATGACATTCATGACATTCATGACATTCATGACATTCATGACATTCATGACATTCCATGGAAAACGAAAACGAAAATG	δí			
146143 AGATECTETCAGGAGACCATCCCATGGAAACAAAAAAAAAA	gg (		ò	
1491 GCTGTCTGGGGGGGCCTTACAAATAGCTGTGAAAAGAAAG	& B			.45303 TAATTTCTATGCAGAG
146143 AGATCTTCTACAAAAAGAAAAAAAAAAAAAAAAAAAAAA	ò			
1551 AAAGGAAAGATTAAAAGCAAGTTCCAAA	qq	GCTGTCTGGGGGGGCCTTACAAATAGCTGTGAAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAA		
146263 AAAGGAAAGTATAGAATATAGAAGTTCCAAAGAATAGCAAGAAGAAGAAGAAGAAGAAAAGAAAAGAAATAGCAAGGATCCAAAGAAATAGCAAGAATATAGAAGATTCATGCAAAGAAATAGAAAATAGAAGAAAATTCATGCAAAGAAAG	ò	AAAGGAAAGATAAAAGCATCTGAAATGCAGAGTTCCAAA		
1589 1588 Db 145123 146203 AGCCTTCCTCAGTGATCAAGGAAATAGAGAAACAACAGAATGGGAAAGACTAG 146144 Qy 2157 1589 1588 Db 145063 146143 AGATCTCTTCAAGAAAATTAGAGATACCAAGGGGACATTTCATGCAAAGATGGGCTCGAT 146084	QQ			
146203 AGCCTTCCTCAGTGATCAAAGAAAATAGAGGAAAACAACAGAAATGGGAAAAGACTAG 146144 Oy 2157 1589 1588 Db 145063 146143 AGATCTCTTCAAGAAAATTAGAGATACCAAGGGACATTTCATGCAAAGATGGGCTCGAT 146084	δλ	1		45123 TGGCTTAAAGCTCAAC
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146143 AGATCTCCTCCAAGAAAATTAGAGATACCAAGGGACATTTCATGCAAAGATGGGCTCGAT	ò			 .45063 GGAAATAGATGG
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NTATGGACCTAACAGAAGCAGAAGATATTAAGAAGAGATGGCAAGA 146024 ratacaaaaagatcttcatgacccagataatcacgatgatgat 145964 STGGAGGTGATGGAATTCCAGTTGAGCTCTTTCAAATACTGAAAGA 145844 IGTTGCACTCAATATGCCAGCAAATTTGGAAAACACAGCAGTGGCC 145784 SGTCAGTTTTCATTCCAATCCCAAAGAAAGGCAATGCCAAAGAATG 145724 AGCAATACGTGAACCGTGAACTTTCTGATGTTCAAGCTGGTTTTAG 145604 PAGACATCCTGGAATGTGAAATCAAGTGGGCCTTAGAAAGCATCAC 145904 PARTIGCACTCATCTCGCATGCTAGTAAAGTAATGCTCAAAATTCT 145664 145484 145424 145304 145244 HAATATCATAACCTCAGATATGCAGATGACACTACCCTTATGGC 145184 145124 145064 1617 1917 2096 2156 1797 ACATCTATTTCTGCTTTATTGACTATGCAAAAGCCTTTGACTGTGG 1737 1976 CCAGAGACCAAATTGCCAACATCCTCTGTATCATGGAAAAGCAAG 1677 ------GAACTTCCAGTTCAAGCTGGTTTTAG COTOGOADATTCTGAAAGGGATGGGAATACCAGACCAGACCTG IGTATGCAGGTCAGGAAGCAACAGTTAGAACTGGACATGGAACAAC PAGGAAAAGGAGTATGTCAAGGCTGTATATTGTCACCCGGCTTGTT AACTAAAGAGCCTCTTGATGAAAGTGAAAGTGGAGGGAGTGAAATGT ACATTCAGAAAACGAAGATCATGGCATCCGGTCCCATCACTTCATG AG-ACATCATGAGAAACGCTGGGCTGGAAGCACCAAGCTGGAAT BAAATAGCAATAACCTCAGATATGCAGATGATACCACCCTTATGGC ACTAMAMAGCCTCTTGATGAAGGTGAAAGAGGAGAGAGTGAAAAGT 

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g  $\delta$ 엄  $\delta$ g ð g

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**NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1193 1292: contig of 1192 bp in length 1193 contig of 1192 bp in length 1292: contig of 1887 bp in length 1293 s2164: contig of 1887 bp in length 1225: gap of unknown length 1233 contig of 1887 bp in length 1231; contig of 1887 bp in length 1723: gap of unknown length 1723: gap of unknown length 1733: contig of 4572 bp in length 1733: contig of 4572 bp in length 1733: contig of 4572 bp in length 1875: contig of 24856 bp in length 1875: contig of 24856 bp in length 1875: contig of 24856 bp in length 1877: contig of 22367 bp in length 1875: contig of 22367 bp in length 1875: contig of 22367 bp in length 1875: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 2266 bp in length 1877: contig of 22367 bp in length 1877: contig of 22367 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: contig of 2266 bp in length 1877: cont
Green, E.D.

Direct Submission
Submitted (02-OCT-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
Grovemont Circle, Gaithersburg, MD 20877, USA
ON Oct 2, 2003 this sequence version replaced gi:31621329.
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unknown length
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/clone="RP42-25714"
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1. .1192
/note="assembly_fragment
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      AUTHORS
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                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                           CTICIAGICAAGGCTAIGGTTTTTCCTGTGGTCATGTATGGATGTGAGAGTTGGACTGTG 144835
                                                        144774 AGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGTCCTGGG 144715
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                                                                                                                                                                                    144954 GTTATGACCAACCTAGATGGCATATTCAAAAGCAGAGACATTACTTTGCCAACAAATGTC 144895
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            2217 ATCACTGCAGATGGTGACTGCAGCCATGAAATTAAAAGACACTTACTCCTTGGAAGAAAA 2276
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
1 (bases 1 to 294688)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2455 AGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGG
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                                                                                                                                                                                                                                               CATCTAGTCAAGGCTATGGTTTTTCCAGTGGTCATGTATGGATGTGAGAGTTGGACTGTG
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Bos taurus (cow)
Bos taurus
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2408 ACTGAAGAATTGATGCTTTTGAACTGTGGGGGTTGGGAAGACTCTTGAGAGTCCCTTGGA 2.	gccaaagaattgatgctttttgaactgtggtgttggagaagactcttgagagtcccttgga	CIGCAAGGAGTCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTTTTGGAAG	CTGCAAGGAGATCCAACCATTCTGAAGGAGATCAGCCTGGGATTTCTTTGGAAG	GAATGATGCTAAAGCTCAAAACTCCAGTACTTTGGCCACCTGATCAGAGAGGTGACTCAC	GAANGANGCTAAAGCTGAAACTCCAGTATTTTGGCCACCTCATGTGAAGAGTTGACTCAT	ZB88   THEEAAAAGANCECTEATIGCTEGEGGGATTIGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	こののようないとうなどものうりつなどうなりつなりつないのです。 プログラウィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック・アラフィック	TGAGATGGCTGGATGGCATCACTGACTCGATGAGCTGAGGTGAGTCTCGGTGAACTCTGGGAGT	2708 TGGTGATGGACAGGGAGGCCTGTCCTGCGGCGATTCATGGGGTCACAAAGAGTTGGACAC 2		2768 GACTGAGCAACTGAACTGAACTGTACTGAAACCTTAGTAGTTTATTACTCAGA 20	2828 ABATAGTAATATGTATATGTATTGA 2851	GGTAAAGAATCTGCCTTCAATGCA	AC135216 153264 bp DNA linear HTG 27-NOV-2	Bos taurus clone RP42-427020, WORKING DRAFT SEQUENCE, 3 pieces. AC135216		1 Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoide: Bovidae; Bovinae; Bos. <ol> <li>(bases 1 to 153264)</li> </ol>	Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks,	<pre>Cariaga,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,SL., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,SQ., Legaspi,R., Maduro,Q.L., Maduro,V.B.,</pre>	Marguitas, E.H., Masiello,C., Maskeri,B., McDowell,J., Paguitigan,C., Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,	Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, B.D.	NISC Comparative Sequencing initiative Unpublished 2 (bases 1 to 153264)	Green,B.D. Direct Submission Submitted (09-OCT-2002) NIH Intramural Sequencing Center, 8717	Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 153264)	Green, E.D. Direct Sub Submitted	saithersburg, MD 2087 is sequence version r ome Center	Center: NIH Intramural Sequencing Center
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83705 TAGAAATCCTGGAATGTGAAGTCAAGTGGGCCTTAGAAAGCATCACTACAAACAA	83645 GIGGAGGIGAIGGAATICCAACIGAGCIATICCAAAICCIGAAAGAIGAIGCIGIGAAAG 83586	1590	83588 TGCTGCACTCAATATGCCAGCAAATTTGGAAAACTCAGCAGGGCCACAGGATTGGAAAA 83526	1590 1589	83525 GGTCAGTTTTCATTCCAATCGCGAAGAAAGGCAATGCCAAAGAATGCTCAAACTACCGCA 83466	1590 1589	83465 CAATIGCACTCATCTCACATGCTAGTAAAGTAATGCTCAAAATTCTCCAAGCCAGGCTTC 83406	AACTTCCAGTTGTTCAAGCTGGTTTTAGAAAAGTCAGAGGAA		1632 CCAGAGACCAAATTGCCAACATCCTCTGTATCATGGAAAAGGAAGAGAGAG	ACATCTATTTCTGCTTTATTGACTATGCAAAAGCCTTTGACTGTGGGGGTCACAATAAAC	83285 ACATCTATTTCTGCTTTATTGACTATGCCAAAGCCTTTGACTGTGTGGATCACAATAAAC 83226	1752 IGTGGAAAATTCTGAAAGGGATGGGAATACCAGACCACCTGACCTGACTCTTGAAAATT 1811 	1812 IGTATGCAGGTCAGGAAGCAACAGTTAGAACTGGACAAGGAACAACAGACTGGTTCCAAG 1871 	1872 TAGGAAAAGGATATGTCAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTATGCAG 1931	AG-ACATCATGAGAAACGCIGGGGCIGGAAG-AAGCACAGGAIIAIIIAACIIAIIAAGAAGAGAGAAGAGAGAG		AGAAATAGCAATAACTCAGATATGCAGATGATGATACACCCTTATGGCAG	AGAAATATCAATAACCTTAGATATGCAGATGACACCACCCTTATGGCAGAAAGTGAAGAG	2050 GAACTAAAAAGCCTCTTGATGAAGGTGAAAAGGGGAGAGTGAAAAAGTTGGCTTAAAGCTC 2109 	AACATTCAGAAAACGAAGATCATGGCATCTGGTCCCATCACTTCATGGGAAATAGATGG	AACATITCAGAAAAACGAAGATCATGGCATCCGGTCCCATCACTITCATGGGAAATAGATGGG	21/0 BARACAGINGSANAGISICAGACTITATITITIGGGGGGCTCCAAAATCACTGAAATG 2229 82805 GAAACAGIGGAAACAGIGTCAGACTTTATITITGGGGGGCTCCAAAATCACTGCAGAIG 82748	2230 GIGACIGCAGCCAIGAAAITAAAAGACACITACICCITIGGAAGAAAAGITAACCAACC 2287	82747 GTGACTGCGAGCCATGAAATTAGAAGATGCTTCCTCCTTGGAAGGAA	82687 TAGACAGCATATCAAAAGCAGAGAGACATTACTTTGCCAACAAATGTCCATCTAGTCAAGG 82628	CTATGGTTTTTCCAGTGGTCATGTATGGATGTGAGAGTTGGACTGTGAAAAGCTGAGC	82627 CTATGGTTTTCCCTGTGGTCATGTATGGATGTGGAGTTGGACTGTGAAGAAGGCTGAGC 82568
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outfard,G.G., Brinkley,C., Brooks,S.,
d., Granite,S., Guan,X., Gupta,J.,
Ho,S.-L., Idol,G.R., Karlins,E.,
pi,R., Maduro,Q.L., Maduro,V.B.,
askeri,B., McDowell,J.,
Schueler,M.G., Sison,C.,
Schueler,M.G., Sison,C.,
onas,P.J., Touchman,J.W., Vogt,J.L.,
itiative AGGAGATCAGCCCTGGGATTTCTTTGGAAG 2527 sgggcaggagagagggacgacagagga 2647 TEGCCACCTGATCAGAGAGCTGACTCAC 2587 TGAAACCTTAGTAGTTTATATTACTCAGA 2827 DNA linear HTG 27-NOV-2002 RKING DRAFT SEQUENCE, 3 ordered aniata; Vertebrata; Euteleostomi; 71a; Ruminantia; Pecora; Bovoidea; amural Sequencing Center, 8717 us10664775-2.rge

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                                                                                                                                                                                                                                version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence with a phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 69855 69854: contig of 68854 bp in length

* 69855 108944: contig of 68854 bp in length

* 108945 109044: gap of unknown length

* 108945 109044: gap of unknown length

* 108945 109044: gap of unknown length

* 109045 103264: contig of 44220 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 153954 bases at least Q40 consensus quality: 153042 bases at least Q30 consensus quality: 153042 bases at least Q20 lnsert size: 140000, agarose-fp lnsert size: 153064; sum-of-contigs Quality coverage: 11.86x in Q20 bases; sum-of-contigs Quality coverage: 10.84x in Q20 bases; sum-of-contigs
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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147690 IGCGCTTTGCTGGAGCAGCCCTGAAGAGATACCCCACATCCAAGGTAAGAGAAACCCAAG 147749 147806 147925 GGTCCACTGGAGAAAGGGAATGGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGA 147984 148043 148103 148104 Changchanahacharaccchacterscarterskriesrichrenberakschasserershied 148163 148223 148344 AATCCCTCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAAGGGTCCGAAATGCAGTAC 148403 148463 148523 147924 148283 1138 718 418 958 358 478 598 658 778 GAAAACTAGTCAATATAATCACA--TGGACCACAGCCTTGTCTAACTCAATGAAACTAAG 148164 GTAAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGG GGTCCTATGAAGACCTACAAGACCTTTTAGAACTAACACCCAAAAAAAGATGTCCTTCTCA 148524 GGTTGTATGAAGACCTACAAGACCTTTTAGAACTAAACACTCACAAAAAGATGTCCTTTTCG TTGGCCTTGGAATACGGAATGAAGCAGGGCAAAGACTAATAGAGTTTTGCCAAGAAAATG 148644 INGCCTIGGAATACGGAATGAAGCAGGGCAAGGCTAATAGAGTTTTGCCAAGAGCCA 148704 CACTGGTCATAGCAAACACCCTCTTCCAACAGCACAAGAGAAGAGAAGACTCTACACATGGACAT 147985 ACAGTATGAAAAGGC-AAATGATAAGGTACTGAAAGAGGAGGTCCCCCAGGTCAGTAGGTG GTAAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGG 839 ATATCACAGTAATCCAAGTCTATGCCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAAC TTATAGGGGACTGGAATGCAAAAGTAGGAAGCAAAGAAACACCTGGAGTAACAGGCAAAT CACTGGTCATAGCAAACACCCTCTTCCAACAACACAAGAGAAGACTCTACACATGGACAT 1139 CACCAGATGGTCAACACCGAAATCAGATTGATTATATTCTTTGCAGCCAAAGATGGAGAA GAAAACTAGTCAAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAG GGTCCACTGGAGAAAGGGAAAT-GCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGA **ACAGTATGAAAAGGCAAAATGATAGGATACTGAAAGAGGAACTCCCCAGGTCAGTAGGTG** AAGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGGAATCAGCGAACTAA AATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATATCTACTGCGGGCAGG 719 AATCCCTCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAAGAGTCCGAAATGCAGTAC 241 CCATG-CCCGTGGGGCAACCCAAGATGGGCAGGTCATGGTGGAGAGATCTGACAGAATGT 479 CAAAGCAAAAAAAATACCCAGCTGTGGATGTGACTGGTGATATAAGCAAGGTCCGATGCT 779 959 300 359 629 899 181 147807 539 599 1019 1079 121

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I (bases I to 223761)

S Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W.,

Bouffard G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,

Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,

Coleman, H., Daki, N., Engle, J., Granite, S., Guan, X., Gupta, J.,

Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B.,

Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P.,

Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, O.L., Maduro, V.B.,

Mullikin, J.C., Paguirigan, C., Portnoy, M.E., Prasad, A.,

Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C.,

Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L.,

Wetherby, K.D., Young, A. and Green, B.D., Tsipouri, V., Vogt, J.L.,

NISC Comparative Sequencing Initiative
                                                                                                                                                             HTG 17-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
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Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 22338 bases at least Q30
Consensus quality: 22338 bases at least Q20
                                                                                                                                                             AC147195 223761 bp DNA linear HTG 17-DEC-;
Bos taurus clone RP42-466M15, WORKING DRAFT SEQUENCE, 4 ordered
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Submitted (06-NOV-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 223761)
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Submitted (17-DEC-2003) NIH Intramural Sequencing Center, 8717
Submitted (17-DEC-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, ND 20877, USA
On Dec 17, 2003 this sequence version replaced gi:38194246.
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Quality coverage: 27.55x in Q20 bases; agarose-fp
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150982 CATGACTGAGCGACTGAACTGA 151003
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HTG; HTGS PHASE2; HTGS DRAFT.
Bos taurus (cow)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 GAGGGCATCAGAGGGCAGACATACTGAAACCATACAGGCAGAAAACTAGTCAATCTAATC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 AAGATGGGCAGGTCATGGTGGAGAGTCTGACAGAATGTGGTCCACTGGAGAAGGGAAT- 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 AGTGGAGAAATAACTCCAGAAAGAATGAAGAGATGGAGCCAAAGCAAAAGAATACCCAG 499
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                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs. * are represented as runs of M. The order of the pieces is balleved to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence as soon as it is available and the accession number will be preserved.

145384 17206: contig of 145383 bp in length 171207 171307 app of unknown length 171307 200669: contig of any and and the accession contig of any and and the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession of the accession 
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76.7%; Pred. No. 0;
iive 0; Mismatches 165; Indels 614; Gaps
Quality coverage: 21.94x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 223761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="RP42"
/note="BAC resource: http://bacpac.chori.org/"
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71307. .209669
'note="assembly_fragment"
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/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="RP42-466M15"
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/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector side:left"
145484. .171206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone end:SP6
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1937   GAMCTICALITICACION	Ω	199267 CTGTGGATGTGACTGGTAATAGAAGCAAGGTCTGATGCTGTAAAGAGCAATATTGCATAG 199326	è	0 0 0
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199477   TIMETCHARTCHARTCHARTCHARTCHARGAGGGGGAATTCCCTCCAAAAAAATTCCAACTTCCAATTCCAATTCCAATTCCAACTTCCAACTTCCAACTTCCAACTTCCAATTCCAACTTCCAACTTCCAATTCCAACTTCCAATTCCAACTTCCAATTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACT	qq	GAAGAGTGAATGTCGACATTCTAGGAATCAGTAAACTGAAATGGACTGGAAAGGGTGAAT	\$	
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19957   TOTAL CONTROLLED   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED   19957   TOTAL CONTROLLED	2 3	TAACICAGAIGACCATTATATCTACTACTGCGGGCAGGAATCCCCCCAGAAGAAATGGAG	ζ	1589
199567   ACADATICATION CONTINUENCE   19956   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199567   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   199667   1	දි දි	TAGCCATCATGGTCAAAAGAGTCCGAAATGGAGTACTTGAATGCAGTCTCCAAAAACG TAGCCAATCATGGTCAAAAAAAAATGAAAATGAATGAATG	qa	200587 GATCTTCAC
199567 ACAGATCATCTCTCTTCCAAGCAACACCTTCAATTCACCAGTATCAACACCTACACCTACAGCT	3 8	・ このこくについていこうできない アンド・ファン・ファン・ファン・コン・コン・コン・コン・コン・コン・コン・コン・コン・コン・コン・コン・コン	Š	1589
860   PIGCCCCAACCAGTAATGCTGAAGATGAAGATGAAGGGTCCTATGAAGACCTACAG 919     195627   ATGCCCCAACCAGTAATGCTGAAGATGAAGATTGAAGGCTCTATATGAGACCTACAG 919     195627   ATGCCCCAACCAGTAATGCTGAAGATGCTGATTGAAGACCTTCAAGACCTACAGA 919     195637   ATGCCCCAACCAGAAGATGCTCTTCATTATAGGCGCATTGCAA 919     195637   ACTTCTACAACTAAGACTCCCAAAAGATGCTTTCATTATAGGCGCATTGCAA 919     195637   AAGTAGGAAGACTAAGACACCCCAAAAAGATGCCTTTTCATTATAGGCGCATTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGC	g 43	ACAGAA IGALICITES I IONI I COMO COMPANCIO CANTO INTERNACIONA I CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO INTERNACIONA CANTO I	අු	200647 GAATGTGAA
199627   ATGCCCCACCACTACTACTACTACTACTACACTACACACTACT	ò	ATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAG	λò	1589
920 ACCITITIORANCIAACCCAAAAAGATGTCCTTCTATTATAGGGGACTGGATGCAA 199687 ACCITITIOGAACTAACACCCCAAAAAGATGTCCTTCATTATAGGGGACTGGAATGCAA 199746 980 AAGTAGGAACTAACACCCGAAGATGTCCTTTTCATTAGGGGACTGGAATGCAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGGAATGCATGAAAAGAATGCATGAAAAAGAATGCATGAAAAAGAATGCATGAAAAAAGAATGCATGAAAAAAGAAAAGAAAG	: 쇰	ATGCCCCAACTAATGTTGAAGAAGTTGAAGTTGAAGGGTTCTATGAAGACCTACAAG	QQ	200707 GGAATTCCA
199687   ACCTITION	ò	ACCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCATTATAGGGGACTGGAATGCAA	ò	
980 AAGTAGGAAGAAAAAACCTGGAGTAACAGGCAATTTGGCCTTGAATTAGGGATTGAATTGGCCTTGAATTAGGGATTGAATTGGCCTTGAATAGGAACCCCAAGAACACCCC 19906  1040 AAGCAGGCCAAGAACACATTAGAGTTTTGCCAAAAAAACACACCCTTGAATACCAACACCCC 19906  1100 TCTTCCAACAACAAAAAAAAAAAAAAAAAAAAAAAAA	q	ACCITITAGAACTAACACCCCAAAAAAGATGTCCTTTTCATTATAGGGGACTGGAATGCAA	අු	200767 ATATGCCAG
199147 AAGTAGGAAACTCAAGAACTCAGGAATTTGGCCTCGAATACGAAACGAAATTTGGCCTCTGAATACGAAACCC 19986 199807 AAGCAGGGAAACACTCAGGAATACCCAAATTTGGCCTCTGAATACGAAACCC 19986 199807 AAGCAGGGAAACACTAATACACACACAAGAAAATTCACACACA	8	<u> AAGTAGGAAGCAAAGAAACACCTGGAGTAACAGGAAATTTGGCCTTGGAATACGGAATG</u>	ò	1589
1040 AAGCAGGGCAAAGACTAATTAGAGTTTTGCCAAGAAATTGCACTGGTCATAACAACACC   19986     199807 AAGCAGGGAAAGACTAATTAGAGAAATTGCACTGGTCATTAACAACCC   19986     190907 AAGCAGGAAACACAAGAAGAACACTGGAAAATTGCACTGACTAACACCGAA   1159     199807 TCTTCCAACAACAAGAAGAACACTCTATACATGGACATGCACACAAAA   1299     1100 ATCAGATTGATTATATTCTTTGCAGCCAAAGATGGACACTCTATTACATCACACAAAA   1219     1200 AATCAGATTGATTATATTCTTTGCAGCCAACACTCATTACACTCACACAAAA   1219     1210 ATCAGATTGATTATATTCTTTGCAGCCAACACTCATTATACCCAATTCAGACTTA   200046     1220 CAAGACCAGAGACCACACACACACACACTCATATTCCAAATTCAGACTTA   200046     1280 AATTGAGAAGAACACACACACACACACACACTCAAATTCAGACTTA   200046     1280 AATTGAGAGAAACACACACACACACACACACATCAAATTCAGACTTA   200046     1280 AATTGAGAGAAACACACACACACACACACACATCAAATTCAAACTTA   200046     1280 AATTGAGAGAAACACACACACACACACACACACATCAAATTCAAACTTA   200106     1280 AATTGAGAGAAAACACACACACACACACACACATCAAATTCAAACTTA   200106     1280 AATTGAGAGAAAACACACACACACACACACACATCAAATTCAAACACTTA   200106     1280 AATTGAGAGAAAACACACACACACACACACACACACATCAAATTCAAACACTTA   200106     1280 AATTGAGAGAAAACACACACACACACACACACACACATCAAATTCAAAATTAAAAATTGAAAACACACAC	: A		ΩD	200827 ATTCCAATC
199807   ABGCKGGGAATAGACTAGTGCAAAGAAAAGGACTGGTCATAACAACACCC   199866   1100   TCTTCCAACAACAACAAAGAATAGACTTGCAAGAAAAAGACTGGTCATAACAACACCCGAA 1159   1100   TCTTCCAACAACAACAACAACAAGAAAACTTGAACACTGAACACCCGAA 1159   1100   TCTTCCAACAACAACAACAACAACAACAACAACAACAACA	S	AAGCAGGGCAAAGACTAANTAGAGTTTTGGCCAAGAAAATGCACTGGTCATAGCAAACACC	ò	1589
1100 TCTTCCAACAACACAAGAAACACACACACACACACACACA	. g		ΩD	200887 ATCTCACAC
199867	8	TCTTCCAACACACAGAAGAGCTCTACACATGGACATCACCAGATGGTCAACACGCAA	ò	1589GAA
1160 ATCAGNTTGATTATATTCTTTGCAGCCAAAGATGGAGAAGCTCTATACAGTCAGCAAAA 1219	: A		QC	200947 AACCATGAA
199927   ATCAGATTGATTATATTCTTTGCAGGAAAGATGGAGAAGCTCTATACAGTCAGCAAAAA   199986     1220   CAAAGCAGGAGCTTACTTGCAGCTCAGAACCCTATACAGTCAGCAATTCAGACTTA   1279     199987   CAACATCAGGAGCTTACTGTGGGCTCAGACCCTAATTCAGACTTA   1279     199987   CAACATCAGGAGCTGACTCAGCTCAGACTCCTAATTCAGACTTA   1279     199987   CAACATCAGGAGCTGACTCAGACCATCAGACTCATATTGCCAAATTCAGACTTA   1339     100047   AATTGAAGAAAACTAGGAAAACCACTAGACCATTCAGGTATCACCTAAATCCATT   1339     100047   AATTGAAGAAAAACAAAACCACTAGACCATTCAGGTATCTGATAACCATTCAGACTTAGACTTGAAATCCATT   1399     111	ò	ATCAGATTGATTATATTCTTTGCAGCCAAAGATGGAGAAGCTCTATACAGTCAGCAAAA	λΌ	1643 ATTGCCAAC
1220 CAAGACCAAGAACTTACTGTGGGTTCAGATCCTTATTGCCAAATTCAGACTTA	අු	ATCAGATTGATTATATTCTTTGCAGCGAAAGATGGAGAAGATCTCTATACAGTCAGCAAAAA	qq	201007 ATTGCCACC
199987   CAAGATCAGGAGCTGACTCAGACCATGAACTCCTINII	à	CAAGACCAGGAGCTTACTGTGGCTCAGATCATGAACTCCTTATTGCCAAATTCAGACTTA	ò	
1280 AATTGAAGAAAGTAGGAAAACCACTAGATCACTCAGGTAAGACCTAAATCCATCC	<u> </u>		qq	201067 TGCTTTAT
200047 AATTGAAGAAAGTGGGAAAACCATTCAGGTATGACTAAATCAAATCCCTT 200106 1340 ATGATTATACAGTGGAAAACCATTCAGGTATGACCTAAATCAAATCCCTT 200106 1340 ATGATTATACAGTGGAAAACGATTTAAGGGCCTAGATCTGATAG 1394 200107 ATGATTGTACAGTGGAAATGATTTAAGGGCCTAGATCTGATAG 200166 1395 AGTACCTAATGAACTATGGAAAAAGGTTTAAGGGCCTAGATCTGATAG 200166 1395 AGTACCTAATGAACTATGGAAAAAGGTTCAGAGTTCTACAGGAATCAACAC 200266 1455 AGTACCTAATGAACTATGGAAAAAGGTTCGTAACAGTTCTACAGAACAGGAACAAGAACAAAAAGAAAAAGAAAAAAAA	ò	AATTGAAGAAAGTAGGGAAAAACCACTAGATCACTCAGGTAAGACCTAAATCCAATCCCTT	δλ	1763 CTGAAAGGG
1340 ATGATTATACAGTGGAAGTGAGATTTAAGGGCCTAGATCTGATAGACAG   1394	셤	ATTGAAGAAAGTAGGGAAAACCACTAGACCATTCAGGTATGACCTAAATCAAATCCATT	đ	201127 CTGAAAGAG
	ò	ATGATTATACAGTGGAAGTGAGAAATAGATTTAAGGGCCTAGATCTGATAGACAG	ò	
1395 AGTACCTAATGAACTATGGACGGTTCATGACATGTACAGGAACAGGGATCAAGACT 1454	임		đ	
200167 AGTGCTGATGGATGGAGGTTCGTGACATTACAGGAGCTGTGATTCAAGACCAGGATCAAGAC 200226 1455 CATCCCCATGGAAAAAGCAAAAAGCAAAATGGCTGTTGGGAGGGGGGGG	ò	AGTACCTAATGAACTATGGACAGAGGTTCATGACATTGTACAGGAGACAGGGATCGAGGAC	δδ i	
1455 CATCCCCATGGAAAAGGAAAAAGGAAAATGGCTGTCTGGGGAGGCCTTACAAAT 1514 200227 CATTCCCATGGAAAAGGAAAAAAGCAAAATGGCTGTCTGGGGAGGCCTTACAAAT 1514 200227 CATTCCCATGGAAAGAAGAAGAAAGAAAAAGGAAAAAAGGAAAAAGAAAA	qq	AGTGCCTGATGAACTATGGACTGAGGTTCGTGACATTGTACAGGAGACAGGGATCAAGAC	තු	
200227 CATTCCCATGGAAAAGAAAAAGAAAAAGGAAAATGGCTGTCTGAGAAGGCCTTACAAAT 200286 1515 AGCTGTGAAAAGAAAGTGAAAAGCAAAAGGAAAAAGGAAAGGAAAGGCCTTACAAAT 200286 200287 AGCTGTGAAAAGAAGGAAAGTGAAAGGAAAAGGAAAAGGAAAAGGAAAAGAAAGAAAGAAAGAAAA	È	CATCCCCATGGAAAAGGAAAAAGCAAAATGGCTGTCTGGGGAGGCCTTACAAAT	ò	
1515 AGCTGTGAAAAGAAGAGAAAAGCAAAGGAAAAAGAAAAG	q	CATICCCATGGAAAAGAAATGCAAAAAGGCAAAATGGCTGTCTGAGAAGGCCTTACAAAT	q <sub>Q</sub>	
200287 AGCTGTGAAAGGAGAGAGGAAAGGAAAAGGAAAAGGAAAAGGAAAA	ò	AGCTGTGAAAAGAAGGAAAAGCAAAAGGAAAAAAAAAAA	λ t	2002 AACCTCAGA
1575 TGCAGAGTTCCAAA 1588                200347 TGCAGAGTTCCAAAGAATAGCAAGAAGAGATAAGAAAGCCTTCTTCAGCGATCAATGCAA 200406	qq	AGCTGTAAAAGAAGAAGAGAAAGTGAAAGGAAAAGGAAAAGGAAAAGATATAAACATCTGAA	3 2	2062 CTCTTGATG
200347 TGCAGAGTTCCAAAGAATAGCAAGAAGAGATAAGAAAGCCTTCTTCAGCGATCAATGCAA 200406	ò	TGCAGAGTTCCAAA	5 E	
	엄	TGCAGACTTCCAAAGAATAGCAAGAAGATAAGAAAGCCTTCTTCAGCGATCAATGCAA	}	

à	1589		1588
qq	200407 ACP	ACAAATAGAGGAAACAACAGAATGAGAAAGACTAGAGATCTCTTCAAGAAAATCAAGAT	200466
λ̈	1589		1588
QQ	200467 ACC	accaaaggaacatttcatgcaaagatgggcttgataaaggacagaaatggtatggaccta	200526
λά	1589		1588
Db	200527 ACP	acagaagcagaagatattaagaagagatggcaataatacacagaagaactgtacaaaaaa	200586
λ̈́o	1589		1588
qq	200587 GAT	GATCTTCACAACCCAGATAATCACGATGGTGTGATCACTGACCTAGAGCCAGACATCCTG	200646
ò	1589		1588
a	200647 GA	GAATGTGAAGTCAAGTGGGCCTTAGAAAGCATCACTACGAACAAAGCTAGTGGAGGTGAT	200706
λ	1589		1588
qq	200707 GG	GGAATTCCAGTTGAGCTATTCCAAATCCTGAAAGATGATGCTGTGAAAGTGCTGCACTCA	200766
δ	1589		1588
qq	200767 ATA	ATATGCCAGCACATTTGGAAAACTCAGCAGTGGCCACAGGACTAGAAAAGGTCAGTTTTT	200826
δ	1589		1588
QQ	200827 ATT	ATTCCAATCCCAAAGAAAGGCAACGCCAAAGAATGCTCAAACTACTGCACAATTGCACTC	200886
ογ	1589		1588
qq	200887 ATC	ATCTCACACACTAGTAAAGTAATGCTCAACATTCTCCAAAGCCAGGCTTCAGCAATATCTG	200946
à	1589	GAACTTCCAGTTGTTCAAGCTGGTTTTAGAAAAGCTCAGAGGAACCAGAGACCAA	1642
QQ	200947 ÀAC	CATGAACTICCTGATGTTCAAGCTGGTTTTAGACAAGGCAGAGGAAGCAAGAGTGCAA	201006
ob Ob	1643 ATJ     201007 ATJ	atigccaacatcctgtatcatggaaaagcaagaggticcagaaaacatctattc 	1702 201066
à	1703 TGC	TITIATIGACIAIGCAAAAGCCTITGACIGIGGGGGTCACAATAAACIGIGGAAAATT	1762
Db	201067 TGC		201126
δ	m	CTGAAAGGGATGGGAATACCAGACCTGACCTGACTCTTGAAAAATTTGTATGCAGGT	(3)
Dp Dp	201127 CTC	saaadadadadadadadadadadadadadadadadadad	201186
ò	1823	CAGGAAGCAACAGTTAGAACTGGACATGGAACAACACTGGTTCCAAGTAGGAAAAGGA	882
අධ	201187 CAC	ggaagcaacagttagaactggacatggaacaacagactggttccaaataggaaaagaa	201246
δλ	1883 GTZ	GTATGTCAAGGCTGTATATTGTCACCGGCTTGTTTAACTTCTATGCAGAG-ACATCATG	1941
QQ	201247 GT	rcorcadocroratarrorcaccrocrivarriaacrivararocagagracaro	201306
٥٨	1942 AG	AGAAACGCTGGGAAGAAGGACACAGCTGGAATCAAGATTGCCGGGAGAATAGCAAT	2001
අු	201307 AG	Nacectica et esa a cara de teca a la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la composição de la com	201366
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ò	2062		2121
Ор	201427 CTC	CICTTGATGAAAGTGAAAGTGGAAGAGTGAAAAAGCTTGGCTTAAAGCTCAACATTCAGAAA	201486

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* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are prepresented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 10239 contig of 10238 bp in length 10339 gap of unknown length 10339 gap of unknown length 10339 gap of unknown length 10339 contig of 20924 bp in length 1486 41585 contig of 20924 bp in length 41585 contig of 1610 bp in length 41586 43195 contig of 88268 bp in length 5164; contig of 88268 bp in length 14032 16032; contig of 88268 bp in length 14033 180432; contig of 88268 bp in length 140032; contig of 88268 bp in length 140032; contig of 88268 bp in length 16033 180432; contig of 40300 bp in length 160433 180432; contig of 40300 bp in length 160433 180432; contig of 40300 bp in length 160433 180432; contig of 40300 bp in length 160433 180432; contig of 88268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 180432; contig of 80268 bp in length 160433 1
                                                                                                                                             Direct Submission
Submitted (03-OCT-2002) NIH Intramural Sequencing Center, 8717
Gerovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 180432)
                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (09-NOV-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
On Nov 9, 2002 this sequence version replaced gi:23477844.

Center: NIH Intramural Sequencing Center
NISC Comparative Sequencing Initiative
Unpublished
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Contact: nisc_zoo@nhgri.nih.gov
Center_project_nformation
Center_project_name: ddc
Center_clone name: 118011
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/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: NISC
                                                                               (bases 1 to 180432)
                                                                                                                   Green, E.D.
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Eukaryota, Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

1 (bases 1 to 180432)
S. Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Boulfard,G.G., Brinkley,C., Brooks,S.,
Cariaga,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J.,
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,
Lario,F., Lee-Lin,S.-Q., Legaspi,R., Maduro,O.L., Maduro,V.B.,
Margulies,B.H., Masiello,C., Maskeri,B., McDowell,J.,
Pagnirigan,C., Pearson,R., Portnoy,M.E., Prasad,A.,
Reddix-Dugue,N., Schandler,K., Schueller,M.G., Sison,C.,
Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,
Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
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Bos taurus clone RP42-118011, WORKING DRAFT SEQUENCE, 7 ordered
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                             2122 ACGAAGATCATGGCATCTGGTCCCATCACTTCATGGGAAATAGATGGGGAAACAGTGGAA
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                                                                                                                                                    ACAGTGTCAGACTTTATTTTTGGGGGGCTCCAAAATCACTGCAGATGGTGACTGCAGCC
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HTG; HTGS_PHASE2; HTGS_DRAFT.
Bos taurus (cow)
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                                                                             729 AAGAAATGGAGTAGCCATCATGGTCAAAAAGAGTCCGAAATGCAGTACTTGGATGCAG
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                                       849 AATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGA
                                                                                                                                                                                                                                                                                                                      909 AGACCTACAAGACCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCATTATAGGGGA
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Db         44301         GGACCTAACAGAAGATATTAAGAAGAGTGGCAAGAATACACAGAACTGTACAA 44360           Qy         1589	1589 1588 44541 CTCAATAIGCCAGCAAATTIGGAAAACTCAGCAGTGGTCACAGGACTGĠAAAAGGTCAGT 44600	TTTCATTCCAATCCCAAAGAAAGGCAATGCCAAAGAATGCTCAAACTACCACACAATCAC	44661 ACTCATCTCGCACGCTAGTCAACTATCTCCAAGCCAGGCTTCAGCAATA 1589GAACTTCCAGTTGTTCAAGCTTTTAGAAAGCTAGGGAACCAGAGA 1689GAACTTCCAGTTGTTCAGGTTGTTTTAGAAAGCTAAGGAACGAGA 44721 TGTGAACTGTGAACTTCCTGATGTTCAGGTTTTTAGAAAGGAACGAAGGAAG	1699 TTTCTGCTTTATTGACTATGCAAAAGCCTTTGACTGTGGGGGTCACAATAAACTGTGGAA 1758 	1759 AATTCTGAAAGGGATGGGAATACCAGACCACCTGACCTG	ACAT	1938 CATCAGAAACGCTGGAAGAACACACAAGCTGGAATCAAGATTGCCGGGGAGAAATAG 1997	45141 CAGTAACCTCAGATATGTAGATGACCACCACCTTATGGCAGAAAGTGAAGAGAACTAAA 45200 2058 AAGCCTCTTGATGAAGGGAAAAAGAGAGAGAGAAAAGTTGGCTTAAAGCTCAACATTCA 2117 45201 AAGCCTCTTGATGAAAGTGAAAGTGAAAAGTTGAAAAAGTTAAAGCTCAACATTCA 45260	2118 GAAAACGAAGATCATGGCATCTGGTCCCATCACTTCATGGGAAATAGATGGGGAAACGT 2177 	2178 GGAAACAGTGTCAGACTTTATTTTTGGGGGCTCCAAAATCACTGCAGATGGTGACTGC 2237 45321 GGAAACAGTGTCAGACTTTTTTTTCTGGGCTCCAAAATCACTGCAGATGGTGC 45378 2238 AGCCATGAATTAAAAGACACTTACTCCTTGGAAAAGTTAACCAACCTAGATAGC 2295

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 53584 53683: contig of 53583 bp in length 53683: contig of 3770 bp in length 53684 57553: gap of unknown length 57554 83676: contig of 26123 bp in length 83677 83776: gap of unknown length 83677 83776: gap of unknown length 83677 83776: gap of unknown length 83777 gap of unknown length 83777 gap of unknown length 83777 gap of unknown length 175702: contig of 87532 bp in length 175703 155803: gap of unknown length 175703 155803: gap of unknown length 175703 165803: contig of 87532 bp in length.
Submitted (24-SEP-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA on Sep 24, 2003 this sequence version replaced gi:34328552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 184412 bases at least Q40 consensus quality: 184461 bases at least Q20 consensus quality: 184992 bases at least Q20 linsert size: 186000; agarose-fp linsert size: 185090; sum-of-contigs Quality coverage: 17.20x in Q20 bases; agarose-fp Quality coverage: 17.20x in Q20 bases; sum-of-contigs
                                                                                      Center: NIH Intramural Sequencing Center Center code: NISC.
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
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/clone="RP42-234I22"
                                                                                                                                                                                                                      Center clone name: 234122
                                                                                                                                                                                                    Center project name: eed
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                                                                                                                                     GenBank Accession Number (center project name eec)"
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                                                                                                                                                                                                                                                                                                   57.5%; Score 2052.6; DB 1; Length 185590;
75.0%; Pred. No. 0;
ive 0; Mismatches 239; Indels 636; Gaps
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Best Local Similarity 75.0
Matches 2624; Conservative
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                                                                                                                                                                                                                                                                                                                     39115 AAAGGAATGATGCTAAAGCTGAAACTCCAGGACTTTGGCCACCTCATGGGAAGAGTTGAT 39174
        38995 GAGCGCCAAAGAATTGATGCTTTTGAACTGTGGTGTTGGAGAGACTCTTGAGAGTCCCT 39054
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Bos taurus clone RP42-56C13, WORKING DRAFT SEQUENCE, 2 ordered
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                                                                                   2464 TGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTTTG 2523
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Direct Submission
Submitted (20-NOV-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 123710)
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                                                                                                                                 2524 GAAGGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                         TCACTGGAAAAGACCCTGATGCTGGGAGGGATTGGGGGGCAGGAGGAGAAGGGGACGACAG
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HTG; HTGS PHASE2; HTGS_DRAFT.
Bos taurus (cow)
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                                                                                                                                                                                                                                                 The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q2D bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence only proper and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence only bare been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid; n/a; 100% of reads consensus quality: 123475 bases at least Q40 consensus quality: 123571 bases at least Q30 consensus quality: 123571 bases at least Q30 consensus quality: 123571 bases at least Q30 consensus quality: 123671 bases at least Q30 consensus quality: 123671 bases at least Q30 consensus quality: 123671 bases at least Q30 consensus quality: 123671 bases at least Q30 consensus quality: 123671 bases at least Q30 consensus quality: 123671 bases at least Q30 consensus quality: 123671 bases at least Q30 consensus quality: 123671 bases; agarose-fp Quality coverage: 10.67x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 35692: contig of 35692 bp in length 35692 bp in length 35793: 123710: contig of 87918 bp in length.
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------- Project Information
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/note="assembly_fragment
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/db_xref="taxon:9913"
/clone="RP42-56C13"
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Center clone name: 056Cl3
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GCTCAGATCATGAACTCCT 1259 CCACTAGATCACTCAGGTA 1319 TTCATGACATTGTACAGGA 1439 GCAAAGGAAAAAGGAAAG 1559 |||||| || ||||||||| GCAAAAGAGAAAGGAAAG 110998 GAGATAAGAAAGCCTTTCT 111058 SAAAGACTAGAAATCTCTT 111118 TGGGCTCGATAAAGGACAG 111178 GGTGGCAAGAATACACAGA 111238 ATGATGTAATCACTCACCT 111298 AAAGCATCACTACGAACAA 111358 TTCTGAAAGATGATGCTGT 111418 AGCAGTGGCCACAGGACTG 111478 CCAAAGAATGCTCAAACTA 111538 CAAAATTCTCCAAGCCAG 111598 AAAAGCAAGAGAGTTCCA 1686 1588 1588 1588 1588 1588 1588

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidea; Bovidea; Bovidea; Bosiae; Bovidea; Bosiae; Bovidea; Bosiae; Bovidea; Bovoidea; Bovidea; Bovidea; Bovoidea; Bovoidea; Bovidea; Bovidea; Cosiae; Bovoidea; Bovoidea; Bovoidea; Cosiae; Bovoidea; Borjamia, B. Blakesley, R.W., Boriffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dierrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Haghighi, P., Hansen, N., Ho, S.-L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pagnirigan, C., Pearson, R., Portnoy, M.B., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wigglins, L., Young, A., Zhang, L.-H. and Green, E.D., NISC, Comparative Sequencing Initiative
                                                                                                   AC091399 181921 bp DNA linear HTG 01-JUN-2002 Bos taurus clone RP42-65K24, WORKING DRAFT SEQUENCE, 5 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-APR-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 181921)
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112797 AGTCGGACATGACTAAGTGACTGAACTGAACTGAA 112836
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Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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Center clone name: 065K24
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AC091399.2 GI:21306657
HTG: HTGS PHASE2; HTGS_DRAFT.
BOS taurus (COW)
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                                                                  RESULT 26
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Jhote="Clone overlaps with GenBank Accession Number
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          * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

27633 27732; gap of unknown length 69703; contig of 27632 bp in length 69703; contig of 41876 bp in length 69703; contig of 41876 bp in length 69703; contig of 41876 bp in length 69703; contig of 41877 bp in length 69703; contig of 41876 bp in length 69703; contig of 72498 bp in length 1109286 181783; contig of 72498 bp in length 118184 181883; gap of unknown length 1181884 181821; contig of 738 bp in length 1181884 181821; contig of 738 bp in length
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REFERENCE AUTHORS TITLE JOURNAL	C (Dases I to 1/9949) Hudson, H., Yoo, Y., Shaull, S., Yao, Z., Seroussi, E. and Roe, B.A. Direct Submission Submitted (15-JAN-2002) Department Of Chemistry And Biochemistry,	λ Ω	513 TGGTGATATAAGCAAGGTCCGATGCTGTAAAGAGCAATATTGCATAGGAACCTGGAATGT 572 
REFERENCE AUTHORS	The University of Oklahoma, 620 Parrington Oval, Roc 07 73019, USA 3 (bases 1 to 175949) Hudson, H., Yoon, Y., Shaull, S., Yao, Z., Seroussi, E. &	oy Op	573 CAGGTCCATGAATCAAGGCAAATTGGAAGTGGTCAAACAAGAGATGGCAAGAGTGAATGT 632 
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REFERENCE AUTHORS TITLE JOURNAL	4 (bases I to 1/5949) Hudson, H., Yoon, Y., Shaull, S., Yao, Z., Seroussi, E. and Roe, B.A. Direct Submission Submitted (27-SEP-2002) Department Of Chemistry And Biochemistry, The Thiverestry Of Oklahoma 200 Barrington Oval	<i>₹</i> 8	693 CCATTATATCTACTACTGCGGGCAGGAATCCCTCAGAAGAAATGGAGTAGCCATCATGGT 752 
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JOURNAL	Submitted (18-SEP-2003) Department Of Chemistry The University Of Oklahoma, 620 Parrington Oval OK 73019, USA	දු පු	813 TGTTTGCAAGGGAAACGATTGAATATGACGTAATCGAAGTGTATGCCCCAACCAG 872
Tigoto)	On Sep 10, 2013 Ults Sequence Version repraced 91:22554011 Genome Center Center: Department Of Chemistry And Biochemistry The University Of Oklahoma Center code 100kNP	දු පු	873 TAATGCTGAAGAGCTGAAGGTGAACGGTCCTATGAAGACCTACAAGACCTTAAGAACT 932 
FEATURES SOUFCE	0	g d	933 AACACCCAAAAAAGATGTCCTTCTCATTATAGGGAACTGGAATGCAAAAGTAGGAAGCAA 992 
	/organism== bos taurus= /mol_type="genomic DNA" /db_xref="taxon:9913" /clone="rp42-513213"	දි දි	993 AGRACACCTGGAGTAACAGGCAAATTTGGCCTTGGAATACGGAATGAAGGGGGGAAAG 1052 
Query Mat Best Loca Matches	cch 56.6%; Score 2022.6; DB 1; al Similarity 75.6%; Proced, No. 0; S541; Conservative 0: Mismatches 194:	දු පු	1053 ACTAATAGAGTTTTGCCAAGAAATGCACTCGTCATAGCAAACACCCTCTTCCAACAACA 1112
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Oy Db 86,	GAGG 	දු පු	1173 TATTCTTTGCAGCCAAAGATGCAGAAGCTCTATACAGTCAGCAAAAACAAGACCAGGAGC 1232
Qy 364	GCAGACATACTGAAACCATACACGCAGAAAACTAGTCAATCTAATCACACTAGGACCACA 	g &	1233 TTACTGTGGCTCAGATCATGAACTCCTTATTGCCAAATTCAGACTTAAATTGAAGAAGT 1292 
. YO 365	GCCTTGTCTAACTCAATGAAACTAAGCCATGCC-CGTGGGGCAACCCAAGATGGGCAGGT 	g &	1293 AGGAAAACCACTAGATCACTCAGGTAAGACCTAAATCCAATCCCTTATGATTATACAGT 1352 
Oy 60	CATGAGAGAATCTGACAGAATGTGGTCCACTGGAGAGAAATGGAAACCACTTCA	Qy Db	1353 GGAAGTGAGAAATTGATTTAAGGGCCTAGATCTGATAGACAGAGTACCTAATGAACTATG 1412 
ò	TGAA 392	\$ a	1413 GACAGAGGTTCATGACATTGTACAGGAGCAGGGATCGAGACCATCCCCATGGAAAAGAA 1472 

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/organism="Bos taurus"

Location/Qualifiers

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Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, K., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P. J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319

Consensus quality: 176756 bases at least Q30

Consensus quality: 177014 bases at least Q20
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

25821 52820; contig of 52820 bp in length 25821 69950; contig of 44030 bp in length 69951 70050; gap of unknown length 70051 170994; contig of 100854 bp in length 170905 171004; gap of unknown length 170905 171004; gap of unknown length 170905 171004; gap of unknown length 170905 171004; gap of unknown length 170905 177095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-FEB-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 177535)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (04-DEC-2002) NIH Intramural Sequencing Center,
Submitted (2012) Gaithersburg, MD 20877, USA
On Dec 4, 2002 this sequence version replaced gi:18640643.
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Insert size: 177235; sum-of-contigs
Quality coverage: 12.93x in Q20 bases; agarose-fp
Quality coverage: 10.65x in Q20 bases; sum-of-contigs
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------- Project Information
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Center clone name: 262G19
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/db_xref="taxon:9913"
/clone="RP42-262G19"
/clone lib="RP42"
1. 25820
/clone lib="genomic DNA"
/clone lib="RP42"
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vector_side:le
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Best Local Similarity 75.7°
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9 AGAACTGTACAAAAAGTTCTTCAAGACCAAGATAATCACAATGGTGTGATCACTGACCT 124108 9 AGAGCCAGACATCCTGGAATGTGAAGTCAAGTGGGCCTTAGAAAGCATCACTACGAACAA 124168 9 AGCTAGTGGAGGTGATGGAATTCCAGTTGAGCTCTTTCAAATCCTGAAAGATGATGCTGT 124228 9 GAAAGIGCTACACTCAATAIGCCAGCAAATTIGCAAAACTCAGCAGGCCACAGGACIG 124288 GAAAACGICCAGITITCAITCCAATCCCAAAGAAAGGCAATGCCAAAGAATGCTCAAACTA 124348 9 CIGCACAATIGIACICATCICACAIGAIAGIAAAGIAAIGCICAAAAITCICCAAGCCAG 124408 9 GCTTCAGCAATATGTGAACCGTGAACTTCCAGATGTTCAAGCTGGTTTTAGAAAAGGCAG 124468 9 AGGAACCAGAGATCAAATTGCCAACATCCCTGGATCATAGAAAAAGCAAGAGAGTTGCA 124528 5 AAACCIGIAIGCAGGICAGAAAGCAACAGIIAGAACIGAGCAIGGAACAACAAAAACIGGII 124704 5 TGCAGAGGCACGTCATGAGAAATGCTGGGCTGGAAGAAGCACAAACTGGAAATCAAGATTTC 124824 s ccaaataggaaaaggagtccatcaaggcrgtatatrgtcacccrgctratrtaacttata 124764 AAGAGGAACTAAAAAGCCTCTTAATGAAGGTGAAAGTGGAGAGTGAAAAAGTTGGCTTAA 124944 125057 -----ACTGCAGTCATGAAATTAAAAGATGC-TACTCTTTTGGAGAAAAGTTATGAC 125108 1588 1866 1686 -----GAACTTCCAGTTGTTCAAGCTGGTTTTAGAAAAGTCAG 1626 1746 CCAAGTAGGAAAAGGAGTATGTCAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTA 1926 TGCAGAG-ACATCATGAGAAACGCTGGGCTGGAAGAAGCACAAGCTGGAATCAAGATTGC 1985 6 CGGGAGAAATAGCAATAACCTCAGATATGCAGA-TGATACCACCCTTATGGCAGAAAGTG 2044 5 AAGAGGAACTAAAAAGCCTCTTGATGAAGGTGAAAGAGGAGAGTGAAAAAGTTGGCTTAA 2104 5 ATGGGGAAACAGTGGAAACAGTGTCAGACTTTTATTTTTGGGGGGCTCCAAAATCACTGC 2224 5 AGATGGTGACTGCAGCCATGAAATTAAAAGACACTTACTCCTTGGAAGAAAAGTTA--AC 2282 7 GAAAAACATCTATTTCTGCTTTATTGACTATGCAAAAGCCTTTGACTGTGGGGGTCACAA 7 AAATTIGIATGCAGGICAGGAAGCAACAGTTAGAACTGGACATGGAACAACAGACTGGTT AGGAACCAGAGACCAAATTGCCAACATCCTCTATCATGGAAAAAGCAAGAGAGTTCCA 

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                                                                                                                                                   Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 205621 bases at least Q40 Consensus quality: 205925 bases at least Q30 Consensus quality: 205925 bases at least Q30 Consensus quality: 206512 bases at least Q30 Insert size: 185000; agarose-fp Insert size: 20755; sum-of-contigs Quality coverage: 12.00x in Q20 bases; sum-of-contigs Quality coverage: 10.70x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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18000 18099: gap of unknown length
18100 35702: contig of 17603 bp in length
18100 35702: contig of 17603 bp in length
18803 58809: contig of 1808 bp in length
18803 58890: contig of 1808 bp in length
1891 68990: gap of unknown length
1891 207875: contig of 140885 bp in length
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Pred. No. 0;
0; Mismatches
Contact: nisc zoo@nhgri.nih.gov
                                    Center project Information
Center project name: eyz
Center clone name: 407L03
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35803. .66890
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
1 (bases 1 to 207875)
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Bos taurus clone RP42-407L3, WORKING DRAFT SEQUENCE, 4 unordered
pieces.
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Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Coleman, H., Daxi, N., Engle, J., Granite, S., Guun, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B.,
Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P.,
Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, C.L., Maduro, V. B.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Mullikin, J.C., Paguirigan, C., Portnoy, M.E., Prasad, A., Puri, O.,
Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C.,
Stantripop, S., Thomas, J. M., Thomas, P. J., Tsipouri, V., Vogt, J.L.,
Wetherby, K.D., Young, A. and Green, E.D.
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Submitted (18-DEC-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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Center: Odde: NISC
Center codd: NISC
Web site: http://www.nisc.nih.gov
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HTG; HTGS PHASE1; HTGS_DRAFT.
Bos taurus (cow)
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Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J.,
Paguirigan,C., Pearson,R., Portnoy,M.E., Prasad,A.,
Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,
Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

the accession number will be preserved.

* 145286 145385; gap of unknown length

* 145386 125540; contig of 47155 bp in length.
                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (15-FEB-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Feb 15, 2003 this sequence version replaced gi:25699528.
                                                                                                                                                                                                                  Direct Submission
Submitted (27-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 192840)
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Web Site: http://www.nisc.nih.gov
Centact: nisc_zoo@nhgri.nih.gov
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1. .145285
/note="assembly_fragment clone_end:SP6
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1. 192540
| Organism="Ros taurus"
| mol_type="genomic DNA"
| /db xref="taxon:9913"
| clone="RP42-22413"
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Center clone name: 224103
                                                                                                                                                                      2 (bases 1 to 192540)
Green, E.D.
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Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakssley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Caringag,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho.S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
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Bos taurus clone RP42-224I3, WORKING DRAFT SEQUENCE, 2 ordered
                                                TATGGCAGAAAGTGAAGAAGCTAAAAAGCCTCTTGATGAAGGTGAAAGAGGAGTGA
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AC137651.2 GI:28394356
HTG: HTGS PHASE2; HTGS_DRAFT.
Bos taurus (COW)
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20456 ATTGGGGGCAGGAGGACGACGACGAGGGTGAGGTGGCTGGTGGCTGCCGCC 20515 2674 TCGATGGACGTCGGGTGAACTCCTGGAGTGGGTGGATGGCTGGTCGTCCT 2733 20516 TCGATGGACTCTGGGTGAACTCCTGGAGTTGGTAATGAACAGGCAGG	1 /C AC092727		TSUTGEON, C., VOGT, J.L., Walker, W.A., Wetherby, K.D., Wiggins, L., TSUTGEON, C., VOGT, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, LH. and Green, E.D. NISC Comparative Sequencing Initiative Unpublished  L Chases 1 to 163604)  S Green, E.D. Direct Submission L Submitted (21-JUL-2001) MIH Intramural Sequencing Center, 8717		Direc Submi Grove On De	Center project Information Center project name: cjb Center project name: cjb Center clone name: 351K05  This sequence was finished as follows unless otherwise noted: all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality, >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
6 6 6 6 6 6	RESULT 31 AC092727/C LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL COMMENT	٠.
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1589				2196 TATTTTTGGGGGCTCCAADATCACTGCAGTGATGCTGCAGCCATGAAATTAAAAGA 2255  20050 TATTTTGGGGGGCTCCAADATCACTGCAGATGGTGACTGCAGCCATG 20096  2256 CACTTACTCCTTGGAAAATCATAACCAACCTAGATAGCATATTGAADAGGAGAGC 2313  20097 -GTTTACTCCTTGGAAGGAAATTATGACCAAACTAGAAAGCATATTGAADAAGCAGAGAC 20155		

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12012 TCTACTACTGCGGGCAGGAATCCCTCAGAAGAAACGGACTGTAGCCATCGTGGTCAACAA 41953
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                                               AAGAGTCTGAAATGCAGTACTTGGATGCAATCTCAAAAACGACAGAATGATGATCTCTGTTTG
                                                                                       TTTCCAAGGCAAACCATTCAATATCACGTAATCCAAGTCTATGCCCCAACCAGTAATGC
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| 11354...| 11341
| Increasion quality single stranded/single chemistry
region = 15246
| Increasion = 15246 | Increase = 15706 | Increasingle clone coverage = 157788...| 137719 | Increasingle clone coverage = 137788...| 137819 | Increasingle clone coverage = 157788...|
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/note="low quality single stranded/single chemistry
                                                                                                                                                                                                                                                                                                                                                                              region" 154683 // Ancee "low quality single stranded/single chemistry region"
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/note="low quality single stranded/single chemistry
               CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlapps are noted in the beginning and end of the Features section.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 163604;
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Pred. No. 0;
0; Mismatches 153; Indels
                                                                                                        /organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="RP42-351KS"
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ilarity 75.9%;
Conservative
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110	SULT 32  AC092410  Bos taurus clone RP42-245C6, WORKING DRAFT SEQUENCE, 5 unordered pleces.  CESSION  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC092410  AC04CANA  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC00A  AC0A  AC00A  AC0A  AC00A  AC0A  AC00A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  AC0A  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA  ACCOA
·	RESULT 32 AC092410 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT
1589	1787 CACCTGACCTGACTTGAAAAATTTGTATGCAGGGAAGCAACAGTAGAACTGGA 10279 1847 CACCTGACCTGCCTCTTGAAAAATTTGTATGCAGGGAAGCAACGTTAGAACTGGA 10279 1847 CATGGAACAACAGGTCCAATTAGGAAAAGGAATACGTCAAGGCTGTAATTGTCA 10219 1907 CATGGAACAACAGACTGGTTCCAAATAGGAAAAGGAATACGTCAAGGCTGTAATTGTCA 10219 1907 CCCGGCTTGTTTAACTTCTATGCAGAAAAGGAATACGTCAAGGCTGTAATTGTCA 10219 1907 CCCGGCTTGTTTAACTTCTATGCAGAAAAAGGAATACGTCAAGAGCTGAAATTGTCA 10159 1906 CAAGCTGGAATTAACTTCTATGCAGAAAATACCAATAACCTCAAGAAAACGTGGAAAAACC 10159 1906 CAAGCTGGAATTAACTTCTATGCGGAAAATACCAATAAACCTCAAGAATAGCAAAAAAAA

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                                                                                                         ATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAACTAA
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                                        GGTCCATGAATCAAGGCAAATTGGAAGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCA
                                                                                         ACATTCTAGGAATCAGCGAACTAAAATGGACTGGAATGGGTGAATTTAACTCAGATGACC
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                     Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 166686 bases at least Q40
Consensus quality: 167007 bases at least Q30
Consensus quality: 167085 bases at least Q30
Consensus quality: 167085 bases at least Q30
Insert size: 159000; agarose-fp
Insert size: 169007; aun-of-contigs
Quality coverage: 12.17x in Q20 bases; agarose-fp
Quality coverage: 11.52x in Q20 bases; sum-of-contigs
                                                                                                                                                                      consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                        143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S4.0%; Score 1930.2; DB 1;
Larity 76.2%; Pred. No. 0;
Conservative 0; Mismatches 143;
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Best Local Similarity
Matches 2376; Conserv
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OY 2141 GTCCCATCACTCATGGGAAATAGATGGGGAAACAGTGGAAACAGTGTCAGACTTTATTT 2200  Db 145958 GTCCCACCACTTCATGGGAAATAGGGGAAACAGTGGAAACAGTGCAGACTTTATTT 146017  QY 2201 TTTGGGGGGCTCCAAATTCACTGCAGTGACTGCAGCCATGAAATTAAAAAGACTT 2260  Db 146018 TTCTGGGCTCCAAATTCACTGCAGTGACTGCAGCCATGAAATTAAAAAGACACTT 260  OY 2261 ACTCCTTGGAAAATTAAAAGAGTGACTGCAGCCATGAAAGAAGACACTT 146075  QY 2261 ACTCCTTGGAAAAGTTAA-ACCAACTAGAAAGACAATATGAAAAGAAGAAACATTAC 2318  Db 146076 ACTCCTTGGAAAAGTTATAACCAACTAGATAACCATATTCAAAAGCAGAGACATTAC 146135  QY 2319 CTGGCCAAAAATTATGACCAAGCTAGATATTCAAAAGCAGAGACATTAC 146135  QY 2319 CTGGCCAAAAAAGTTATGACCAAGCTATTTCCAAGGGTGATGTATTAC 146135	Db 146136 TTTGCCAACAAACATCCATCTATATCAACGCTTTTCTGTGGTCATGTTTTGTTTTTTTT	AC130787  AC130787  LOCUS  BOS taurus clone RP42-206224, WORKING DRAFT SEQUENCE, 3 ordered pieces.  ACCESSION  VERSION  HTG3. HTG2 PHASE2; HTG3_DRAFT.  AC130787.2 G1:23334708  HTG3. HTG2 PHASE2; HTG3_DRAFT.  AC130787.2 G1:23334708  HTG3. HTGS PHASE2; HTG3_DRAFT.  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  BOS Taurus (cow)  Carlaga,K., Antonollis,A., Ayele,K., Bockstrom-Sternberg,S.M.,  KATILIS, B., Laric,P., Lee-Lin,SQ., Leegspi,R., Maduro,Q.L.,  MAGUINO,V.B., Margulies,E.H., Masiello,C., Maskeri,B.,  MAGUINO,V.B., Margulies,E.H., Masiello,C., Maskeri,B.,  RATILIS, MCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C., MCCLOSKEY,J.C.,
144818 CAAGGAGAGATAAGAAAGCCTTCCTCAGGGATCAATGCAAAGAAATAGAGGAAAACAACA 144877  1589	ATCACGATGGTGTGATCACTCACCTAGAGCCAGACATCCTGGAATGTGAAGTCAAGTGGG	1722

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* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* B9790 89889: contig of 8978 bp in length 89790 86759: contig of 6870 bp in length 86760 96859: gap of unknown length 86760 96859: gap of unknown length 96760 96859: contig of 77093 bp in length.
                                                                                                               Direct Submission
Submitted (27-SEP-2002) NIH Intramural Sequencing Center, 8717
Grovemont Gircle, Gaithersburg, MD 20877, USA
On Sep 27, 2002 this sequence version replaced gi:22218457.
                                                  8717
                               Direct Submission
Submitted (14-AUG-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (Dassa I to 173952)
                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center
Center code: NISC
                                                                                                                                                                                                                                          Web site: http://www.nisc.nlh.gov
Contact: nisc_zooSnhgri.nih.gov
------- project Information
Center project name: ddb
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                                                         Gaps
                          Length 173952
                                                         627;
missing SP6 clone_end from 3' end of insert
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reacreacadaaaadaceerdargerggaaagarrgaggeraggaggaagggarg 102470
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                                                                                                                                                                                                                                                                                                                                                                                                HTG 30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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Direct Submission
Submitted (13-JUN-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 216698)
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Submitted (30-MAY-2002) NIH Intramural Sequencing Center, 8717
Submitted (30-MAY-2002) MI 20877, USA
Grovemont Circle, Gaithersburg, MD 20877, USA
On May 30, 2002 this sequence version replaced gi:14389328.
                                                ACAGAGGATGAGATGGCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACT
                                                                                          102471 Acadaadardaarderredardecarcaccaacrcagadacacdedriredereder
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Bos taurus clone RP42-456A17, WORKING DRAFT SEQUENCE.
AC092006
                                                                                                                                                                                                                                                             TTGGACACGACTGAGCAACTGAACTGAACTGAACTGTACTGA 2801
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HTG; HTGS PHASE2; HTGS_DRAFT.
Bos taurus (cow)
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DEFINITION
ACCESSION
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KEYWORDS
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ORGANISM
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TITLE
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AC092006
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

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17882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

I 16698 contig of 216698 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18123 TGAATCAAGGCAAATTGGAAGTGGTCAAACAGGAGATGGCAAGAGTGAACATCGACATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 GCCTTGAGAACCCCATGAACAGTATGAAAAGGCAAAATGATAGGATACTGAAAAGAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCCCAGGTCAGTAGGTGCCCCATATGCTACTGGAGATCAGTGGAGAAATAACTCCAGAA
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Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 216492 bases at least Q40
Consensus quality: 216689 bases at least Q20
Consensus quality: 216689 bases at least Q20
Insert size: 187000; agarose-fp
Insert size: 216698; sum-of-contigs
Quality coverage: 14.77x in Q20 bases; sum-of-contigs
Quality coverage: 12.74x in Q20 bases; sum-of-contigs
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1. .216698
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="RP42-456A17"
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clone_end:T7
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	<b>4</b> 0	19321 GGTGGCAAGAATACACAGAAGAACTGTACAAAAAAGATCTTCATGACCCAGATAATCACG 19380
TCTACTACTGCAGGCAAGAATCCCTCAGAAGAAGAAGGAGCCATCATGGTCAACAAAA 18301 GAGTCCGAAATGCAGTACTTGGATGCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTT	δ d	1589 1588 19381 ATGGTGTGACGTGACCTAGAGCCAGACATCCTGGAATGTGAAGTCAAGTGGCCTTAG 19440
TGCTG 880	ò a	1589
CTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAACTAACACCCA 940 	ò a	TCCTAAAAGATGACGCTGTGAAAGTGCTGCACTCAATATGCCAGCAAATTTGGAAAACTC
AAAAAGATGTCCTTCTCATTATAGGGGACTGGAATGCAAAGTAGGAAGCAAAGAAACAC 1000 	& A	AGCAGTGGCCACAGGACTGGAAAAGGTCAGTTTTCATTCCAATCCCAAAGAAAAAGCAATG
CTGGAGTAACAGGCAAATTTGGCCTTGGAATACGGAATGAAGCAGGGCAAAGACTAATAG 1060 	& 43	CCAAAGAATGCTCAAACTACCGCACAGTTGCACTCATCTCACATGCTAGTAAAGTAGTGC
AGTTTGCCAAGAAATGCACTGGTCATAGCAAACACCCTCTTCCAACACACAAGAGAA 1120 	දු පු	1589CAACTTCCAGTTGTTCAG 1607 19681 TCAAAATTCTCCAAGCCTTCAGCAATATGTGAACCGTGAACTTCCTGATGTTCAAG 16740
TCTTT	& g	1608 CTGGTTTTAGAAAGTCAGAGCAACCAGAGACCAAATTGCCAACATCTCTGTATCATGG 1667 
	<i>≿</i> 8	1668 AAAAAGCAAGAGGTTCCAGAAAAACATCTATTTCTGCTTTATTGACTATGCAAAAGCCT 1727 
3AAAA        -	yy da	1728 TTGACTGTGGGGGTCACAATAAACTGTGGAAAATTCTGAAAGGGATGGGAATACCAGACC 1787 
AGTGA	% dd	1788 ACCTGACCTGAAAAATTTGTATGCAGGTCAGGAAGCAACAGTTAGAACTGGAC 1847 
AGAGG	& 43	1848 AIGGAACAACAGGTTCCAAGTAGGAAAAGGAGTAIGTCAAGGCIGIATATIGICAC 1907 
Appara	op o	1908 CCGGCTTGTTTAACTTCTATGCAGAG-ACATCATGAGAAACGCTGGGCTGG
SAAAA 	& a	1967 AAGCTGGAATCAAGATTGCCGGGGAGAAATAGCAATAACCTCAGATATGCAGATGATACCA 2026 
 AAGAA	\$ g	2027 CCCTTATGGCAGAAAGTGAAGAGGAACTAAAAAGCCTCTTGATGAAGGTGAAAGAGAGA 2086 
AATGG	S G	2087 GT-GAAAAGTTGGCTTAAAGCTCAACATTCAGAAAACGAAGATCATGGCATCTGGTCCC 2145 
	ð 6	2116 ATCACTTCATGGGAAATAGATGGGGAAACAGTGGAAAACAGTGTCAGACTTTATTTTTTGG 2205
GAAAGACTAGAGATCTCTTCAAGAAAATCAGAGATACCAAAGGAACATTTCATGCAAAGA 19260	3 8	ALCALLICATOGRAPHING HOUSE GRANCHOUS GRANCHOUS GRANCH TING. GGGGCTCCAAAATCACTGCAGATGGTGACTGCAGCCATGAAATTAAAAGACACTTACTCC
1588	, 3	GOGGCTCCAAAATCACTGCAGATGGTGATTGCAGCCATGAAATTAAAAGATGCTTACTCC
TGGCCTCGATAAAGGACAGAAATGGTATGGACCTAACAGAAGCAGAAGATATTAAGAAGA 19320	යි දී	GGGGCTCCAAAATCACTGCAGATGGTGATTGCAGCCATGAAATTAAAAGATGCTTACTCC

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Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. Ungublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contign has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigns have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid; n/s; 100% of reads Semblary: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap, version 0.990319

Consensus quality: 17182 bases at least Q30

Consensus quality: 171845 bases at least Q20

Insert size: 146000; agarose-fp

Insert size: 146000; agarose-fp

Quality coverage: 10.76x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-NOV-2001) NIH intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 171875)
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1124483 123583: gap of unknown length 137443 137442: gap of unknown length 137443 142844: contig of 5402 bp in length 142844 contig of 5402 bp in length 142845 171875; contig of 28931 bp in length 142845 171875; contig of 28931 bp in length 160cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (30-MAY-2002) NIH Intramural Sequencing Center, 8
Grovemont Circle, Gaithersburg, MD 20877, USA
ON MAY 30, 2002 this sequence version replaced gi:17017550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
Center project name: crh
Center clone name: 244N18
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/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="RP42-244N18"
/clone lib="RP42"
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Bos taurus clone RP42-244N18, WORKING DRAFT SEQUENCE, 4 ordered
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1 (bases i to 171875)

2 Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Brojamin,B., Blakesley,R.W., Bordatad,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Hachighi,P., Masiepi,R., Maduro,Q.L., Maduro,V.B., Margulies,B.H., Masiello,C., Waskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
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/note="assembly_fragment clone_end:T7 vector side:left"  1. 22552 /note="clone overlaps with GenBank Accession Number AC099407 clone RP42-270J1 (center project name crg)" 123583. 137342 /note="assembly_fragment" /note="clone overlaps with GenBank Accession Number /note="clone overlaps with GenBank Accession Number /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembl	282 AGAGITCTGACAGATGGTCCACTGGAGGAAT-GCAACCATTCAGTATTTT 340 146977 AGAGITCTGACAGATGTGTTTTTTT 1111111111111111111111111		09   761   GAGTCCGAAATGCAGTACTTGGATCTCAAAACGACAGATGATCTTTGTTT   820

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* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 49759 sooning of 49788 bp in length

* 49759 contig of 70182 bp in length

* 120041 120140 gap of unknown length

* 120041 120140 gap of unknown length

* 16955 180549; contig of 49314 bp in length

* 16945 180549; contig of 13494 bp in length

* 16945 180548; contig of 13494 bp in length

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Consensus quality: 182395 bases at least Q40
Consensus quality: 182646 bases at least Q20
Consensus quality: 182726 bases at least Q20
Insert size: 140000; agarose-fp
Insert size: 182748; sum-of-contigs
Quality coverage: 10.60x in Q20 bases; sum-of-contigs
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11; Conservative 0; Mismatches 164;
                                 Center code: NISC
Web site: http://www.nisc.nih.gov
                                                                      Contact: nisc_zoo@nhgri.nih.gov
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43769 TAGAACTGGACACGGAACAGACTGGTTCCAAATAGGAAAAGGAGTTCGTCAAGGCTG 43825 1897 TATATTGTCACCCGGCTTGTTTAACTTCTATGCAGA-ACATCATGAGAAAAGGCTGGGGCT 1955		4 6	2016 AGATGATACCCCCTTATGGCAGAAAGTGAAGAACTAAAAAGCCTCTTGATGAAGGT 2075 	2076 GAAAGAGGAGAGTGAAAAAGTTGGCTTAAAGCTCAACATTCAGAAAACGAAGATCATGGC 2135	ATCTGGTCCCATCACTTCATGGGGAAATAGATGGGGAAAACAGTGGAAAACAGTGCAAACTTCT 2195	ATCCGGTCCCACCACTTCATGGGAAATAGATGGGGAAAACAGTGGAAACAGGGTCAGACTT 4	2196 TATTTTTTGGGGGGCTCCAAAATCACAGGGGTGACTGCAACCATGAATTAAAAA 2255 	2		) 4.		GGATGTGAGAGTTGGACCGTGAAGAAGGCTGAGTGCCGAAGAATGATGCTTTTGAACTG 443	2434 TGGTGTTGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGAGATCCAACCAGTCCAT: 2493	CTGAAGGAGATCAGCCCTGGGATTTCTTTGGAAGGAATGATGCTAAAGCTGAAACTCCAG 2	GIGAAGGAGATCAGCCCTGGGATTTCTTTGGAAGGAATGATGATAAAGCTGAAACTCCAG 44	2554 TACTITGGCCACCTGATCAGAAGAGCTGACTGAAAAAAAAAGACCCTGATGCTGGGAGGG 2613	TACTTIGGCCACCICATGCGAAGAGTTGATTCATTGGAAAGACTCTGATACTGGAAGGG	2614 ATTGGGGGCAGGAGAAGAGGGACAAGAATGGCTGGATGGCTGGATGGCATGCCATGCCATGCATG	2674 TCGATGGACGTGAGGTCTGGGAGTTGGTGATGGACAGGAGGGCGTGTCCT 2733	TUGATAGACITUGGGTCTIGGGTGAACTUCGGAAGTTGGTGATAGAACAGAGAGAGAGAGAGAGAGAGA	44664 GCTGCGATTCATGGGGTTCCAAAGACTCGACTCAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA	2794 TGTACTGA 2801                 44724 TGATCTGA 44731			, and and as
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                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos (1 to 223717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Jul 20, 2002 this sequence version replaced gi:18464072.
                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (01-FEB-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 223717)
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Center code: NISC
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Center clone name: 089G03
                PHASE2; HTGS DRAFT
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2 (bases 1 to 223717)
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91800 CCATGCCTGTGGGGCCATCCAAGACGGCGGGTCCATGGTGGAG-GGTCTGACAGAATGTG 91742
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AC108175 clone RP42-250120 (center project name axf)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GAAAACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCAGGAAGGGCGCCAGTAAGGAGGTACCTACCTCGTCCAAGGTAAGGAGCAGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TGCGCTTTGCTGGAGCAGCCGTAAAGAGATACCCCACGCCCAAGGTAAGAGAAACCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAGATGGTAGGTGTTGTGAGAGGGCATCAGAGGCCAGACATACTGAAACCATACACGCA
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1. 11524
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AC108176 clone RP42-57H8 (center project name axg)"
1 3266: contig of 3266 bp in length
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3367. 53961: contig of 50595 bp in length
1062 115545: contig of 61484 bp in length
1064 115545: contig of 61484 bp in length
1064 115645: gap of unknown length
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1084 200320: contig of 23297 bp in length
1084 200320: contig of 23297 bp in length
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               3267
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	90433 TCAGCGATCAGTGCAAAGACATAGAGGAAAACAACAGAATGGGAAAGACTAGAGATCTTT 90374	TCAAGAAAATCAGAGATACCAAGGGAACATTTCATGCAAAGATGGGCTCAATAAAGGACA 9	1589 1588 1588 1588 1588 1588	1589 1588 1588 90253 GAGAACTGTACAGATGACCCAGATAATCACGATGGTGTGATCACTCAC	1589 1588 90193 TAGAGCCAGACATCCTGGAATGTGAAGTCAAGTGGGCCTTAGGAAGTAACACAACGAACA 90134	1589 1588 90133 AAGCTAGTGGAGGGGAATTCCAGTTGAGCTATTTCAAATCCTGAAAGATGATGCTG 90074	TGAAAATATTGCACTCAATATGCCAGCAAATTTGGAAAACTCAGCAGTGGCCACAGGACT	1589 1588 90013 GGAAAAGGICACCTITICGITICCAAICCCAAAGAAAGGCAAIGTCAAAGAATGCICAAACT 89954	1589 1588 1588 89953 ACCGCACAATTGCACTCACACGCTAGTAAAGTAACGCTCAAAATTCTCCAAGCCA 89894	1589GAACTTCCAGTTGTTCAAGCTGGTTTTAGAAAGTCA 1625 89893 GGCTTCAGCAATACGTGAACTGTGAACTTCCAGATGTTCAAGCTGGTTTTAGAAAAGGCA 89834		1686 AGAAAACATCTATTTCTGCTTTATTGACTATGCAAAAGCCTTTGACTGTGGGGGTCACA 1745 	1746 ATAAACTGTGGAAAATTCTGAAAGGGATGGGAATACCAGACCTGACCTGACTCTTGA 1805 	1806 AAATTTGTATGCAGGTCAGGAAGCAACAGTTAGAACTGGAACATGGAACAACAGGT 1865 		1926 ATGCAGAG-ACATCATGAGAAACGCTGGGCTGGAAGCACAGCTGGAATCAAGATTG 1984		2045 AAGAGGAACTAAAAAGCCTCTTGATGAAGGTGAAAGAGGAGAGTGAAAAGTTGGCTTAA 2104
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                                                                                                                                                                                                                                                 AGATGGTGACTGCAACCATGAAATTAAAAGACACTTACTCTTTAGAAGGAAAGTTATGAT 89178
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                                                                                      89296
                                                                                                                                                                               99295 ATGGGGAAATAGTCGAAACAGTGGCTGACTTTATTTTCT--TGGGCTCCAAAATCACTGC 89238
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Bos taurus clone RP42-57H8, WORKING DRAFT SEQUENCE, 2 ordered
bieces.
                                                                                                                                                                                                                          GACACGACTGAGCAACTGAACTGAACTGAACTGTACTGAAACCTTAGTAGTTTATATTAC 2822
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1 (bases 1 to 154440)
Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.,W.; Bordiard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Trinsley,C., Haghighi,P., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P.,
                                                                             CAAGGCTATGGTTTTTCCAGTGGTCATGTATGGATGTGAGAGTTGGACTGTGAAGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88997 AIGGACIACAAGGAGATCCAACCAGGGCAIICIAAGGGAGAICAGICCIGGGTGIIIIII
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                                                                                                                                   ATGGGGAAACAGTGAAACAGTGTCAGACTTTATTTTTGGGGGGCTCCAAAATCACTGC
                                                                                                                                                                                                                                                                                                                CAACCTAGATAGCATATTGAAAAGCAGAGACATTACCTTGCCAACAAAGCCCCATCTAGT
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Bos taurus (cow)
Bos taurus
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Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
Margulies,E.H., Masiello,C., Maskeri,B., Maetrian,S.D.,
McCloskey,J.C., McDowell,J., Pagnirigan,C., Pearson,R.,
Portnoy,M.E., Prasad,A., Schueler,M.G., Stantripop,S., Thomas,J.W.,
Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 96915: contig of $9615 bp in length

* 97016 154440: contig of 57425 bp in length.
                                                                                                                                                                                                                                         Submitted (26-JAN-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 154440)
                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-JUL-2002) NIH Intramural Sequencing Center, 8717
                                                                                                                                                                                                                                                                                                                                                                                 Grovemont Circle, Gaithersburg, MD 20877, USA
On Jul 20, 2002 this sequence version replaced gi:18376875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: NISC
Web alte: http://www.nisc.nih.gov
Contact: nisc zoo@nhgri.nih.gov
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/organism="Bos taurus"
/mol_type="genomic DNA"
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/clone="RP42-57H8"
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1. 96915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: axg
Center clone name: 057H08
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                                                                                                                                                                                (bases 1 to 154440)
                                                                                                                                                                                                     Green, E.D.
Direct Submission
                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                    Green, E.D
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TATCACAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACG 899  TATCACTGTAATCCAAGTCTATGCCCCAACCAGTAACACTG-AGAAGCTAAAATTGAACA 134  GTCCTATGAAGACCTACAAGACCTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCAT 959  GTCTATGAAGACCTACAAGACCTTTTAGAACTACACCCAAAAAAGATGTCCTTTTCAT 134  GTTCTATGAAGACCTATAAGACCTTCTAGAACTACACCCCAAAAAAGATCCTTTTCAT 134  TATAGGGGACTGGAATGCAAAAGTAAGAACAACACCCGGAGTAACAGGCAAATT 101  TATAGGGGACTGGAATGCAAAAGTAAGAACAACACCTGGAGTAACACGCAAATT 131  TATAGGGGACTGGAATGCAAAAGTAAGAACACACCTGGAGTAACACGCAAATT 133	1020 TGGCCTTGGAATACGGAATGAAGCACAAGACTAATAGAGTTTTGCCAAGAAATGC 1079 133939 TGGCCTTGGATACAGATGAGCAGGCAAAAGGCTAATGGCAAGAAAATGC 133880 1080 ACTGCTCATACAAACACCTTTCCAACAAAGAAAAAAAAAA	1140   ACCAGATGGTCAACAGATTGATTATTCTTTGCAGCCAAAGATGGAGAG   1199	1260 TAITGCCAAATTCAGACTTAAATTGAAGAAGTAGGGAAAACCACTAGATCACTCAGGTA 1319 133708 TAITGCCAAATTCAGACTTAAA TGAAGAAAGTAGGAAAAACACACTCAGCCATTCAGGTA 133650 1320 AGACCTAAATCCCATATGATTATACAGGGAAGTGAGAAATAGAATAGGCCT 1379 1310 AGACCTAAATCCCATACGATTATAACAGGGAAATAGATTAAGGGCT 1379 133649 TGACCTAAATCCAAATCCAAATCCATACGATTATAACAGGAATAAATA	1380 AGATCTGATAGACAGAGTACCTAATGAACTATGGACAGAGGTTCATGACATTGTACAGGA 1439	1499 GGGAGGCCTTACAAATAGCTGGAAAAGAAGAAGTGAAAAGCAAAAGGAAAAAA 1558	TCAGCGATCAGTGCAAAGACATAGAGGAAAACAACAGAATGGGAAAGACTAGAGATCTTT 13329	289 TCAAGAAAATCAGAGATACCAAGGGAACATTTCATGCAAAGATGGGCTCAATAAAGACACA589	9 GAGAACTGTACAAAAAAGATCTTCATGACCCAGATAATCACGATGGTGTGATCACTCAC
8 6 8 6 8 6	8 8 8	8 8 8 8	8 8 8	8 6 8 6	8 8 8	ò & ò	8 8 8 8	68686
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AGATCAGCCCTGGGATTTCTTT 2522
                                                                                  SCCACCTGATCAGAAGACTGA 2582
                                                                                                                                                           ACGIGAGICIGGGIGAACICCI 2702
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G.G., Brinkley, C., Brooks, S.,
ite, S., Guan, X., Gupta, J.,
L., Idol, J.R., Karlins, E.,
ladurc, Q.L., Madurc, V.B.,
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I., Prasad, A.,
I., Prasad, A.,
I., Touchman, J.W., Vogt, J.L.,
I., Touchman, J.W., Vogt, J.L.,
Id Green, E.D.
SGAGAAGACTCTTGAGAGTCTC 131914
                                                                                                                                          GCAGGAGAGAGGGGACGACA 2642
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AFT SEQUENCE, 6 ordered
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inantia; Pecora; Bovoidea;
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, USA
laced gi:25699231.
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, USA
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The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been releved to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 58795 $8895 $4062: contig of 58794 bp in length 58895 $4062: contig of 25168 bp in length 84163 100779: contig of 15677 bp in length 100890 133011: contig of 16677 bp in length 133012 144769: contig of 11658 bp in length 113312 144769: contig of 11658 bp in length 114870 145899: gap of unknown length 114869: contig of 11658 bp in length 114869: contig of 11658 bp in length 144870 165992: contig of 21123 bp in length 144870 165992: contig of 21123 bp in length
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114737. 165992
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AC137906 clone RP42-73K10 (center project name crs)"
133112. .144769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 165185 bases at least Q40
Consensus quality: 165185 bases at least Q20
Consensus quality: 165454 bases at least Q20
Insert size: 155000; agarose-fp
Insert size: 165492; sum-of-contigs
Quality coverage: 11.30x in Q20 bases; agarose-fp
Quality coverage: 10.58x in Q20 bases; sum-of-contigs
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vector side:left"
58895. 84062
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Center project Information
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100880. .133011
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1. .58794
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                                           project name: crr
clone name: 127F18
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clone end:SP6

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                                                       GGAATGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAACAGTATGAAAAGGCA
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                               Gaps
Score 1887; DB 1; Length 165992;
Pred. No. 0;
0; Mismatches 145; Indels 602;
 Query Match 52.8%;
Best Local Similarity 75.8%;
Matches 2335; Conservative
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                                                                                                                                                                                                                                                                                                   Sirran, N. Musbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S. Birran, N. Bastien, V., Bastien, V., Boyalavkiy, L., Boylakari, S. Musbaun, C., Lander, E., Ali, A., Devar, Y., Collymore, A., Camarata, J., Chazaro, B., Choepel, Y., Collymore, A., Camarata, J., Chazaro, B., Choepel, Y., Collymore, A., Ganarata, J., P., Fizzderalano, K., Devar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fizzderald, M., Gage, D., Galagan, J., Dodge, S., Faro, S., Ferreira, P., Fizzderald, M., Gage, D., Galagan, J., Dodge, S., Gord, S., Gordam, L., Grand-Petre, N., Halao, E., Malle, W., Iliav, I., Johnson, R., Chong, C., Rata, M., Karaa, A., Kalle, C., McClarm, M., Menden, C., Macle, M., Menden, C., Macle, M., Moya, J., Roy, A., Schauer, S., Schubback, R., Saeman, S., Severy, P., Smith, C., Spencer, B., Stanger-Indaman, N., Schanen, S., Severy, P., Smith, C., Spencer, B., Stanger-Indaman, N., Schanen, S., Zewery, P., Smith, C., Spencer, B., Stanger-Indaman, N., Schanen, S., Zewery, P., Camar, J., Roy, A., Wilson, B., Wann, D., Young, G., Zainoun, J., Roy, M., Wilson, B., Wann, D., Young, G., Zainoun, J., Roy, M., Wilson, B., Wann, D., Young, G., Zainoun, J., Roy, M., Wilson, B., Wann, D., Young, G., Zainoun, J., Roy, M., Wilson, B., Wann, D., Young, G., Zainoun, J., Roy, M., Wilson, B., Wann, D., Young, G., Zainoun, J., Roy, M., Wilson, B., Wann, D., Young, G., Zainoun, J., Roy, M., Wilson, B., Wann, D., Young, G., Anderson, S., Arachchi, H.M., Barten, W., Bloom, T., Rate, S., Lodge, S., Booley, K., Dorrish, L., Erickeon, J., Hago, B., Hall, J., Machasan, C., Gook, M., Cook, B., Cook, M., Cook, M., Cook, M., Cook, M., Cook, M., Cook, M., Cook, M., Cook, M., Wilson, B., Wathews, C., McCarthy, M., Wann, D., Young, G., Lui, A., Mathews, C., McCarthy, M., Wann, D., Young, G., Tanders, M., Melle, M., Wath, Wann, D., Young, G., Tanders, M., Melle, M., Wath, Wann, D., Young, G., Tander, S., Schoper, M., Melle, M., Wath, Wann, D., Young, G., Tander, S., Schoper, M., Mathews, C., Wann, M., Young, G., Zainoun, W., Wann, D., Young
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 362 K 14
------ Summary Statistics
Sequencing vector: Plasmid, n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                            HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Bos taurus (cow)
Bos taurus
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                     . and Lander, E.
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                                                                                                                                                                                                          Darren, S. Nusbaum, C. and Lanc
Bos taurus, clone RP42-362K14
Unpublished
2 (bases 1 to 190441)
                          AC129960.2 GI:27901861
                                                                                                                                                                      Bovidae; Bovinae; Bos. 1 (bases 1 to 190441)
                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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AUTHORS
ACCESSION
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137789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AAGATGGTAGGTGTTGTGAGAGGCCATCAGAGGCCAGACATACTGAAACCATACACGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 AAAACTAGTCAATCTAATCACACTAGGACCACAGGCTTGTCTAACTCAATGAAACTAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137841 ACAACAATCTGAT-----CACATGGACCACAGCTCTGTCTAACTAAGCCATGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 CATGCCCGTGGGCAACCCAAGATGGGCAGGTCATGGTGGAGAGATCTGACAGAATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137788 GGGGCCACCCAAG--ACCCCACATGGTGGGTCATGGTGGAGAGGTCTGACAGAATGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137550 AAGCAAAAACAACACCCAGCTGTGGATGTGATTGGTGATAGAAGCAAGGTCTGATGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGCTTTGCTGGAGCAGCCGTAAAGAGATACCCCAAGCCCCAAGGTAAGAGAAACCCAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCAAAAAGAATACCCCAGCTGTGGATGTGGTGGTGATATAAGCAAGGTCCGATGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 619; Gaps
                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* I 190441: contig of 190441 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 190441;
                   Consensus quality: 190436 bases at least Q40 Consensus quality: 190441 bases at least Q30 Consensus quality: 190441 bases at least Q20 Insert size: 198000; agarose-fp Insert size: 190441; sum-of-contigs Quality coverage: 16.1 in Q20 bases; agarose-fp Quality coverage: 16.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.8%; Score 1885.1; DB 1; Length 73.9%; Pred. No. 0; ive 0; Mismatches 254; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
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   version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
Assembly program:
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Best Local Similarity 73.9
Matches 2467; Conservative
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88660 ..12656

/note="assembly_fragment"

e 126757 ...154577
                                                                                                                                                                                                                                                                                     The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence control has been established using one or more of the following: read-pair data from individual subclones, overlags with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been triumed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 154307 bases at least Q40 consensus quality: 154367 bases at least Q20 consensus quality: 154358 bases at least Q20 insert size: 121000; agarose-fp insert size: 124377; sum-of-contigs Quality coverage: 12.74x in Q20 bases; sum-of-contigs Quality coverage: 9,99x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 88559: contig of 88559 bp in length 88560 126556: contig of 37937 bp in length 12657 126556: contig of 37937 bp in length 12657 154577: contig of 27821 bp in length.
Grovemont Circle, Gaithersburg, MD 20877, USA
On Dec 5, 2002 this sequence version replaced gi:18581925.
------ Genome Center
Center: NHH Intramural Sequencing Center
Center code: NISC
                                                                                                                                  Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
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                                                                                                                                                                                                                 Center project name: cjr
Center clone name: 136015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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vector_side:right"
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                                      COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135159 AACCTAGACAGCATATTAAAAAGCAGAGACATTACTTTGTCAAAAAAAGATCCGTCTAGTT 135100
                                                                                                                                                                                                                                                                                                                                                                                               134982 TGGACTGCAAGGAGATCCAACCAGTCCATTCTAAAGGAGATCAGTCCTGGGTGTTCATTG 134923
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S2.3%;   Score 1868.9;   DB 1;   Length 154577;   Cal Similarity   75.7%;   Pred. No. 0;   2363;   Conservative   0;   Mismatches 141;   Indels 619;   Gaps 266   GGCAGGTCATGGTGGAGAATGGTCCACTGGAGAAGGAAT-GCAAA 9292   GGGCAGGTCATGGTGGACAGAATGTGGTCCACTGGAGAAGGGAAT-GCAAA 325   CCACTTCAGTATTCTTGCCGTGGAACCCCATGAACGTATGATAGGCAAAAGGCAAAATGATAGGAAGGCAAAAAGGCAAAAAGGCAAAAAGATAGAT		S9532 GAIGHGACTGGTGATAGAGGTCCGATGCTGTAAAGGAGCAATATTGCATAGGAAC 59591 565 TGGAATGTCAGGTCCATGAATCAAGGCAAATTGGAAGTGATCAAACAAGAAGAAGAAGA 624 59592 TGGAATGTTAGGTCCATGAATCAAGGCAAATTGGAAGTGGTCAAACAAGAAGATGGCAAGA 624 59592 TGGAATGTTAGGTCCATGAATCAAGGCAAATTGTAAGTGGTCAAACAGGAGATGGCAAGA 59651	625 GTGAATGTCAACATTCTAGGAATCAGCGAACTAAAATGGACTGGAATGGGTGAATTTAAC 684 	685 TCAGATGACCATTATATCTACTGCGGGCAGGAATCCCTCAGAAGAAATGGAGTAGCC 744	745 ATCATGGTCAACAAAAGGTCCGAAATGCAGTACTTGGATGCAGTCTCAAAAACGACAGA 804 	805 ATGATCTCTGTTTGTTTCCAAGGCAAACCATTCAATATCACAGTAATCCAAGTCTATGCC 864	865 CCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTT 924 	925 TTAGAACTAACACCCAAAAAAGATGTCCTTCTCATTATAGGGGACTGGAATGCAAAAGTA 984 	985 GGAAGCAAAGACACCTGGAGTAACAGGCAAATTTGGCCTTGGAATACGGAATGAAGCA 1044 	1045 GGGCAAAGACTAATAGAGTTTTGCCAAGAAAATGCACTGGTCATAGCAAACACCCTCTTC 1104 		1165 ATTGATTATATTCTTTGCAGCCAAAGATGGAGAAGCTCTATACAGTCAGCAAAAACAAGA 1224 60190TGATTATATTCTTTGCAGCCAAAQATGGAGACTCTATACAGTCAGCAAAAAAAAA 60247	CCAGGAGCTTACTGTGGCTCAGATCATGAACTCCTTATTGCCAAATTCAGACTTAAATTG	60248 CCAGGAGCTGTGGGCTCAGATCATGAACTCCTTATTGCCAAATTCAGACTGAAATTG 60307 1285 AAGAAAGTAGGGAAAACCACTAGATCACTCAGGTAAGACCTAAATCCAATCCCTTATGAT 1344

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rive 0; Mismatches 126; Indels 596;
                                        is available
* provided by the submittor.

* This sequence will be replaced

* the finished sequence as soon as it is available

* the accession number will be preserved.

* 18859: contrig of 88559 bp in length

* 88660 126656: contrig of 88559 bp in length

* 12667 12656: contrig of 37997 bp in length

* 12667 126577: contrig of 27821 bp in length

* 12657 154577: contrig of 27821 bp in length

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Bos taurus (cow)

Hose taurus (cow)

Bos taurus (cow)

Horazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bostaurus

Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bovidae; Bovinae; Bos.

1 (bases 1 to 20118)

RS Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.W.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,

Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,

Laric, P., Lee-Lin, S., C., Legaspi, R., Maduro, Q.L., Maduro, V.B.,

Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,

Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C.,

Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,

Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D. 84706 84646 84586 2667 2727 2787 bp DNA linear HTG 05-DEC-2002 WORKING DRAFT SEQUENCE, 5 ordered Submitted (07-FBB-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 201118) 8717 34765 creragractriresceaericarsceaaeaerreaerearresarasaaaeaerereaere GGAGGGATTGGGGGCAGGAGAAGGGGACGACAGAGGATGAGATGGCTGGATGGCATC 2668 ACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAC CTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGACTCACTGGAAAAGACCCTGATGCTG 2728 TGTCCTGCGGCGATTCATGGGGTCACAAAGAGTTGGACACGACTGAGCAACTGAACTGAA The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence connig has been established using one or more of the following: read-pair Direct Submission
Submitted (05-DEC-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
On Dec 5, 2002 this sequence version replaced gi:18582035. Center: NIH Intramural Sequencing Center Center code: NISC.
Web Site: http://www.nisc.nih.gov
Contact: nisc\_zoo@nhgri.nih.gov
Center project name: cjq
Center project name: cjq
Center clone name: 071E11 AC109798 201118 Bos taurus clone RP42-71E11, (bases 1 to 201118)

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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

70539 77543 6904 by in length 77543 77543 13346; contig of 6904 bp in length 77543 13346; contig of 55774 bp in length 77543 13356; contig of 1533 bp in length 133517 149909; contig of 1533 bp in length 133517 149909; contig of 1533 bp in length 149910 150009; gap of unknown length 150010 150009; gap of unknown length 150010 150009; gap of unknown length 150010 150009; gap of unknown length 150010 150009; gap of unknown length 150010 150009; gap of unknown length
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ACTOSTS Clone overlaps with GenBank Accession Number
ACTO9787 clone RP42-136015 (center project name cjr).
                                                                                                                      Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 199764 bases at least Q40
Consensus quality: 200201 bases at least Q20
Consensus quality: 200271 bases at least Q20
Insert size: 157000; agarcse-fp
Insert size: 200718; sum-of-contigs
Quality coverage: 12.42x in Q20 bases; sum-of-contigs
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133517. .149909
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/clone="RP42-71E11"
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30257 30076 TGGCCATCACGGTCAACAAAAGAGTCCGAAATGCAGTACTTGGATGCAATCTCAAAAACG 30017 CCATGG-AAAGAAATGCAAAAAAGCAAAATGGCTGTCTGGGGAGGCCTTACAAATAGCTG 29298 30196 CAAGAGTGAATGTCGACATTCTAGGAATCAGCGAACTGAAATGGACTGGAATGGGTCAAT 30137 30136 TTPACTCAGATGACCATTATATCTACTACTACGGGGCAGGAATCCCTCAGAAGAAATGGAG 30077 30016 ACAGAATGATCTCTTTCGTTTCCAAGGCAAACCATTCAATATCACAGTAATCCAAGTCT 29957 29837 29477 2956 ATGCCCCAAACAGTAACACTGAAGAAGCTGAAGTTGAACGGTTCTATGGAGACCTACAAG 29897 29717 29417 29777 1099 1279 1459 29357 1039 ATCAGATTGATTATATTCTTTGCAGCCAAAGATGGAGAAGCTCTATACAGTCAGCAAAAA 1219 619 739 559 619 799 859 919 30316 CTGTGGATGTAACTGGTGATAGAAGGTCTGATGCTGTAAAGAGCAATATTGCGTAG 680 TTAACTCAGATGACCATTATATCTACTACTGCGGGCAGGAATCCCTCAGAAGAATGGAG 500 CTGTGGATGTGACTGGTGATATAAGCAAGGTCCGATGCTGTAAAGAGCAATATTGCATAG 740 TAGCCATCATGGTCAACAAAAGAGTCCGAAATGCAGTACTTGGATGCAGTCTCAAAAACG ATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACGTCCTATGAAGACCTACAAG 29896 ACCTTTTAGAACTAACACCCCCAAAAGATGTCCTTTTCATTATAGGGGACTGGAATGCAA 19776 AAGCAGGGCAAAGACTAATAGAGTTTTGCCAAGAAATGCACTGGTCATAGCAAAGACCC . 29656 ATCAGATTGATTATATTCTTTGCAGCCAAAGATGCAGAAGCTCTATACAGTCAGCAAAAA 29596 caagaccaggagcrgacrgrggcrcagaccargaacrccrrarrgccaaarrcagacrra 560 GAACCTGGAATGTCAGGTCCATGAATCAAGGCAAATTGGAAGTGGTCAAACAAGAGATGG CAAGAGTGAATGTCAACATTCTAGGAATCAGCGAACTAAAATGGACTGGAATGGGTGAAT 800 ACAGAATGATCTCTGTTTCCAAGGCAAACCATTCAATATCACAGTAATCCAAGTCT ACCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCATTATAGGGGACTGGAATGCAA AAGTAGGAAGCAAAGAAACACCTGGAGTAACAGGCAAATTTGGCCTTGGAATACGGAATG 29836 AAGTAGGAAGTCAAGAAACAGCTGGAGTAACAGGCAAATTTGGCCTTGGAATACGGAATG AAGCAGGGCAAAGACTAATAGAGTTTTTGCCAAGAAAATGCACTGGTCATAGCAAACACCC TCTTCCAACAACACACAAGAGAACTCTACACATGGACATCACCAGATGGTCAACACGGAA 1220 CAAGACCAGGAGCTTACTGTGGCTCAGATCATGAACTCCTTATTGCCAAATTCAGACTTA 29536 AATTGAAGAAAGTAGGGGAAACCACTAGACCATTCAGGTATGACCTAAATCAAATCCGTT 1340 ATGATTATACAGTGGAAGTGAGAATAGATTTAAGGGCCTAGATCTGATAGACAGAGTAC CTAATGAACTATGGACAGAGGTTCATGACATTGTACAGGAGACAGGGATCGAGACCATCC CCATGGAAAAGAAATGCAAAAAAGCAAAATGGCTGTCTGGGGAGGCCTTACAAATAGCTG AATTGAAGAAAGTAGGGAAAACCACTAGATCACTCAGGTAAGACCTAAATCCAATCCCTT

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Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Iaric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Magulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Paskeri, B., E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P. J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

** 18393 18492: contig of 18392 bp in length 18392: contig of 6985 bp in length 25478 25578 (6985 bp in length 25478; contig of 6985 bp in length 46407: contig of 28639 bp in length 46507; gap of unknown length 46507; gap of unknown length 46507; gap of unknown length 46507; gap of unknown length 46507; gap of unknown length 46507; gap of unknown length 46507; gap of unknown length 46507; gap of unknown length 46507; gap of unknown length 49175; gap of unknown length 89137; gap of unknown length 89137; gap of unknown length 89137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; gap of unknown length 189137; ga
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Submitted (27-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 121609)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-FEB-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Feb 6, 2003 this sequence version replaced gi:25699809.
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Center: NIH Intramural Sequencing Center
Center code: NISC
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2 (bases 1 to 121609)
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COMMENT

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68587 GAGAAGGGAGTGGCAAACTACTTCAGTGTTCTTGCCTTGAGAACCCCATGAACAGTATGA 68646
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69122 TAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACAGTTCTATG 69181		69182 AAGACCTACAAGACCTTTTAGAACTAACACCCCAAAAAGATGTCCTTTTTCATTATAAGGG 69241	968 ACTGGAATGCAAAAGTAGGAAGCAAAGAAACACCTGGAGTAACAGGCAATTTGGCCTTG 1027 69242 ACTGGAATGCAAAACTACCAAACAAAAAAAAAAAAAAAA	GAATACGGAATGAAGCAAGCAAACAAAAAAAAAAAAAAA	GAACACGGAATGAAGGCCAAAGTCTAATAGACTTTTGCCAAGAGAACGCACTGGTCA	1088 TAGCAAACACCCTCTTCCAACAACAACAAGAAGAACTCTACACATGGACATCACAGATG 1147	69362 TAGCAAACACCTCTTCCAACACACAGAGAGACTCTACACATGGACATCACCAGATG 69421	GTCAACACGGAAATCAGATTGATTATATTCTTTGCAGCCAAAGATGGAGAAGCTCTATAC		69482 AGTTAGCAAAAACAGGACCAGGAGCTGACTCAGAACTCATGAACTCTTTATTGCCA 69541	1268 AATTCAGACTTAAATTGAAGAAAGTAGGGAAAACCACTAGATCACTCAGGTAAGACCTAA 1327	69542 AATTCAGACTTAAATTGAAGAAGTAGGGAAAACCACTAGACCGTTCAGGTATGACCTAA 69601	ATCCAATCCCTTATGATTATACAGTGGAAGTGAGAAATAGATTTAAGGGCCTAGATCTGA		1500 IANALAMANIAKUTANIAKUTANIARAKARAGATIKATAKATI'GIRAKAGAGAKAGGGA 1447	1448 TCGAGACCATCCCCATGGAAAAGGAAATGCAAAAAGCAAAATGGCTGTCTGGGGAGGCCT 1507		1508 TACAATAGCTGTGAAAAGAAGAAGTGAAAAGGAAAAGGAAAAAAGGAAAGATAAAAGC 1567	69782 TACAAACATGTGGAAAAAAGAGAAGAGAAAGGAAAGGAA	1568 ATCTGAATGCAGAGTTCCAAA1588	69842 ATCTGAATGCAGAGTTCCAAAGAATAGCAAGGAGAAATAAGAAAGCCTTCCTCAGCGACC 69901		AGTGCAAAGAAACAGAGGAAAACAATAGAATGGGAAAGACTAGAGATCTCTTCAAAAAA		ITAGAGATACCAAGGAACATTTCATGCAAAGATGGGCTCGATAGAGGACAGAAATGGTA		I'GCACCTAAAAGAAGCTGACAATATTAAGAAGAGGTGGCAAGAATACACAGAAGAACCGT	1002	ウザンフラのカル・ファンド・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・	ACATCCTGGAACGTGAAGTGGGCCTTAGAAAAGCATCACTATGAACAAAGGTG		70202 GAGGTGATGGAATTCCAGTTGAGCTATTTCAAATCCTGAACGATGATCCTGTGAAAGTGC 70261
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70561 70621 70681 70801 70861 TCATCTCACACACTAGGAAAGTAATGCTCAAAATTCTCCAAGCCAGGTTTCAGC 70441 70501 1940 71041 71100 71280 CAATATGCCAGCAAATTTGGAAAACTCAGCAGGGGCCACAGGACTGGAAAAAGT 70321 TCATITCAATCCCAAAGAAAGGCAATGCCAAAGAATGCTCAAACTACCACATAA 70381 1641 1761 1821 2000 2180 1701 1881 2298 2358 2418 TGAACTACCAGATGTTTAAGCTGGTTTTAGAAAAGGCAGAGGAACCAGAGGTCA GATCATGGTATCTGGTCCCATCACTTCATGGGAAAGAGATGGGGAAACAGTGGA -GAACTICCAGITGITCAAGCIGGITTIAGAAAAGICAGAGGAACCAGAGACCA CAACATCCTCTGTATCATGGAAAAGCAAGAGAGTTCCAGAAAAAACATCTATTT AGCAACAGTTAGAACTGGACATGGAACAACAGACTGGTTCCAAGTAGGAAAAGG TCAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTATGCAGAG-ACATCAT CCCTGGGCTGGAAGAAGACCACAAGCTCGAAGATTGCCGGGAGAAATAGCAA ATTAAAAGACACTTACTCCTTGGAAGAAAAGTTA--ACCAACCTAGATAGCATA GATCATGGCATCTGCTCCCATCACTTCATGGGAAATAGATGGGGAAACAGTGGA GTCATGTATGGATGTGGAGTTGGACTGTGAAGAAAGCTGAGCACTGAAGTT GICATGTATGGATGTGAGAGTTGGACTGTGAAGAAACTGAGGCGCTGAAGATT AGCAGAGACATTACCTTGCCAACAAGCCCCATCTAGTCAAGGCTATGGTTTTT

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** NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**This sequence will be replaced to the pieces of the finished sequence as soon as it is available and the accession number will be preserved.

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order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence esequence assembly is based on at least 8% average coverage in 020 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a phrap-derived quality score.

Sequencing vector: plasmid; n/a; 100% of reads chemistry: bye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
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Consensus quality: 153316 bases at least Q20
Consensus quality: 15384 bases at least Q20
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Consensus quality: 154212 bases at least Q20
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Consensus quality: 154212 bases at least Q20
Consensus quality: 154212 bases at least Q20
Consensus quality: 154212 bases; sum-of-contigs
Quality coverage: 8.56x in Q20 bases; sum-of-contigs
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1 (bases 1 to 155001)

2 Akhter, M., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, K.R., G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-C., Legaspi, R., Maduro, O.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J. W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Maggins, L., Young, A. and Green, E.D.
                                                                              71521 GATGGCTTCACCGACAATGGACATGAGTTTCAGTGAACTCCGGGAGTTGGTGATG--- 71577
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Bos taurus clone RP42-262C3, WORKING DRAFT SEQUENCE, 8 ordered
                                                                                                                                                                                                           AAGCTGAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGACTCACTGGAAAAGACC
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Submitted (21-FEB-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 155001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated
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Center code: NISC
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Bos taurus (cow)
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	1558   AGATAAAAGCATCTGAATGCAGAGTTCCAAAGAACTTCCAGTTG	1638 1637 120956 AGAAATGGTATGGACCTAACAGAAGCAGAAGATATTAAGAAGAGGGGCGAGAATATACA 120897 1638	1638	1638
4 6 6 6 6 6	8 4 8 4 8 4	666666	6 6 6 6 6	<ul><li>6</li></ul>
/note="assembly_fragment clone_end:SP6 vector_side:right"  52.1%; Score 1861.5; DB 1; Length 155001; Similarity 75.0%; Pred. No. 0; 31; Conservative 0; Mismatches 215; Indels 561; Gaps 3 AACAGTATGAAAAGGCAAATGATAGGATACTGAAAGGGAACTCCCCAGGTCAGTAGGT	122276 GCCCAATGTGCTACTGGAGATCAGTGGAGATATAACTCCAGAAAGAA	658 AAATGGACTGGAATTGACTCAGATGACCATTATATCTACTGCGGCAG		1018 121676 1078 121616 1138 121556 1198 121496 1258 121436

Search completed: August 24, 2004, 12:54:03 Job time : 14990 secs

## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- nucleic search, using sw model OM nucleic

August 24, 2004, 13:00:13 ; Search time 650 Seconds (without alignments) 3.920 Million cell updates/sec Run on:

US-10-664-775-2 3572 1 gtcaggaagggcggcagtga......gcaacaacagcagaaagctt 3572 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 0.5 Scoring table:

41 segs, 356661 residues Searched:

82 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

rng2.seq:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	2000	Description	Bovine Claudin-16	Bovine Claudin-16		Bovine BSE-resista	tide seguen	t-de	tide sequ	86	Bovine BSE-resista	Bovine tracheal an	r bovine	Bovine Claudin-16	A nucleotide seque	Platelet-derived g	Goat beta-casein g	Bovine embryonic d	Bovine-derived DNA	Sheep alpha (1, 3)	Bovine 1-80 protei	Bovine EST associa	Bovine EST associa	Bovine EST associa	Bovine EST associa	EST	Bovine EST associa			Sheep PrP gene nuc	Sheep BSE-resistan	alpha (1,	EST as	OCI	-derived DN
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16137 AACAATATGAAAAGGCAAAATGATAGATACTGAAAGAGGAACTCCCCAGGTCAGTAGGT 16078

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358 AACAGTATGAAAAGGCAAAATGATAGGATACTGAAAGAGGAACTCCCCAGGTCAGTAGGT

Query Match 51.6%; Score 1842.4; DB 1; Length 54842; Best Local Similarity 75.6%; Pred. No. 4.8e-05; Matches 2295; Conservative 0; Mismatches 131; Indels 608; Gaps

7; 417 

Bovine EST associa Bovine EST associa	Bovine EST associa Bovine EST associa	Human immune/haema Bovine EST associa	Bovine-derived DNA Bovine EST associa	Calf acetyl cholin Bovine EST associa	Bovine EST associa Sheep alpha (1, 3)
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                                                                                                     Gene diagnosis of type 2 mutation for bovine claudin-16 deficiency, comprises checking for mutation in 1-161 position in claudin-16 sequence.
                                                                                                                                                                                      The invention describes gene diagnosis of type 2 mutation for bovine claudin-16 deficiency. The method involves (a) getting a bovine nucleic acid sample; (b) subjecting the sample to a gene amplification reaction to give a nucleic acid fragment; (c) checking the presence of mutation it he nucleic acid fragment of step (b). The method is used for gene diagnosis of type 2 mutation for bovine claudin-16 deficiency. This sequence represents a polymucleotide from the bovine Claudin-16 deficiency associated gene in which the type 2 mutation occurs
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                                                                                                                                                                                                                                                                                                                                                Sequence 38793 BF; 11758 A; 7706 C; 7060 G; 12139 T; 0 U; 130 Other;
                                                                                                                                                                                                                                                                                                                                                                                  Length 38793;
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Pred. No. 0.03;
0; Mismatches 123;
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   CHIKUSAN GIJUTSU KYOKAI SH.
KACHIKU KAIRYO JIGYODAN SH.
DOKURITSU GYOSEI HOJIN KACHIKU KAIRYO
                                                                                                                                                         Example 1; Page 28-41; 43pp; Japanese
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larity 67.4%;
Conservative
                                                                        WPI; 2002-744759/81
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ABS55700 standard; DNA; 38793
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Qy 2391 TGTGAAGAAGCTGAGCACTGAAGAATTGATGCTT  A 2390	245	32246	2511	32186 T	2571	32126	Qy 2631 AAGGGGACGACAAGGATGAGATGGCTGGATGGC	32068 GAGGGATGACAGAGGATGAGATGGCTGG	2691	Db 32008 GAATGAACTCCGGGAGTTGATGATGGACAGGAGGGGGGGG	в	Qy 2811 A 2811	Db 31888 A 31888	RESULT 3 AAD26486/c ID AAD26486 standard; DNA; 17141 BP.	XX AC AAD26486;	26-MAR-2002	Bovine, xenotransplantation, Gal-alpha (1,	KW alpha(1,3) galactosyltransferase; alpha (1, KW surgery; gene therapy; gamma globin gene; ds XX	Bos sp.	EN WO200188096-A2. XX XX PD 22-NOV-2001.		XX	XX PA (GERO-) GERON CORP.	XX PI Denning C, Clark J;	WPI; 2002-089848/	New ovir	Claim 18; Page 70-	XX CC The patent discloses immunologically compatic CC for xenotransplantation into human patients. CC to an ovine tissue devoid of antibody-detect
1589 1588	33382 TCACTATGAACAAAGCTAGTGGAGGTGATGGAATTCCAGTTGAGCTATTTCAAATCCTGA 33323	1589 1588	33322 AAGATGATGCTGTGAAAGTGCTGCATTCAATATGCCAGCAAATTTGGAAAATTCAGCAGT 33263	1589 1588	33262 GCCACAGGACTGGAAAAGGTCAGTTTTCATCCCAATCTCAAAGAAAG	1589 1588		1589GAACTTCCAGTTGTTCAAGCTGGT 1612		TITAGAAAAGGCAGAAAAACCAGAGAGCCAAATIGCCAACATCGGCIGGAICAGGAAAAA	1673 GCAAGAGATCCAGAAAAACATCTATTTCTGCTTTATTGACTATGCAAAAGCCTTTGAC 1732	GCAAGAGAG-TCCAAGAAACATCTATTTCTGCTTTATTGACAAAGGCCT++GAC	1733 TGTGGGGGTCACAATAAACTGTGGAAATTCTGAAAGGGATGGGAATACCAGACCACTG 1/92 	1793 ACCTGACTCTTGAAAATTTGTATGCAGGTCAGGAAGCAAACAGTTAGAACTGGACATGGA 1852 	ACAACAGACTGGTTCCAAGT	32843 ACAACAGACTGGTTACAAACAGGAAAAGGAGTACATCAAGGCTGTATATTGTCACCCTGC 32784	1913 TTGTTTAACTTCTATGCAGAGACATCATGAGAAAGGCTGGGCTGGAAGAAGCACAGGCTG 1972 	GAATCAAGATTGCCGGGAGA	32723 GAATCAAGATTGCTGGGAGAAATATCAATAACCTCAGATATGCAGATGACACATTCTTA 32664	2033 TGGCAGAAAGTGAAGAAGTAAAAAGCCTCTTGATGAAGGGGGGAAAGAGGAGAAA 2092				CATGGCAAATAGATGGGGAAACAGTGGAAACAGTGTCAGACTTTATTTTCTGGGCTC 324	2213 CAAAATCACTGCAGATGGTGACTGCAGGCATGAAATTAAAAGACACTTACTCCTTGGAAG 22/2 2213 CAAAATCACTGCAGATGGTGACTGCAGGCATGAATTAAAAGACACTTACTCCTTGGAAG 22/2 2213 CAAAATCAATGCAAG 22/2			2331 GCCCATCTAGTCAAGGCTATGGTTTTTCCAGTGGTCGTAGAATGGAGTTGGAC 2390 32366 GGTCCGTCTAGTCAAGGCTATGGTTTTCCTGTGGTCATGTATGGATGAAGGTAGAC 32307
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CCAGTCCATTCTGAAGAGATCAGCCC 2510 CATCACTGACTCGATGGACGTGAGTCT 2690 SCTGGGAGGGATTGGGGGCGAGGAG 2630 agectigredecearitearedegr 2750 trible animal tissue, suitable s.s. The invention also relates sctable Gal alpha (1,3)Gal (GAL) able Gal-alpha(1,3)Gal in the treatment of the human 3)Gal; GAL determinant; , 3) GT; drug screening; ds. ò

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determinants which are made by alpha(1,3) galactosyltransferase (GT). The ovine tissue is useful for treatment of human body by surgery or therapy and in xenotransplantation, by transplanting the ovine tissue into a mammal having circulating and alpha(1,3) GT determinants. Polymucleotide constructs of the invention are useful for inactivating solymucleotide in an ovine cell. Alpha (1,3) GT sequences are useful for drug soreening and for the production of GAL containing synthetic oligosaccharides. Sequences of the invention are also useful in gene therapy. The present sequence is bovine gamma globin gene
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Sequence 17141 BP; 5078 A; 3416 C; 3372 G; 5275 T; 0 U; 0 Other;

Ouery Match Best Local S Matches 1117 16837 16837 16777 1709 16777 1829 16557 1889 16577 1989 1657 1989 16357 2068 16357 2188 16297 2188 2248 16179 2366 16179 2366	28.8%; Score 1028.7; DB 1; Length 17141; nilarity 91.9%; Pred. No. 0.079; Conservative 0; Mismatches 93; Indels 5; Gaps 3;	ACTICCAGTIGITCAAGCTGGTTTTAGAAAGTCAGAGGAACCAGAGACCAAAATTGCC 1648		AACATCCTCTGTATCATGGAAAAAGCAAGAGAGTTCCAGAAAAACATCTATTTCTGCTTT 1708	ACATCTGCTGGATCATGGAAAAAGCAAGAGATTCCAGAAAAGCATCTATTTCTGCTTT 16718	TTGACTATGCAAAAGCCTTTGACTGTGGGGGTCACAATAAACTGTGGAAAATTCTGAAA 1768	TIGACTATGCCAAACCCTTTGACTGTGGGATCACAATCAACTGTGGAAAATTCTGAAA 16658	GGGATGGGAATACCAGACCACCTGACCTGAAAAATTTGTATGCAGGTCAGGAA 1828	GAGATGGGAATACCATACCTGATCTGCCTCTTGAGAATTTGTATGCAGGTCAGGAA 16598	CAACAGITAGAACTGGACATGGAACAGACTGGTTCCAAGTAGGAAAGGAGTATGT 1888	CAACAGTTAGAACTTGGAACAACAACAGATTCCAAATAGGAAAAGGAGTTCGT 16538	CAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTATGCAGAG-ACATCATGAGAAAC 1947	CAAGGCTGTATTGTCACCCTGTTTTAACTTCTGTGCAGAGTACATCATGAGAAAC 16478	GCTGGGCTGGAAGAAAGCTGGAATCAAGATTGCCGGGGAGAAATAGCAATAACCTC 2007	CTGGACTGGAAGAAACACGGCCGGAATCAAGATTGCCGGGACAAATATCAATAACCTC 16418	MATAIGCAGATGATACCACCTTATGGCAGAAAGTGAAGAGGGAACTAAAAAGCCTCTTG 2067	AGATATGCAGATGACACCACCTTATGACAGAAAATGAAGAGGAACTCAAAAGCCTCTTG 16358	ATGAAGGTGAAAGAGGAGAGTGAAAAAGTTGGCTTAAAGCTCAACATTCAGAAAACGAAG 2127	ATGAAAGTGAAAGTGGAAGTGAAAAGTTGACTTAAAGCTCAACATTCAGAAATGAAG 16298	AICAIGGCAICTGGICCCAICACTITCAIGGGAATAGAIGGGAAACAGIGGAAACAGIG 2187	Arcarggcarccggrcarcactrcargggaaaragargggaaacagrggaaacagrg	TCAGACTITATITITIGGGGGGCTCCAAAATCACTGCAGATGGTGACTGCAGCCATGAAA 2247	GCAGACTITATTITCTGGGCTCCAAAATCACTACAGATGGTGACTGCAGCCATGAAA 16180	TAAAAGACACTTACTCCTTGGAAGAAAAGTTAACCAACCTAGATAGCATATTGAAAA 2305	TAAAAGATGCTTACTCCTTGGAAGGAAAGTTATGACCAACCTAGATAGA	GCAGAGACATTACCTTGCCAACAACAAGGCCCCATCTAGTCAAGGCTATGGTTTTTCCAGTGG 2365	CAGAGACATTACTTTGCCAACAAAGGTTCGTCTAGTCACGGCTATGTTTTTTCCTGTGG 16060	CATGTATGGATGTGAGAGTTGGACTGTGAAGAAAGCTGAGCACTGAAGAATTGATGCTT 2425	CATGTATGGATGTGAGGATTGGACTGTGAAGAAGGCTGAGCACCGAAAAATTGATGCTT 16000	TTGAACTGTGGTGTTGGAGAAGACTCTTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACC 2485
Ouery Match Best Local Matches 111 16837 16777 16777 16777 16777 16597 16597 16417 16357 16357 16357 16357 16357 16357 16357 1637 1637 2188 2188 2306 2306 2306	milarity Conserv	GAACTTCCAGTTGTT	GAACTTCTAGATGTT	AACATCCTCTGTATC	AACATCTGCTGGATC	ATTGACTATGCAAAA	ATTGACTATGCCAAA	GGGATGGGAATACCA	GAGATGGGAATACCA	GCAACAGTTAGAACT	gcaacagrragaacr	CAAGGCTGTATATTG	CAAGGCTGTATATTG	GCTGGGCTGGAAGAA	GCTGGACTGGAAGAA	GATATG	AGATATGCAGATGAC	ATGAAGGTGAAAGAG	ATGAAAGTGAAAGTG	ATCATGGCATCTGGT	Arcareccarceer	TCAGACTITATITIT	GCAGACTTTATTTT	TTAAAAGACACTTAC	TTAAAAGATGCTTAC	GCAGAGACATTACCT	GCAGAGACATTACTT	TCATGTATGGATGTG	rcargrarggargra	TIGAACIGIGGIGII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New transgenic bovine and cervid useful for producing animals which are resistant to bovine spongiform encephalopathy and transmissible spongiform encephalopathy disease, comprise a transgene encoding a mutant PrP polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                       Transmissible spongiform encephalopathy; neuroprotective; prion protein; bovine spongiform encephalopathy; transgenic; BSE; bovine; cervid; PrP;
TIGAACTGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACC
                                                                                                                                       15759 TCACTGACTCGATGGACGTGAGTCTGAGTGCTCCGGGAGTTGGTGATGGACGGGAGG
                                                                                                                                                                                                             CCTGTCCTGCGGCGATTCATGGGGTCACAAAGAGTTGGACACGACTGAGCAACTGAACTG
                                   2546 AACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGACTCACTGGAAAAGACCCTGATGC
                                                                                                                       2606 TGGGAGGGATTGGGGGCAGGAGAAGGGAACGACGACAGAGGATGAGATGGCTGGATGGCA
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                                                                                                                                                                                                                                                                     15639 ATCTGATCTGATCTG 15625
                                                                                                                                                                                                                                                       2786 AACTGAACTGTACTG 2800
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P-PSDB; ABP57900.
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The invention relates to a novel transgenic bovine/cervid comprising a transgene encoding a mutant prion protein (PrP) polypeptide, in which a substitution has been made at position 171 of the sequence, which renders the bovine/cervid resistant to bovine spongiform encephalopathy (BSB) and transmissible spongiform encephalopathy (TSE) disease, respectively. The transgene of the invention has neuroprotective activity. The method is useful for producing a transgenic bovine or cervid resistant to BSE and

Disclosure; Page 60-82; 98pp; English.

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(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
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TSE diseases. The bovine prion gene is useful for producing transgenic cattle exhibiting resistance to bovine spongiform encephalopathy. The sequence represents the transgene encoding the mutant bovine PrP polypeptide
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pBC734 expression disease; ij Platelet-derived growth factor; PDGF; transgenic; milk; gene; wound healing; diabetic foot ulcer; decubitus ulcer; ophthalmic venous stasis ulcer; periodontal regeneration; bone formation; prosthetic vascular graff; pBC734; ds. cassette insert used Production of platelet derived growth factor (PDGF) comprises in the milk of a non-human transgenic animal.

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bovine spongiform encephalopathy; transgenic; BSE; bovine; cervid; PrP;
TSE; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 promoter sequences of the myostatin gene used to diagnose muscle disorders.
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                                         CATTCAGAAAACGAAGATCATGGCATCTGGTCCCATCACTTCATGGGAAATAGATGGGGA
                                                                                               <u> AACAGTGGAAACAGTGTCAGACTTTATTTTTTGGGGGGCCTCCAAAATCACTGCAGATGGT</u>
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                                                                                                                                                                                                                                                                                               The invention relates to a novel transgenic bovine/cervid comprising a transgene encoding a mutant prion protein (PrP) polygeptide, in which a substitution has been ande at position 171 of the sequence, which renders the bovine/cervid resistant to bovine spongiform encephalopathy (BSE) and transgene of the invention has neuroprotective activity. The method is useful for producing a transgenic bovine or cervid resistant to BSE and cattle exhibiting resistance to bovine spongiform encephalopathy. The sequence represents the bovine prion gene is useful for producing transgenic cattle exhibiting resistance to bovine spongiform encephalopathy. The sequence represents the transgene encoding the mutant bovine prp
                                                                                                                                                                                                  New transgenic bovine and cervid useful for producing animals which are resistant to bovine spongiform encephalopathy and transmissible spongiform encephalopathy disease, comprise a transgene encoding a mutant PrP polypeptide.
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24.8%; Score 885.401; DB 1; Length 78056;
Best Local Similarity 86.6%; Pred. No. 0.053;
Matches 1063; Conservative 0; Mismatches 151; Indels 14; G
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3308 AGAGACATTACCTTGCCAACAAAGCCCCATCTAGTCAAGGC---TATGGTTTTTCCAGTG
                            TTTGAACTGTGGTGTTGGAAAAAACTCTTGATAGTCTTTTGGACTGCAAGGAGAATCCAAC
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Pred. No. 6.1;
0; Mismatches 85; Indels 10
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                                                                                                                                                                                                                                                                                   (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
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P-PSDB; AAR66205.
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                                                                                                                           AAGGCAAAATGATAGGATACTGAAAGAGGAACTCCCCAGGTCAGTAGGTGCCCCATATGC
                                                                                                      Gaps
                 esent sequence encodes the bovine brain protein p97, which is in genetic engineering techniques for carrying out various
                                                                                                     <u>ن</u>
                                                                                  Length 2830;
                                                             0 Other;
                                                                                 Score 667.9; DB 1; Length
Pred. No. 7.4;
0; Mismatches 166; Indels
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                                                             C; 686 G;
3; Page 6-8; 12pp; Japanese.
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Similarity 81.7%;
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Best Local Simil
Matches 782; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes gene diagnosis of type 2 mutation for bovine claudin-16 deficiency. The method involves (a) getting a bovine nucleic acid sample; (b) subjecting the sample to a gene amplification reaction to give a nucleic acid fragment; (c) checking the presence of mutation in the nucleic acid fragment of step (b). The method is used for gene flagnosis of type 2 mutation for bovine claudin-16 deficiency. This sequence represents a polymuclecide from the bovine claudin-16 deficiency associated gene in which the type 2 mutation occurs
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1559 TATTGCAAAGTTCAGGCTTAAGTTGAAGATAATACCAAAAACGACTCGGCCATTCAG 1615
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KACHIKU KAIRYO JIGYODAN SH.
DOKURITSU GYOSEI HOJIN KACHIKU KAIRYO
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Matches 1166; Conserv
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                                                                                                                                                                                                                                                                                                                                                           1828
sex chromosome. The mammal, as well as the method is useful for preselecting the sex of mammalian offspring. The present sequence represents a sequence 3' of the bovine SRY gene, which was used as the homologous arm in targeting vectors of the invention
                                                                                                                                                                                                                                                                                                                CAGATGGGAATACCAGACCACTTGACAGCTCTTGAGAACTCTGTATGCAGGTCAAGAA
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                                                                                                                                       Gaps
                                                                            Sequence 6620 BP; 2279 A; 1161 C; 1449 G; 1731 T; 0 U; 0 Other;
                                                                                                                                       24;
                                                                                                         DB 1; Length 6620;
                                                                                                                                     76; Indels
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Pred. No. 5.8;
0; Mismatches
                                                                                                        Query Match
Best Local Similarity 87.8%;
Matches 717; Conservative
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BP.

standard; DNA; 23653

ABK14793

RESULT 14

ABK14793

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The invention relates to the production of platelet-derived growth factor (PDGF) comprising a transgenic mammal whose sonatic and garm cells comprise a nucleic acid sequence (1) encoding PDGF, operably linked to a promoter directing expression into mammalian gland epithelial cells, and obtaining the milk from the transgenic mammal where at least 30% of the PDGF in the milk from the transgenic mammal where at least 30% of the ransgenic mammal capable of expressing an active PDGF molecule in milk. Pharmaceutical compositions can be obtained from this milk and can be transgenic pode to enhance the wound healing process; in particular diabetic foot ulcers, decubitus ulcers and venous stasis ulcers.

Transgenic PDGF (11) can also be used in the treatment of periodontal regeneration, stimulation of bone formation, ophthalmic diseases or healing of prosthetic vascular grafts. (11) can also be used for nonmedical applications, e.g., as a supplement for cell culture media or as a component of diagnostic kits. The present sequence represents the platelet-derived growth factor expression cassette insert used in p80734 vector of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of platelet derived growth factor (PDGF) comprises expression in the milk of a non-human transgenic animal.
                                                         in pBC734
                                                                                                                   disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TGCCGGGGAGAAATAGCAATAACCTCAGATATGCAGATGATGATCACCCCTTATGGCAGAAAG
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                                                                                              Platelet-derived growth factor; PDGF; transgenic; milk; gene; wound healing; diabetic foot ulcer; decubitus ulcer; ophthalmic venous stasis ulcer; periodontal regeneration; bone formation; prosthetic vascular graff; pSC734; ds.
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                                                         Platelet-derived growth factor expression cassette insert used
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15.6%; Score 557.9; DB 1;
Best Local Similarity 78.4%; Pred. No. 2.1;
Matches 820; Conservative 0; Mismatches 191;
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                                                                                                                                                                                                                                                                                                                                                                                                     (GENZ ) GENZYME TRANSGENICS CORP.
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                   (first entry)
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This invention relates to the goat beta-casein gene, represented by the present sequence. There are 18 positions in the 5'-flanking region, 21 positions in intron sequences and 1 position in exon VII that conflict with the sequence reported for this gene by Roberts et al (1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13723 BP; 4471 A; 2396 C; 2470 G; 4386 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTIGGACACGACTGAGCIGAACTGAACTGAACTGTACTGAAACCTTAGTA
                                                                                                                                                                        UNA molecules containing goat beta-casein gene
                                                                                                                                                                                                                                                                                                                                                                 Query Match
13.8%; Score 494.6; Dest Local Similarity 90.6%; Pred. No. 5.6; Matches 538; Conservative 0; Mismatches
                                                                                                                                                                                                           Chinese
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                                 97TW-00107261
                                                                                                                                                                                                           Claim 1; Page 1-13; 41pp;
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                                                                  (NASC-) NAT SCI COUNCIL
                                                                                                                                     WPI; 2001-264857/27
                                                                                                     Lin J;
                                   28-MAY-1997;
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                                                                                                     Huang M,
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TTCTGGGAGAAATATCAATAAAC-GAGATACAAAGAT-ACACCACACTTATGGCAGAAAA
                                                                                                                                       AAAACCCAACATTCAAAATCAAGA--------TCATCATTTCATGGCAAAT
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                                                                                                    AAAGCTCAACATTCAGAAAACGAAGATCATGGCATCTGGTCCCATCACTTCATGGGAAAT
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DB 1; Length 13723; 54; Indels 2637 9187 9247 2757 9307

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GATACCACCTTATGGCAGAAAGTGAAGAGGAACTAAAAAGCCTCTTGATGAAGGTGAAA 2079
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AAH21005 standard; DNA; 1333
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Best Local Similarity 85.3%;
Matches 453; Conservative
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(DURS/) DURSTEWITZ G.
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                                                                                                                                                                                                                                                                                                                                                       The present invention describes an expressed sequence tag (EST), where the EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell. Molecules which induce developmental competence in a cell line are useful for inducing incompetence in one or more cells. Molecules which induce developmental incompetence in a cell line are useful for preventing a full term pregnancy in an animal and inhibiting totipotence. The molecules are also useful for treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type. The present the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1960 GAAGCACAAGCTGGAATCAAGATTGCCGGGAGAAATAGCAATAACCTCAGATATGCAGAT 2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 ACTIGGACATIGGAACAACAGACTIGGGTTTGGAAAAGGAGTACATCAAGGCTGTCTA 414
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                                       Bos taurus; EST; expressed sequence tag; totipotence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 908 BP; 251 A; 210 C; 174 G; 248 T; 0 U; 25 Other;
                                                                                                                                                                                                                                                                                        An expressed sequence tag (EST), the expression of which, o complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.6%; Score 413.4; DB 1
85.6%; Pred. No. 1.5e+02;
ive 0; Mismatches 68
             embryonic germ (EG) cell cDNA EST #609
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                                                                                                                                                                                                                                        Childs
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                                                                                                                                                                           07-JUN-2000; 2000US-0209874P.
                                                                                                                                                    07-JUN-2001; 2001WO-US018576
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Best Local Similarity 85.67
Matches 501, Conservative
                                                     development; gene; ss
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                                                                                                                                                                                     174
                                                                                                                                                                                                                                                                                                                                                    173 GGTCCCATCACTTGATCGCNAATAAATGGG-----AATTGTGGCTGNCTTTATT 125
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                                                                                                                                                                        GTGGAGAGTGAAAAAGTTGGCTTAAAGCTCAACATTCAGAAAAACTAAGATCATGCATCT
293 GACACTACCCTTATGGCAGAAAGTGAAGAACTAAAGAGCTCTTGATGAAAGTGAAA
                                                                                                           GAGGAGAGAGAAAAAGTTGGCTTAAAGCTCAACATTCAGAAAACGAAGATCATGGCATCT
                                                                                                                                                                                                                                                                  GGTCCCATCACTTCATGGGAAATAGATGGGGAAACAGTGGAAACAGTGTCAGACTTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine, digital DNA signature; breeding; animal product origin; identification; genetic association; breed; population; race; ds
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Pred. No. 1.10+02;
0; Mismatches 78; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTGGGGGGCTCCAAAATCACTGCAGATGGTGACTGCAGCCATG 2244
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for xenotransplantation into human patients. The invention also relates to an ovine tissue devoid of antibody-detectable Gal-alpha (1,3)Gal (GAL) determinants which are made by alpha(1,3) galactosyltransferase (GT). The ovine tissue is useful for treatment of human body by surgery or therapy and in xenotransplantation, by transplanting the ovine tissue into a mammal having circulating antibody against Gal alpha(1,3)GT determinants. Polymucleotide constructs of the invention are useful for inactivating an alpha1,3 GT gene in an ovine cell. Alpha (1,3)GT sequences are useful for drug screening and for the production of GAL containing synthetic oligosaccharides. Sequences of the invention are also useful in gene therapy. The present sequence is alpha (1,3)GT post-exon 4 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               chaargitrahagcaraitcaaaagcagagagaritacitrigccaacaaaggccaiciar
                                                                                                                                                                                                                                                                                                                                                                                                                       GTCAAGGCTATGGTTTTTCCAGTGGTCATGTATGGATGTGAGAGTTGGACTGTGAAGAAA
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                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                Score 388.9; D
Pred. No. 88;
O; Mismatches
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Best Local Similarity 88.2%;
Matches 455; Conservative (
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     1056 CCGTCTAGTCAAGGCTATGGTTTTTCCAGTAGTCATGTATGGATGTGAGGTTGGACTGT 997
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                                                                                                                                             936 GAGAGTCCCTTGGACTGCAAGGAAATCCAACCAGTCCATTCTGAAGGAGATCAGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                           876 GATTTCTTTGGAAGGAATGATACTGAAGCTGAAACTCCAGTACTTTGGCCACCTCACGCA
                                                                                                                                                                                                                                                                  2574 AAGAGCTGACTGGAAAAGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGAAG
                                                                                                                                                                                                                                                                                                      816 AAGAGTTGACTCATTGGAAAAGACTCTGATGCTGGGAGAACTGGGGGCAGGAGGAAG
                                                                                                                                                                                                                                                                                                                                                                 756 GGGACAACAGAGGATGAGATGGCTGGACGGCATCACCTACTCGATGGACGTGAGTCTGAG
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                                                                                                                 2454 GAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGG
                                                                                                                                                                                                                                                                                                                                           GGGACGACAGAGGATGAGATGGCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGGG
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determinants, for xenotransplantation, and in the treatment of the
body by surgery or therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 AATTCACAGGAAAATATGTATCTTGTTAAACATTTGCAATTTTTGTAAA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1, 3) galactosyltransferase post-exon 4 DNA #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 79; 86pp; English.
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2731 CCTGCGGCGATTCATGGGGTCACAAAGAGTTGGACACGACTGAGCAACTGAACTGAACTG 2790
                                                                                                                                                                                                                                                                                                                                      This invention relates to novel isolated bovine 1-80 and Leu-13 proteins whose expression is induced by interferon and elevated during bovine pregnancy. The invention is useful for detecting pregnancy in a bovine animal. The method involves taking biological samples from a test animal and from a non-pregnant animal and detecting bovine 1-80 protein or Leu-13 protein in which an elevation of the protein from the test animal relative to that from non-pregnant animal indicates pregnancy in the test animal. The present sequence is that of the upstream region of the gene which encodes the bovine 1-80 protein and which is related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     717 GACTGGATGGACATGAGTTTGAGCAAGGTCCGGGAGTTGGTAATGGTCAGGGAAGCCTGG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 AAAGGGAATTGCAAAATATAAAATGTAAAAATGTAGACAGCATATTAAAAAGCAGA 356
                                                                                                                                                                                                                                  Novel isolated bovine 1-8U protein and Leu-13 protein whose expression is induced by interferon and elevated during bovine pregnancy, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 967 BP; 313 A; 173 C; 238 G; 243 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.7%; Score 380.6; DB 1; Length 5 Best Local Similarity 81.0%; Pred. No. 1.7e+02; Matches 443; Conservative 0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                       Claim 13; SEQ ID NO 11; 33pp; English
                                                                                                                                                                                                                                                                    detecting pregnancy in bovine animal.
                                                                                                                                                          Pru JK;
             18-NOV-2002; 2002US-00299497
                                                16-NOV-2001; 2001US-0337090P
                                                                                                                                                          Hansen TR, Austin KJ,
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                                                                                                                                                                                             WPI; 2003-829789/77.
                                                                                 (HANS/) HANSEN T R.
(AUST/) AUSTIN K J.
(PRUJ/) PRU J K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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ABX48667 standard; cDNA; 419 BP

RESULT 20 ABX48667

(first entry)

21-FEB-2003

ABX48667;

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The invention relates to a purified mucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nuclectide sequences, appearing a ransformed call having a nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic of functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and c(2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (detecting the level or pattern of the complementary nucleic acid surface acid sequences or its complementary nucleic acid permits the detection of the molecule; and (detecting the level or pattern of the molecule in a bovine cell or tissue. The detection of the molecule or acid is used for level or pattern of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid is used for the second or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the complementary control or the complementary control or constructs for use in cattle gene expression, or control or control or control or control or control or control or control or control or control or control or control or control or control or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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                                                                                                                                                                                 Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                        Bovine EST associated with lactation/muscle/fat deposition #13832.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-2001; 2001US-00960352.
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                                                                                                                                                                                                                                                                                             Bos Taurus.
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muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                                                                                                                                                                       GATCCTGAAGCTGAAATTCCAGTACTTTGGCCACCTCATGCGAAGAGTTGACTTATTGGA
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   Length 419;
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Score 372.6; DB 1
Pred. No. 4.2e+02;
0; Mismatches 29
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                                                       2352 GGTTTTCCAGTGGTCATGTATGGATGTGAGAG1
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Query Match
Best Local Similarity 93.1%;
Matches 390; Conservative C
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11-JAN-2000; 2000US-00480902.
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX4836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic caid linked to a promoter and a 3 non- translated sequence that functions in the cell to cause termination of transcription and addition of plyadenylated ribonuclectides to a 3 end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or the detection of the molecule. The LMFD nucleic acid is predictive of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is predictive of the detecting the level or pattern of a molecule in a bovine cell or tissue.

It is useful for genome mapping, gene identification and analysis, cattle of the second molecule in a bovine cell or the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is not of the complementary nucleic acid is not of the complementary nucleic acid is not of the complement of the molecule in a bovine cell or pattern of a molecule in a bovine cell or pattern of a molecule acid sequence is one of the compl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          electronic format from the USPTO web site:
segdata.uspto.gov/sequence.html?DocID=20020137139
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20-FEB-2003 (first entry)

ABX40996;

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49347, or complements of them. Also included are if in a transformed cell having a nucleic acid comprising an LMFD nucleic caid linked to a promoter and a 3 non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and close to proportion of the comprising and complementary nucleic acid sequences or its complement equipment along the complement of the sequence obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for detectining a level or pattern of a molecule acid is predictive of the complementary nucleic acid sequence to reduce mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the correction of the molecule to pattern of expensive tell or tissue. The correction of the molecule construction and analysis, cattle present sequence was not shown in the specification but was obtained in construct for electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1951 GGGCTGGAAGAAGCAAGCTGGAATCAAGATTGCCGGGAGAAATAGCAATAACCTCAGA 2010
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                                           Bovine, ss; EST; expressed sequence tag; lactation; LMFD; mussle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
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Pred. No. 4.38+02;
0; Mismatches 23; Indels 6;
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ilarity 93.4%;
Conservative C
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MATHIALAGAN N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
410; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      (TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                     US2002137139-A1.
                                                                                                                                                                                                        26-SEP-2002.
                                                                                                                                Bos Taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Byatt JC,
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                   (MATH/)
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9

Gaps

2190 GACTITATITITIGGGGGGCTCCAAAATCACTGCAGATGGTGACTGCAGCCATGAAATTA 2250 2251 AAAGACACTTACTCCTTGGAAGAAAAGTTA--ACCAACCTAGATAGCATATTGAAAAGCA 2308 The invention relates to a purified nucleic acid molecule associated with discration or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49347, or complements of them. Also included are ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that 2011 TATGCAGATGATACCACCTTATGGCAGAAAGTGAAGGAGGAACTAAAAAGCCTCTTGATG 2070 241 ATGGCATCCAGTCCCACTTCATGGAAATAGATGGGGAAACAGTGGAAACAGTGTCA 300 301 GACTITATICITI---GGGCTCCAAAATCACTGCAGATGGTGACTGCAGCCATGAAATTA 357 181 AAAGTGAAATTGGAGAGGGAAAAGTTGGCTTAAAGTTCAACATTCAGAAAATGAAGATC 240 New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle. Bovine, ss; EST, expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. TATGCAGATGACACCACCCTTATAGCAGAAAGTGAAGAGAACTCAAAAAGCCTCTTGATG 2071 AAGGIGAAAGAGAGAGIGAAAAAGIIGGCIIAAAGCICAACAIICAGAAAACGAAGAIC Bovine EST associated with lactation/muscle/fat deposition #5090. Warren WC; Claim 2; SEQ ID NO 5090; 245pp; English Tao N, 2309 GAGACATTACCTTGCCAAC 2327 418 GAGACATTACTTTGCCAAC 436 BP. 12-JAN-1999; 99US-0115707P. 24-SEP-2001; 2001US-00960352. ABX39925 standard; cDNA; 432 Byatt JC, Mathialagan N, (first entry) BYAT/) BYATT J C. MATH/) MATHIALAGAN N. WPI; 2003-110599/10. (MATH) MATHIALAGAN (TAON/) TAO N. (WARR/) WARREN W C. US2002137139-A1. 20-FEB-2003 26-SEP-2002. Sos Taurus. ABX39925; 121 2131 2191 RESULT 23 ABX39925 ò g 8 셤 ò d ò g à g

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functions in the cell to cause termination of transcription and addition of polyademylated ribnnucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any centre the 15112 bovine Last acid (compression) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the detection of the molecule. The LMPD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for penetically improving cattle. The present sequence is one of the complementary nucleic acids, Note: The complement LMPD EST (expressed sequence tag) nucleic acids. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1589 GAACTICCAGIIGIICAAGCIGGIITIIAGAAAAGICAGAGGAACCAGAGACCAAAIIGCC 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1769 GGGATGGGAATACCAGACCACCTGACTCTTGAAAATTTGTATGCAGGTCAGGAA 1828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAACAGTTAGAACTGGACATGGAACAACAGCTGGTTCCAAGTAGGAAAAGGAGTATGT 1888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 ATTGACTATGCCAAGGCCTTTGACTGTGTGGATCACAATAAACTGTGGAAAATTCTGAAA 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
                                                                                                                                                                                                                                                                                                                                                                                                         present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGACTATGCAAAAGCCTTTGACTGTGGGGGTCACAATAAACTGTGGAAAATTCTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 aagargegaaraccagaccaccrescrescrescresagaaarcrerarecageccagaa
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Pred. No. 4.4e+02;
0; Mismatches 22; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 432 BP; 146 A; 87 C; 100 G; 99 T; 0 U; 0 Other;
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Matches 384; Conservative
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Claim 2; SEQ ID NO 4684; 245pp; English
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                                                                                         Tao N,
                            12-JAN-1999; 99US-0115707P.
               24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                                                                                                                                                                                          90.5%;
                                                                                      Byatt JC, Mathialagan N,
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                                                  (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                      WPI; 2003-110599/10.
                                                                         WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                 TAO N.
26-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine EST associated with lactation/muscle/fat deposition #4684.
                                                                                                                                                                                                                                                                                                                                                                                                                              ABX39519 standard; cDNA; 433 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene analysis; cattle breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2003 (first entry)
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The invention relates to a purified nucleic acid molecule associated with lactation or mussle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, 1, 1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic caid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of plyddepylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid server or the detection of the molecule in a bovine cell or tissue.

Clevel or pattern of the molecule in a bovine cell or tissue.

It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for greent sequence is one of the laborate sequence the sequence is not of the complement sequence is not of the complement sequence is not of the complement sequence in the complement sequence in the complement of a processed sequence the sequence is not of the complement of the complement sequence is not of the complement of the complement of the complement of the complement of the complement of the complement of the complement of the complement of the complement of the complement of the complement of the complement of the co
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                                                                                                                                                                                                         New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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Warren WC;
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Wed Aug 25 15:11:56 2004

D111.7-C// 4000T8D

The invention relates to a purified mucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX14836-ABX49947, or complements of them. Also included are [1] a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of 20 determining a level or pattern of a molecule in a bovine cell or [2] determining a level or pattern of a molecule acid (comprising any complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid, where the detection of the complementary nucleic acid, where the detection of the complementary nucleic acid, where the detection of the complementary nucleic acid, where the detection of the complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for 2360 2300 409 -----CTGACTTTATTTTGGGGGGCTCCAAAATCACTGCAGATGGTAACTGCAGCCA 289 New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle. Bovine, ss; EST; expressed sequence tag; lactation; LWFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. 350 AAATAGCAGAGACATCACTTTGTCAACAAAGGTCCATCTAGTCAAGGCTATGGTTTTTTC 2243 TGAAATTAAAAGACACTTACTCCTTGGAAGAAAAGTTA--ACCAACCTAGATAGCATATT 2301 GABABGCAGAGACATTACCTTGCCAACAAAGCCCCATCTAGTCAAGGCTATGGTTTTCC Bovine EST associated with lactation/muscle/fat deposition #5347. Tao N, Warren WC; Claim 2; SEQ ID NO 5347; 245pp; English 2383 ABX40182 standard; cDNA; 433 BP 12-JAN-1999; 99US-0115707P. 24-SEP-2001; 2001US-00960352 Byatt JC, Mathialagan N, (first entry) BYATT J C. MATHIALAGAN N. TAO N. (BYAT/) BYATT J C. (MATH/) MATHIALAGAN 1 (TAON/) TAO N. (WARR/) WARREN W C. WPI; 2003-110599/10. US2002137139-A1. 20-FEB-2003 26-SEP-2002. Bos Taurus. 238 ABX40182 à 셤 ò g ò

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2059
                                                                                                                                                                                                                                                     1701 TCTGCTTTATTGACTATGCAAAAGCCTTTGACTGTGGGGGTCACAATAAACTGTGGAAAA 1760
                                                                                                                                                                                                                                                                                                                      1761 ITCTGAAAGGGATGGGAATACCAGACCACCTGACCTGACTCTTGAAAATTTGTATGCAG 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGAAACGCTGGGCTGGAAGAAGCACAAGCTGGAATCAAGATTGCCGGGAGAAATAGCA 1999
determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the present sequence is one of the present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                           62 TICTGAAAGAAGAAGGAATACCTGCCCACCTGACCTCTTGAGAAACCTATATGCAG 121
                                                                                                                                                                                                                                                                                                                                                                                                               122 GTCAGGAAGCAACAGTTAGAACTGGACATGGAACAACAGACTGGTTCCAAATAAGAAAAG 181
                                                                                                                                                                                                                                                                          2 TCTGCTTTATTGACTATACCAAAGTCTTTGACTGTGTGGATCACAATAAACTGTGGAAAA 61
                                                                                                                                                                                                                                                                                                                                                                                    1821 GTCAGGAAGCAACAGTTAGAACTGGACATGGAACAACAGCTGGTTCCAAGTAGGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1881 GAGTATGTCAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTATGCAGAG-ACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 TGAGAAATGCTGGACTGGATGAAGCCCAAGCTGGAGTCAAAATTGCCGGGAGAGATATA
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                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine, digital DNA signature, breeding, animal product origin, identification, genetic association, breed; population, race; ds
                                                                                                                                                                                     9.9%; Score 353.3; DB 1; Length 433; 90.0%; Pred. No. 4.6e+02; Live 0; Mismatches 42; Indels 1;
                                                                                                                                                        Sequence 433 BP; 159 A; 81 C; 94 G; 99 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine-derived DNA fragment contigl 445_67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH21025 standard; DNA; 1848
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                                                                                                                                                                                                          Best Local Similarity 90.0 Matches 389; Conservative
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DURSTEWITZ
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Best Local S
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(DURS/)
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AAH21025/c
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9.8%; Score 348.7; DB 1; Length 1848;
                                                                                                                                         Sequence 1848 BP; 513 A; 413 C; 407 G; 467 T; 0 U; 48 Other;
                                                                                                                                                                 Indels
                                                                                                                                                                 63;
                                                                                                                                                           Pred. No. 1.1e+02
0; Mismatches 6
                                                     Claim 1; Page 22-23; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                     ABX41993 standard; cDNA; 436 BP.
                                                                                                                                                           86.48;
                                                                                                                                                          Local Similarity 86.4 tes 418; Conservative
                                                                                                                             standardization feature
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Matches
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AC ABX4
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20-FEB-2003 (first entry)

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Bos Taurus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1138 AIGGAIGIGA-AGIICGACIGIAAAGAAAGCIGAGIGCIGAAGAAIIGAIGCIIIIIGAAC 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2729
                                                                                                                                                                                   This invention describes bovine DNA sequences (A) which are used in a method to establish a digital, standardized DNA signature. DNA signatures established from (A) are used to monitor breeding; to determine origin of animal products; to identify individual animals; to study genetic animal products; to identify individual animals; to study genetic association and to establish signatures that are specific at the level of breed, population or race. The method is based on individual base exchanges in DNA, and these are inherited more stably (by an order of studies (as a high throughput test) and the presence of unequivocal sequences flanking the variable position provides a built-in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2730 TCCTGCGGCGATTCATGGGGTCACAAAGAGTTGGACACGACTGAGCAACTGAACTGAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGATCCAACCAG-TCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGATTGGGGGCAGGAGGAGGAGGACGACAGAGGATGAGATGGCTGGATGGCCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      779 GTGTGCTGCAGTTCATGGGGTTGCAAGAGTCAGACTGAGCGACTGAGCGACTGTACTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATACTTTGGCCACCTGATGCGAAGAGCTGACTCATTTGAAAAGACCCTGGATGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2670 TGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             839 CAACACAATGGACATGGGTTTGGGTAAAGTCCGGGAGTTGGTGATGGACAAGAAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                 New bovine genomic DNA sequences, useful for establishing genetic signatures, e.g. for breeding control, contain specific variable
            Durstewitz G;
                                              WPI; 2001-376309/40.
                                                                                                                  positions.
            Fries HR,
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cattle, and the LMFD nucleic acid can specifically hybridise to a second nuclear, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleicide sequences, appearing as ABX-4886-ABX49947, or complements of them. Also included are included are included acid linked to a promoter and 3' non- translated sequence that cunctions in the cell to cause termination of the mRNA molecule; and cid linked to a promoter and 3' non- translated sequence that the cell to cause termination of the mRNA molecule; and of determining a level or pattern of a molecule in a bovine cell or itsue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule optained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the molecule. The LMPD nucleic acid is used for level or pattern of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breathing a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breathing apprentation of constructs for use in cattle gene expression, or present sequence as not shown in the specification but was obtained in a partance in and in the partance is none of the molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a purified nucleic acid molecule associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 GAAATATCAATAAGGCTTGATATGCAGATGACACCCCTTATGGCAGAAAGTGAAGAAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                              Bovine, ss; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GATACATCATGAAAAACCCTGGGCTGGAGGAAGTAAAAGCTGGAATCAAGATTGCCAGGA
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Bovine EST associated with lactation/muscle/fat deposition #7158
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92.8%; Pred. No. 4.7e+02;
tive 0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    segdata.uspto.gov/sequence.html?DocID=20020137139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 7158; 245pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tao N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-2001; 2001US-00960352.
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Best Local Similarity 92.8°
Matches 385, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN
(TAON/) TAO N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                US2002137139-A1.
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2288 2171 AAACAGTGGAAACAGTGTCAGACTTTATTTTTTGGGGGCTCCAAAATCACTGCAGATGG 2230 264 AAACAGIGGAAACAGIGICAGACIIIA--IIIIGGGGGGCICCAAAAICACIGCAGAIGG 321 204 ACATTTAGAAAACTAAGATCATGGCATCTGGTCCCATCACTTCATGGGAAATAGATGGGG 2111 ACATTCAGAAAACGAAGATCATGGCATCTGGTCCCATCACTTCATGGGAAATAGATGGGG 2231 TGACTGCAGCCATGAAATTAAAAGACACTTACTCCTTGGAAGAAAAAGTTA--ACCAACCT 2289 AGATAGCATATTGAAAAGCAGACATTACCTTGCCAACAAAGCCCCATCTAGTC 2343 382 AGATAGCATATTGAAAAGCAGAGACATTACTTTGCCAACAAAGGTCCATCTAGTC 436 셤 엄 ò Db ð g à ò

9

0; Mismatches 208; Indels

Matches 492; Conservative

RESULT 28

ABQ75995 standard; DNA; 31412

(first entry) 05-NOV-2002 Sheep PrP gene nucleic acid sequence

Sheep; PrP; prion; transmissible spongiform encephalopathy; TSE; scrapie; breeding; selection; gene; ds.

Ovis aries

GB2371048-A

10-JAN-2001; 2001GB-00000702

10~JAN-2001; 2001GB-00000702

(UYYO-) UNIV YORK

Ross J, Bowles D;

WPI; 2002-577556/62

Assay for comparing nucleic acid sequence with a reference, useful for determining prion gene alleles, comprises determining the profile of heteroduplexes.

Claim 2 (i)(a); Fig 1; 36pp; English.

The invention relates to an assay for determining allelic variations in prion protein genes, involving comparing a nucleic acid sequence with a reference. The method is used for determining the PrP allele in an animal (or human) in order to assess susceptibility to transmissible spongiform encephalopathies (TSB), most especially scrapie in sheep. This assists in the selection, for breading, of animals having the alleles known to be associated with lowest risk. The method is reproducible and rapid, provides high resolution between allelic variants and is suitable for sheep PrP gene, that is used in the context of the invention as a comparison nucleic acid 

Sequence 31412 BP; 8889 A; 6517 C; 6464 G; 9542 T; 0 U; 0 Other;

Score 344.199; DB 1; Length 31412; Pred. No. 6.9; 9.68; Query Match Best Local Similarity

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17973 AGATGGCTGGATGGCATCACCGACTCGATGGACGTGAGTCTGAGTGAACTCCGGGAGTTA 18032
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ABV99702

ABV99702 standard; cDNA; 31412 BP.

ABV99702;

(first entry) 12-FEB-2003 Sheep BSE-resistant prion protein cDNA.

Transmissible spongiform encephalopathy; neuroprotective; prion protein; bovine spongiform encephalopathy; transgenic; BSE; bovine; cervid; PrP; ISE; gene; ss; sheep. 

Ovis aries

WO200279416-A2

28-MAR-2002; 2002WO-US009652.

(TEXA ) UNIV TEXAS A & M SYSTEM 30-MAR-2001; 2001US-0280549P.

Dunne PW, Piedrahita J; WPI; 2003-092895/08. P-PSDB; ABP57901.

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17733 İGATAACAGTAGGTİTİTİGAACİGTGGTAİTIGGAGAAGACİTCİTIGAGAĞİCCCİTIGGACİ 17792
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                                                                                                                                                                                                                                                                                                            The invention relates to a novel transgenic bovine/cervid comprising a transgene encoding a mutant prion protein (PrP) polypeptide, in which a bubstitution has been made at position 171 of the sequence, which renders the bovine/cervid resistant to bovine spongiform encephalopathy (BSE) and transmissible spongiform encephalopathy (TSE) disease, respectively. The transgene of the invention has neuroprotective activity. The method is useful for producing a transgenic bovine or cervid resistant to BSE and TSE diseases. The bovine prion gene is useful for producing transgenic cattle exhibiting resistance to bovine spongiform encephalopathy. The sequence represents the transgene encoding the mutant PrP polypeptide in
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                                                                                                                                                                        New transgenic bovine and cervid useful for producing animals which are resistant to bovine spongiform encephalopathy and transmissible spongiform encephalopathy disease, comprise a transgene encoding a mutant
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Pred. No. 6.9;
0; Mismatches 208; Indels
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Matches 492; Conservative
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18332 CTÍTAGTÁGTGTÍCAGÍTÍCTÍTTTCCCCAGTCTÍACTÍTÍCTÍTTGAGTTAAGTCAATCC 18391
     'AAAAAGACTTTAAAAT 3064
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                                                                                                                                                                                                                                                                                                                                               surgery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New ovine tissue devoid of antibody-detectable Gal-alpha(1,3)Gal
determinants, for xenotransplantation, and in the treatment of the human
                                                                                                                                                                                                                                                                                                                                   Sheep; xenotransplantation; Gal-alpha (1,3)Gal; GAL determinant; s: alpha(1,3) Galactosyltransferase; alpha (1,3) GT; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11034 BP; 3010 A; 2426 C; 2435 G; 2972 T; 0 U; 191 Other;
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                                                                                                     18392 TAGATACTTTACAGTATGATAGTGAAGTTGTATCTGACTCTTTGT 18437
                                                                                                                                                                                                                                                                                                   Sheep alpha (1, 3) galactosyltransferase post-exon 4 DNA #2
                                                                   3065 TATTAATTTCTCTTTAGTGTTTTACCAGTTCTTTCAGGCTACTTCT
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3005 TATITITATIGATITITICIAAIAAAAICCAGICCIIGII
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ilarity 77.2%; Pred. No. 20;
Conservative 0; Mismatches
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                                                                                                                                                                                              AAD26491 standard; DNA; 11034 BP
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Matches 455;
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4602

4601 Grcaaggcrarggrirriccagregrcarafarafggargrigaggriggacrargaggg 4542

2341 GTCAAGGCTATGGTTTTTCCAGTGGTCATGTATGGATGTGAGAGTTGGACTGTGAAGAA

2282 CCAACCTAGATAGCATATTGAAAAGCAGAGACATTACCTTGCCAACAAAGCCCCATCTA-4661 CTAATGTTTATAGCATATTCAAAAGCAGACATTACTTTGCCAACAAAGGTCCATCTAT

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4541 GCTGAGCCCCGAAGAATCGATGCTTTTGAACTGTGGTGTTGGAGAAGACTCTTHSYCNST 4482
                                                             ------CTGAGCACTGAAGAATTGATGCTTTTGAACTGTGTGTGGAGAAG 2447
                                                                                                                                              ACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTAAAGGAGATCAG 4362
                                                                                                                                                                                                                                                                                                                                     4481 HATGHNGNSNASYCCTGAGCCCCGAAGAATCGATGCTTTTGAACTGTGGTGTTGGAGAAG 4422
                                                                                                                         2448 ACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAG 2507
                                                                                                                                                                                       CCCTGGGGATTTCTTTGGAAGGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGCCACCT 2567
                                                                                                                                                                                                                      4361 CCCTGGGTGTTCTTTGGAAGGAATGATGCTAAAGCTGAAACTCCAGTACTAAGGCCACCT 4302
                                                                                                                                                                                                                                                     GAICAGAAGAGCT---GACTCACTGGAAAAGACCCTGATGCTGGGAGGGATTGGGGGCCAG 2624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine EST associated with lactation/muscle/fat deposition #8154.
                                                                                                                                                                                                                                                                                                                                                                                                                                               2744 ATGGGGTCACAAAGAGTTGGACACGACTGAGCTGAACTGAACTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 8154; 245pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX42989 standard; cDNA; 428 BP
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MATH/) MATHIALAGAN N.
TAON/) TAO N.
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(TAON/) TAO N.
(WARR/) WARREN W C.
2401 G-----
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, of 11 a transformed cell having a nucleic acid comprising an LMFD nucleic acid inked to a promoter and a 3' non- translated sequences that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid acquences or its complement or fragment) with a complementary nucleic acid acquences or its complement or fragment) with a complementary nucleic acid acquence of the molecule; and detecting the level or pattern of the detection of the molecule; and (b) detecting the level or pattern of the detection of the molecule; and (complementary nucleic acid permits the detection of the molecule; and (complementary nucleic acid permits the detection of the molecule. The MMPD nucleic acid is predictive of the detection of the molecule. The MMPD nucleic acid is predictive of the molecule. The molecule in a bovine cell or tissue.

The susful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the list useful for expense a sequence tag) nucleic acid so of the list become the user of shown in the specification but was obtained in electronic format from the USPTO webs site:

Sequence of sequence was not shown in the specification but was obtained in electronic format from the USPTO webs site:
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9.4%; Score 335.8; DB 1; Length '
Best Local Similarity 86.4%; Pred. No. 5.2e+02;
Matches 370; Conservative 0; Mismatches 58; Indels
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ABX36143 standard; cDNA; 406 BP.

ABX36143;

RESULT 32 ABX36143/c ID ABX361 XX AC ABX3614 XX

The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are if it is a transformed call having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that the call to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and ccomplementing a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the molecule acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue, the detection of the complementary nucleic acid molecule obtained from the bovine cell or the complementary nucleic acid molecule. The LMFD nucleic acid, where the detection of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the certain properation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence cell or tissue content to the present sequence was not shown in the specification but was obtained in a laborator. New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle. Bovine, SS; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. Bovine EST associated with lactation/muscle/fat deposition #1308 electronic format from the USPTO web site: segdata.uspto.gov/seguence.html?DocID=20020137139 Warren WC; Claim 2; SEQ ID NO 1308; 245pp; English Tao N, 24-SEP-2001; 2001US-00960352. 12-JAN-1999; 99US-0115707P, 11-JAN-2000; 2000US-00480902. 20-FEB-2003 (first entry) Byatt JC, Mathialagan N, BYATT J C. MATHIALAGAN N. WPI; 2003-110599/10. (WARR/) WARREN W C. US2002137139-A1. 26-SEP-2002 Bos Taurus. BYAT/) MATH/) TAON/)

Sequence 406 BP; 95 A; 138 C; 77 G; 95 T; 0 U; 1 Other;

2464 ö 2405 AGCACTGAAGAATTGATGCTTTTGAACTGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTT 0; Gaps Length 406; Score 333; DB 1; Length 40 Pred. No. 5.6e+02; 0; Mismatches 31; Indels Query Match 9.3%; Best Local Similarity 91.9%; Matches 351; Conservative ઠે

2524 2465 GGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGACATCAGCCCTGGGATTTCTTTGG

406 AGTCCCGAAGAATTGATGCTTTNGAACTGTGGTGTTTGGAGAAGACTCTTGAGTGTCCCTT

a

347

2644 2704 2764 167 227 101 47 226 CATTGGAAAAGACTCTGATGCTGGGAGGGATTGGGGGCAGGAGAGAGGGGACGCCAGA 2705 AGTIGGIGALGGACAGGGAGGCCIGICCIGCGGCGATICAIGGGGICACAAAGAGITGGA 346 GGACTGCAAAGAGTTCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTTTGG 286 AGGGAATGATGCTGAAGATGAAACTCCAGTACTTTGGCCACCTCATGCGAAGAGCTGGCT 2645 GGATGAGATGGCTGGATGGCATCACTGATGGACGTGAGTCTGGGTGAACTCCTGG 106 AGTTGGTGATGGACGGAGGCCTTGCGTGTGTGTTCATGGGGTCGCAAAGAGTCGGA 2585 CACTGGAAAGACCCTGATGCTGGGAGGGATTGGGGGCCAGGAGGAGAAGGGGACGACAGA New bovine genomic DNA sequences, useful for establishing genetic signatures, e.g. for breeding control, contain specific variable positions. Bovine; digital DNA signature; breeding; animal product origin; identification; genetic association; breed; population; race; ds. Bovine-derived DNA fragment contig1 487\_67. 2765 CACGACTGAGCAACTGAACTGA 2786 46 TAGGGCTGAGCGACTGAACTGA 25 Claim 1; Page 23-24; 26pp; German. AAH21026 standard; DNA; 1529 BP. 99DE-01059751. 99DE-01059751. 31-AUG-2001 (first entry) Fries HR, Durstewitz G; (FRIE/) FRIES H R. (DURS/) DURSTEWITZ G. WPI; 2001-376309/40. DE19959751-A1 11-DEC-1999; 11-DEC-1999; 13-JUN-2001 Bos taurus. AAH21026; g 유 영 ò g g ઠે à

This invention describes bovine DNA sequences (A) which are used in a method to establish a digital, standardized DNA signature. DNA signatures established from (A) are used to monitor breading, to determine origin of animal products; to identify individual animals, to study genetic association and to establish signatures that are specific at the level of bread, population or race. The method is based on individual base exchanges in DNA, and these are inherited more stably (by an order of studies in DNA, and these resident its suitable for population-wide studies (as a high throughput test) and the presence of unequivocal sequences flanking the variable position provides a built-in standardization feature

Sequence 1529 BP; 589 A; 299 C; 239 G; 358 T; 0 U; 44 Other;

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                                                         1678 AGAGTICCAGAAAAACAICTATITCIGCITIATIGACTAIGCAAAAGCCTTIGACIGG
                                                                             GGGTCACAATAAACTGTGGAAAATTCTGAAAGGGATGGGAATACCAGACCACCTGACCTG
                                                                                                                                                                        ACTICTTGAAAATTTGTATGCAGGTCAGGAAGCAACAGTT----AGAACTGGACATGGA
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 Length 1529;
Score 326.3; DB 1; Length
Pred. No. 1.6e+02;
0; Mismatches 152; Indels
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ABX43146 standard; cDNA; 423 BP.
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11-JAN-2000; 2000US-00480902.
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Similarity 73.7%; Conservative (
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muscle deposition;
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 Query Match
Best Local Simi
Matches 452;
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing a transformed cell having a nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid aliaked to a promoter and a 3 and of the mRNA molecule, and cc of polyadenylated ribonucleotides to a 3 and of the mRNA molecule, and cc (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any cc of the 1512 nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid, where the detection of the complementary nucleic acid is predictive of the detection of the molecule. The LMFD nucleic acid, is used for the detection of the molecule. The LMFD nucleic acid, is used for determining a level or pattern of the molecule. The LMFD nucleic acid, is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle compensation on constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the complement sequence was not shown in the specification but was obtained in a latert not all the inspired in a per sepecification but was obtained in a latert not a latert not an inspired in a per sequence as not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                  New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis,
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                                                                                                                                                                                                                                                                                               deposition, useful for genome mapping, gene identific
cattle breeding, or for genetically improving cattle.
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                                                                                                                                                               Warren WC;
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                         BYATT J C.
MATHIALAGAN N.
TAO N.
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                                                                                                         WARR/) WARREN W C.
                                                                                                                                                            Syatt JC,
                         (BYAT/)
(MATH/)
(TAON/)
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Query Match 9.1%; Score 324; DB 1; Length 423;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 357; Conservative 0; Mismatches 55; Indels 0; Gaps

2439 2499 2559 2739 2620 GGCAGGAGGAGGAGGACGACAGAGGATGAGATGGCTGGATGGCATCACTGACTCGATG 2679 364 304 244 124 243 GGTCACCTGATGGGAAAAACTGACTGATCTGAAAAGACCCTGGTGGGGAAAGATTGAA 184 64 363 TGGAGAAGACTCTTGAGAGTCCCCTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAG 183 GGCAGGAGGAGGACGACGACGAGGATAAGATGGTTGGATAGCATCACCTACTCATG 2380 GAGAGTTGGACTGTGAAGAAAGCTGAGCACTGAAGAATTGATGCTTTTGAACTGTGTGT 423 GAGAGTIGGACTGTGAAGAAGAGCTGAGCCCAAAGAATIGAIGCTTTIGAACTGTGGGTGT 2440 TGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGCAGTCCATTCTGAAG 303 GAGATCAGCCCTGGGTGTTCATTGGAAGGAATGATGCTGAAGCTGAAACTCCAACACTTT 2680 GACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAGGCCTGTCCTGCGGCG 2500 GAGAICAGCCCTGGGGATTTCTTTGGAAGGAATGATGCTAAAAGCTGAAACTCCAGTACTTT 셤 qq a g ò ਨੇ 8 d à à ઠે

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The Intention relates to a purinted muclence acid medicale associated with cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectie sequences, appearing as ABX49947, or complements of them. Also included are included are included to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyademylated ribonucleotides to a 3' non- translated sequence that functions in the cell to cause termination of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) includating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complementary nucleic acid sequences or its complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid sequence or its such as a second of the complementary nucleic acid sequence or its complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is used for detecting in for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the recomplement and analysis, cattle breeding. Devine LMPD EST (expressed sequence tes one of the recomplement and provine and analysis, cattle breader and analysis, cattle breader and manalysis.
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                                                                                                                                                                                                                                                                                                                  Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
2740 ATTCATGGGGTCACAAAGAGTTGGACACGACTGAGCTGAACTGAACTGA 2791
                                                                                                                                                                                                                                                                              Bovine EST associated with lactation/muscle/fat deposition, #13834
                           63 GTCCATGGGGTTGCAAAGAGTTGGACACAACTAAGTGACTGAACTGA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 13834; 245pp; English.
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                                                                                                                                                  ABX48669 standard; cDNA; 410 BP
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(MATH/) MATHIALAGAN N
(TAON/) TAO N.
(WARR/) WARREN W C.
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AGCTGAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGACTCACTGGAAAAGACCC 2599
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                                                                                                                                                                                                                                                                                                     241 CCAACCAGTCTATTCTAAAGGAGATCAGTCCTG----TTCTTTGGAAGGACTGAAGCTAA
                                                                                                                                                                CAGTGGTCATGTATGGATGTGAGGGTTGGACTGTGAAGAAAGCTGAGCACTGAAGAATTG
                                                                                                                                                                                   2242 ATGAAATTAAAAGACACTTACTCCTTGGAAGAAAAGTTA--ACCAACCTAGATAGCATAT
                                                                                1 ATGAAATTAAAAGATGCTTACTCCTTGTTAGGAAAGTTATGACCAACCTAGATAGCATAT
                                                                                                          TGAAAAGCAGAGACATTACCTTGCCAACAAAGCCCCATCTAGTCAAGGCTATGGTTTTTC
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                                                                                                                                                                                                                     ATGCTTTTGAACTGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGAT
                                                                                                                                                                                                                                               181 ATGCTTTTGAACTGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGT
                                                                                                                                                                                                                                                                           AGCTGAAACTCAAATTCTTTGGCCACCTGACATGAAGAGTTGACTCATTGGAAAAGACTT
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                    TGATGCTGGGAGGGATTGGGGGCAGGAGAAGGGGACGACAGAGAGGATGAGAT 2653
                                                                                                                                                                                                                                                                                                                                                                                                    Bovine EST associated with lactation/muscle/fat deposition #5499
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 Length 410;
                           40; Indels
Score 321.6; DB 1;
Pred. No. 5.9e+02;
0; Mismatches 40;
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Similarity 88.9%;
89; Conservative C
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MATHIALAGAN N.
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(WARR/) WARREN W C.
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                           368;
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    Query Match
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Matches
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Sequence 410 BP; 132 A; 67 C; 104 G; 106 T; 0 U; 1 Other;

segdata.uspto.gov/sequence.html?DocID=20020137139

from the USPTO

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are; (1) a transformed cell havying a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non- translated sequence that functions in the cell to cause termination of transcription and addition of plyddenylated ribonucleotides to a 3 end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or the detection of the molecule. The Mercentonion of the molecule, and (b) detecting the level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breath or pattern of a molecule in a bovine cell or tissue. The present sequence easi or so of the complement of the molecule of the molecule of the complement of the molecule or pattern of a molecule in a bovine cell or tissue. The breath in a bovine LMFD best cannow mapping, gene identification and analysis, cattle breath in the level or pattern of a molecule in a bovine cell or the complement of the molecule or pattern of a molecule in a bovine cell or the complement of the molecule or pattern of a molecule or pattern of the molecule or pattern of a molecule or pattern of the molecule or pattern of a molecule or pattern of the molecule or pattern of a molecule or pattern of or pattern of a molecule or pattern or pattern or pattern or pattern or p
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Gaps . 0 DB 1; Length 423; 9.0%; Score 320.8; DB 1; Length 86.2%; Pred. No. 5.7e+02; ve 0; Mismatches 57; Indels Sequence 423 BP; 93 A; 128 C; 72 G; 130 T; 0 U; 0 Other; 86.2%; Matches 355; Conservative Similarity Query Match Local

2499 2559 2619 2680 GACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAGGCCTGTCCTGCGGGCG 2739 2439 2620 GGCAGGAGGAGAGGGGACGACAAGAGGATGAGATGGCTGGATGGCATCACTGACTCGATG 2679 244 243 Gercacenganggaaaaacngaengarengaaaagaeeengangenggaaagangaa 184 123 AACTTGAGTTTGAATAAGCCCCAGGAGTTGGTGATGGACAGGGAAGCATAGCATACTGCA 64 303 GAGATCAGCCCTGGGTGTTCATTGGAAGGAATGATGCTGAAGCTGAAACTCCAACACTTT 2380 GAGAGTTGGACTGTGAAGCTGAGCACTGAAGAATTGATGCTTTTGAACTGTGGTGT 2440 TGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAG 363 TGGAGAAGACTCTTGAGAGTCCCTGGAACTGCAAGGAGATCCAACCAGTCCATTCTGAAG 2500 GAGATCAGCCCTGGGATTTCTTTGGAAGGAATGATGCTAAAGCTGAAACTCCAGTACTTT 423 g ⊹≿ g 8 임 à 쉱 ð à g 요 ò

Grecardoggradaagagradaacacaacraagagagagagagagagaga 12 2740 ATTCATGGGGTCACAAAGAGTTGGACACGACTGAGCAACTGAACTGAACTGA 63

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2791

ABX49143 standard; cDNA; 409 (first entry) 21-FEB-2003 ABX49143; RESULT 37 ABX49143/ XEXEXEX

BP.

Bovine EST associated with lactation/muscle/fat deposition #14308.

1867

290

409 AAACTGTGGACAATTCTGAAAGAGATGGGAATACCAGACCACCTGATCTGCCTCTTGAGA 350

1868 CAAGTAGGAAAAGGGGTAGAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTAT 1927

349 AATCTGTATGCAGGTCAGGAAGCAACAGTTAGAACTGGACATGAGACAACAGACTGGTTC

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1808 AATTIGIATGCAGGICAGGAAGCAACAGTTAGAACTGGACATGGAACAACAGACTGGTTC

The invention relates to a purified nucleic acid molecule associated with cattation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX34936-ABX49947, or complements of them. Also included are cid allocation of a promoter and a 3 non-translated sequence that control or a promoter and a 3 non-translated sequence that control or polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid, swhere the detection of the molecule. The LMFD nucleic acid, is used for complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid, is used for the detection of the molecule. The LMFD nucleic acid, is used for complementary nucleic acid is used for complementary nucleic acid is used for the molecule or a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle complements is present sequence tag not shown in the present sequence is one of the complement requence was not shown in the respecticities of the incomplement in the respective of the complement of the nucleum of the respective of the complement and such shown in the respective of the complement of the nucleum of the respective of the complement of the nucleum of the respective of the complement of the nucleum of the sequence was not shown in the respective of the respective of the respective of the respective of the respec 1748 AAACTGTGGAAATTCTGAAAGGGATGGGAATACCAGACCACCTGACCTGACTCTTGAAA 1807 New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. Gaps .; 7 9.0%; Score 320.4; DB 1; Length 409; 89.3%; Pred. No. 6e+02; tive 0; Mismatches 42; Indels 2; Sequence 409 BP; 90 A; 97 C; 84 G; 137 T; 0 U; 1 Other; deposition, useful for genome mapping, gene identific cattle breeding, or for genetically improving cattle electronic format from the USPTO web site: segdata.uspto.gov/seguence.html?DocID=20020137139 Warren WC; Claim 2; SEQ ID NO 14308; 245pp; English. Tao N, 24-SEP-2001; 2001US-00960352. 12-JAN-1999; 99US-0115707P. 11-JAN-2000; 2000US-00480902. Mathialagan N, Matches 366; Conservative (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. WPI; 2003-110599/10. Query Match Best Local Similarity (TAON/) TAO N. (WARR/) WARREN W C. US2002137139-A1. 26-SEP-2002. Bos Taurus Byatt JC, ò

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30-4400-2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000
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                                                                                                                 1928 GCAGAG-ACATCATGAGAAACGCTGGCTGGAAGAAGCACAAGCTGGAATCAAGATTGCC
                                                                                                                                                                                                                                  229 GCAGAGTCCATGATGAGAAACTCTGGGCTGGAAGAACACAGAGCTGGAATCAAGATTGCC
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ID AAK56452 standard; cDNA; 529 BP.
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962 TAGGGGACTGGAATGCAAAAGTAGGAAGCAAAGAAACACCCTGGAGTAACAGGCAAATTT 1020
                                                                                                               CACAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAACGTC 902
                                                                                                                                                                        CTATGAAGACCTACAAGACCTTTTAGAACTAACACCCAAAAA-AGATGTCCTTCTCATTA 961
GACTGGAATGGGTGAATTTAACTCAGATAACCATTATATCTACTACCGTGGGCAGGAATC 294
                                                                                                                                                                                                                                   Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                     783 ATGCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCAATAT
                                  CCTCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAAGAGTCCGAAATGCAGTACTTGG
                                                                                                                                                                                                                                                                                                            59 TGGGGGACTGGAATGCAAAGTAGGAAGCCAAGAAACATCTGGGGTAACAGAGAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine EST associated with lactation/muscle/fat deposition #9545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 9545; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                           ABX44380 standard; cDNA; 425 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
(WARR/) WARREN W C.
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ABX44380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GICAAACAAGAGAIGGCAAGAGIGAAIGICAACAIICIAGGAAICAGCGAAC-IAAAAIG 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 GTCAAACAGGAGATGGCCAGGAGTGACCNTGACATTCTRGGAATCAGTGAACTTAAAATG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                claim 1; SEQ ID NO 1512; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.9%; Score 316.4; DB 1
88.8%; Pred. No. 4.7e+02;
cive 1; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC, Ruben SM;
        17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-025198P.
0S-DEC-2000; 2000US-025186P.
0S-DEC-2000; 2000US-025186P.
0S-DEC-2000; 2000US-025186P.
0S-DEC-2000; 2000US-025186P.
0S-DEC-2000; 2000US-025186P.
0S-DAN-2001; 2000US-025198P.
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Matches 372; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483426/52
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3 end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or
New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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| GACTOGAAIGGGGGAAITIAACTCAGAIGACCAITATATCTACTACTGCGGGGAGGAAIC 722

663

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99DE-01059751, 99DE-01059751

11-DEC-1999; 11-DEC-1999;

13-JUN-2001.

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tissue comprising: (a) incubating a marker nucleic acid (comprising any coff the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid, where the detection of the complementary nucleic acid; so used for the detecting of the molecule. The LMFD nucleic acid is used for determining a level or pattern of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle or preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 1512 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence as not shown in the specification but was obtained in electronic format from the USPPO web site:

seqdata.uspto.gov/sequence.html?DocID=20020137139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGTGAAAGAGGAGAGAAAAAGTTGGCTTAATTCTCAACATTCAGAAAACTAAGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCATCTGGTCCCATCACTTCATGGGAAATAGATGGGGAAACAGTGGAAACAGTGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2253 AGACACTTACTCCTTGGAAGAAAGTTA--ACCAACCTAGATAGCATATTGAAAAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGGTTGTGAGATTGGACTATAAAGAAAGCTGAGTGCTGAAGAACTGATGGTTTTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTATGTTTT - TGGGCTCCAAATCACTGCAGATGGTGAATGCAGCCATGAAATTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGGATGTGAGAGTTGGACTGTGAAGAAAGCTGAGCACTGAAGAATTGATGCTTTTTGAA
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8.8%; Score 313.4; DB 1; Length 425;
Best Local Similarity 87.4%; Pred. No. 6e+02;
Matches 375; Conservative 0; Mismatches 46; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 425 BP; 144 A; 70 C; 100 G; 111 T; 0 U; 0 Other;
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This invention describes bovine DNA sequences (A) which are used in a method to establish a digital, standardized DNA signature. DNA signatures setablished from (A) are used to monitor breeding; to determine origin of animal products; to identify individual animals; to study genetic association and to establish signatures that are specific at the level of breed, population or race. The method is based on individual base exchanges in DNA, and these are inherited more stably (by an order of magnitude) than conventional markers: It is suitable for population-wide studies (as a high throughput test) and the presence of unequivocal sequences flanking the variable position provides a built-in

ew bovine genomic DNA sequences, useful for establishing genetic ignatures, e.g. for breeding control, contain specific variable

Fries HR, Durstewitz G;

WPI; 2001-376309/40

New bovine genomic

positions.

(FRIE/) FRIES H R. (DURS/) DURSTEWITZ G.

Claim 1; Page 22; 26pp; German

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1525 AGAAGAGAGAGAAAGGAAAGGAAAAAAAAGATAAAAGCATCTGAATGCAGAGTTC 1584
                                                                                                                                      1079 CAAGAGAACATACTGATCAGAGCAAACACCCTCTTCCAATAACACAAGAGATGACTCTAC
                                                                                                                                                                                                                                                                          1189 AGATGGAGAAGCTCTATACAGTCAGCAAAAACAAGACCAGGAGCTTACTGTGGCTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ACATTGTACAGGAGACAGGATCGAGACATCCCCATG
                                                                                           1069 CAAGAAATGCACTGGTCATAGCAAACACCCTCTTCCAACAACAACAAGAAGAAGACTCTAC
                                                                                                                                                                                    1019 ACATGGACATCACCACGGGTCAATACCGCAATCAGACTGATTATATTCTTTAGGGCTGA
                                                                                                                                                                                                                                                                                                                     959 AGATGGACAAACTCTATACAGTCAGCAAAAACAAGACCTAGAG-----TTGACTCAGAT
                                                                                                                                                                                                                                                                                                                                                                   1249 CATGAACTCCTTATTGCCAAATTCAGACTTAAATTGAAGAAAGTA-GGGAAAACCACTAG
                                                                                                                                                                                                                                                                                                                                                                                                              905 TATTAGCACCICACTGCAAAAGTCAGGCTTAAATTGAAGAAAGTAGGGGAAAACTACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1308 ATCACTCAGGTAAGACCTAAATCCAATCCCTTATGATTATACAGTGGAAGTGAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       845 GCCATTCAGGCATGACCTAAATCAAATCTCTTATGATTACACAGTGGGGGTGATGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1368 ATTTAAGGGCCTAGATCTGATAGACAGAGTACCTAATGAACTATGGACAGAGGTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      665 AAAAAGAAATGCAAGAAGGCAAAGTGATCATCTACAGAGGCTTTACAAATAGCTGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAAAGAAATGCAAAAAGCAAAATGGCTGTCTGGGGAGGCCTTACAAATAGCTGTGAAA
8.7%; Score 312.4; DB 1; Length 1435; ilarity 74.5%; Pred. No. 1.8e+02; Conservative 0; Mismatches 116; Indels 30;
                        Local Similarity
                                                427;
  Query Match
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Matches
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1020 1188

30;

Sequence 1435 BP; 309 A; 301 C; 241 G; 584 T; 0 U; 0 Other;

standardization feature

1248

906

960

1307

846

1367

786

1426

1464

999

605

DE19959751-A1

Bos taurus

31-AUG-2001

AAH21024

Length 422;

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New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                    Bovine EST associated with lactation/muscle/fat deposition #3391
1585 CAAAGAACTICCAGTIGIICAAGCIGGIITIAG 1617
                                                   545 chahardandandandandadaridadariha 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tao N, Warren WC;
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                                                                                                                                                                                                      ABX38226 standard; cDNA; 422 BP
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                                                                                                                                                                                                                                                                                                                    (first entry)
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(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
(WARR/) WARREN W C.
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ABX33226

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ABX32226

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The invention relates to a purified nucleic acid molecule associated with catcation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising an specifically hybridise to a second appearing as ABX34836-ABX4937, or complements of them. Also included are a promoter and a 3 non-translated sequence that acid linked to a promoter and a 3 non-translated sequence that call to cause termination of transcription and addition of polyadenylated ribbnucleotides to a 3' end of the mRNA molecule; and comprising a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the last or acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the detection of the molecule. The detection of the molecule complementary nucleic acid molecule obtained from the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the molecule. The LMFD nucleic acid, is used for the detection of the molecule. The LMFD nucleic acid, is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle complements proved for molecule in a bovine cell or tissue. The breath sequence was not shown in the sequence is one of the content of the molecule in a powine caids. Note: The present sequence was obtained in a part of the molecule. electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139

Sequence 422 BP; 152 A; 73 C; 100 G; 97 T; 0 U; 0 Other;

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                                                                                                                          61 ĠĠĠATAĊĊAĠAAGAĊĊŦTATĊŦĠĊŦŦĊĊĬĠAĠAAĊĊĬĠĬĠĬĠĬĠĬĠĠĠĬĊAAĠĀĠĠŦĀ
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                                                  1714 CTATGCAAAAGCCTTTGACTGTGGGGGTCACAATAAACTGTGGAAAATTCTGAAAGGGAT
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide(s) useful in treatment of myasthenia gravis - also i
diagnosis, having acetyl:choline receptor-alpha like activities
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hACR-alpha; myasthenia gravis; MG; neuromyopathy; ds.
Score 307.8; DB 1;
Pred. No. 6.2e+02;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calf acetyl choline receptor alpha cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAN50416 standard; cDNA; 3649 BP.
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86.0%;
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 Query Match
Best Local Similarity 86.0
Matches 363; Conservative
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08-JAN-1992
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Best Local Similarity 93.2%;
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    Ā
reaction to ACR. See also AANS0415. (Updated on 25-MAR-2003 to correct field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine, ss; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                                                                                                                              2820 GCTGGGAGGGATTGGGGGCAGGAGAAGAGGGATGACAGAGGATGAGATGAGATGGCTGGATGG
                                                                                                             TTTTGAACTGTGGTGTTGGAAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAA
                                                                                                                                                               2940 ccadiccarrcraaagaagarcagrccraggriricrirgaaagaaargargcraaagcr
                                                                                                                                                                                                               2544 GAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGACTCACTGGAAAAGACCCTGAT
                                                                                                                                                                                                                                       GAAACTCCAGTACTTTGGCCACCTCATGCGAAGAGTTGACTCATTGGAAAAGACTCTGAT
                                                                                                                                                                                                                                                                GCTGGGAGGATTGGGGGCAGGAGGAGAAGGGGACGACAGAGGATGAGATGGCTGGATGG
                                                                                                                                                                                                                                                                                                                  CATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGA
                                                                                                                                                                                                                                                                                                                                       2760 CATCACTTACTTGATGGACGTGAGTTTGAGTGAACTCGGGAGTTGGTGATGGACAGGA
                                                                                         Gaps
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                                                              DB 1; Length 3649;
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                                    Sequence 3649 BP; 1007 A; 912 C; 780 G; 950 T; 0 U; 0 Other;
                                                                                      28; Indels
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                                                                          Pred. No. 74;
0; Mismatches
                                                             Score 306.2;
Pred. No. 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                             8.6%;
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11-JAN-2000; 2000US-00480902.
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                                                                                      Conservative
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MATHIALAGAN N.
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(MATH/) MATHIALAGAN !
(TAON/) TAO N.
(WARR/) WARREN W C.
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                                                                         Similarity
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                                                             Query, Match
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                                                                          Best Loca
Matches
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The invention relates to a purified mucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are if a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non-translated sequence that the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cf polyadenylated ribonucleotides to a al' end of the mensa any acid tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complementary nucleic acid sequences or its complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid sequences or its complementary nucleic acid molecule obtained from the molecule; and (b) detecting the level or pattern of the complementary nucleic acid so the complementary nucleic acid is used for complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for determining a level or pattern of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle to genetically improving cattle. The present sequence is one of the complementary nucleic acid is used for the genetically improving cattle. The present sequence is one of the complementary nucleic acid is used for the genetically improving cattle. The present sequence is one of the complementary nucleic acid is used for the genetically improving cattle. The present sequence was not shown in the specification but was obtained in cell cross sequence. The present sequence format from the USPPTO web site:

**Complementary**

**Complementary**

**Complementary**

**Complem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AAGAATTGATGCTTTTGAACTGTGGGAGAAGACTCTTGAGACTCTTGAGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2592 AAAGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGGAGAAGGGGACGACAGAGGATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2532 GATGCTAAAGCTGAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGACTCACTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGCTGAAGCTGAAATTCCAGTACTTTGGCCACCTCATGCGAAGAGTTGACTTATTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2652 ATGGCTGGATGGCATCACTGACTCGATGGACGTGAG 2687
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1408 CTATGGACAGAGGTTCATGACATTGTACAGGAGACAGGGATCGAGACCATCCCCATGGAA 1467

380 CTATAGACAGAGGTTCATGACATTGTACAGGAGACAGGGAGCAAGACACCATCCCCAAGATA 439

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320 ACAGTGGAAGTGGGAAATATATTTAAGGGACTAGATCTGATAGACAGAATGCCTGATGAA 379

1348 ACAGTGGAAGTGAAAATAGATTTAAGGGCCTAGATCTGATAGACAGAGTACCTAATGAA

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1288 AAAGTAGGGAAAACCACTAGATCACTCAGGTAAGACCTAAATCCAATCCCTTATGATTAT 1347

260 AAAGTAGGGAAAACCACTAGATCATTTAGATATGACCTATATCAAACCCCTTACTACTATT

200 GGAGCTGACTGTGCTCTGTGAACACCTAATTGCAAAATACAGACTTAAATTGAAG 259

g 8

GGAGCTTACTGTGGCTCAGGATCATGAACTCCTTATTGCCAAATTCAGACTTAAATTGAAG

141 GATTATATTCTTTGCAGACAAAATGG-GGAGCTCTATACAGTCAGCAAAAGCAAGACTG 199

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (i) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non- translated sequence that functions in the cell to cause termination of transcription and addition of plyddepylated Tibonucleotides to a 3 end of the mRNA molecule, and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequence be arised for the molecule; and (b) detecting the level or pattern of the complementary nucleic acid sequence to detecting of the molecule obtains a bovine cell or the molecule. The LMFD nucleic acid is predictive of the detection of the molecule. The LMFD nucleic acid is used for the molecule of the molecule in a bovine cell or tissue.

CC level or pattern of the molecule in the molecule acid is used for the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breading, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the lactoric format from the USPTO web site:

CS sequence was not shown in the specification but was obtained in election in a bovine of sequence. The security of the molecule of the present sequence as not shown in the specification but was obtained in a bovine and an analysis of the electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Byatt JC, Mathialagan N, Tao N, Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 11945; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-SEP-2001; 2001US-00960352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-110599/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                               US2002137139-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2002
                                                                                                                                                                                                                                           Bos Taurus.
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The patent discloses immunologically compatible animal tissue, suitable for xenotransplantation into human patients. The invention also relates to an ovine tissue devoid of antibody-detectable Gal-alpha (1,3)Gal (GAL) determinants which are made by alpha (1,3) galactosyltransferase (GT). The ovine tissue is useful for treatment of human body by surgery or therapy and in xenotransplantation, by transplanting the ovine tissue into a marmal having circulating antibody against Gal alpha (1,3)G determinants. Polynucleotide constructs of the invention are useful for inactivating an alphal, 3 GT gene in an ovine cell. Alpha (1,3) GT sequences are useful for drug screening and for the production of GAL containing synthetic oligosacoharides. Sequences of the invention are also useful in gene therapy. The present sequence is alpha (1,3) GT post-exon 4 DNA
                                                                                                                                                                                            Sheep; xenotransplantation; Gal-alpha (1,3)Gal; GAL determinant; surgery; alpha(1,3) galactosyltransferase; alpha (1,3) GT; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New ovine tissue devoid of antibody-detectable Gal-alpha(1,3)Gal determinants, for xenotransplantation, and in the treatment of the human
                                                                                                                                                     Sheep alpha (1, 3) galactosyltransferase post-exon 4 DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 76; 86pp; English.
                   AAD26490 standard; DNA; 815 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                          .4-MAY-2001; 2001WO-US015765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-2000; 2000US-0204148P.
13-JUN-2000; 2000US-00593316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    body by surgery or therapy
                                                                                                          26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Denning C, Clark J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-089848/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GERO-) GERON CORP.
                                                                                                                                                                                                                                          gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                   WO200188096-A2.
                                                                                                                                                                                                                                                                                                                                                                            22-NOV-2001.
                                                              AAD26490;
                                                                                                                                                                                                                                                                                        Ovis sp.
AAD26490/
                                                              1048 CAAAGACTAATAGAGTTTTGCCAAGAAAATGCACTGGTCATAGCAAACACCCTCTTCCAA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1109 CAACACAAGAGAAGACTCTACACATGGACATCACCAGATGGTCAACACCGAAATCAGATT 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1168 GATTATATTCTTTGCAGCCAAAGATGGAGAAGCTCTATACAGTCAGCAAAAACAAGACCA 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 CGGCGCAAGATACATCTACATGTGGACATCATCAGTTAGTCAACACCCAAAATCAGATT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 CGAAGGCCAGTAAAGTCTTCACAAGAGAHATATTGGTGATAGG-AAGAACCTTTTTCAA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.4%; Score 299.4; DB 1; Length 447; Best Local Similarity 84.1%; Pred. No. 6.2e+02; Matches 360; Conservative 0; Mismatches 66; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 447 BP; 162 A; 88 C; 94 G; 103 T; 0 U; 0 Other;
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Best Local Similarity
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                                                                                           2402 CTGAGCACTGAAGAATTGATGCTTTTGAACTGTGGTGGTGGAGAAGACTCTTGAGAGTCC 2461
                                                                                                                                                         2462 CTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTT 2521
                                                                                                            635 GACTCATATGGAAAAGACTCATGAAGCTGGGAGGATTGGGGGCAAGAGGAGAAGAGGGAC 576
                                                                                                                                                                                                                                                                                                                                                                 Query Match
8.4%; Score 298.6; DB 1; Length 815;
Best Local Similarity 87.8%; Pred. No. 3.4e+02;
Matches 347; Conservative 0; Mismatches 44; Indels 4; Gaps
Sequence 815 BP; 217 A; 189 C; 186 G; 221 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2758 AGTIGGACACGACTGAGCAACTGAACTGAACTGAA 2792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 AGTMGGACACGACTGAACGACTGAACTGAA 421
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Search completed: August 24, 2004, 13:11:25 Job time : 671 secs

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August 24, 2004, 13:21:40; Search time 604 Seconds (without alignments) 3.966 Million cell updates/sec
                                                                                                                                                                                                                                                         US-10-664-775-2
3572
1 gtcaggaaggcggcagtga......gcaacaacagcagaaagctt 3572
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                 OM nucleic - nucleic search, using sw model
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Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

45 seqs, 335272 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

rni2.seg:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 5, Appli Sequence 23, Appli Sequence 7, Appli Sequence 7, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-08-232-463-14 US-110-204-708-3 US-110-204-708-23 US-110-204-708-21 US-110-204-708-21 US-110-204-708-33 US-08-998-411-1137 US-110-204-708-31 US-08-206-176-20 US-08-206-176-20 US-08-076-506-5 US-08-071-601-3 US-09-930-3778-1 US-09-930-3778-1 US-09-487-8262-1 US-08-487-8262-1 US-08-487-8262-1 US-08-487-8262-1 US-08-998-416-595 US-10-204-708-22 US-10-204-708-57 US-10-204-708-57 US-10-204-708-69 US-10-204-708-35 US-10-204-708-10 US-10-204-708-80 US-10-204-708-29 US-08-060-822A-5 PCT-US94-05257-5 US-08-756-506-23 SUMMARIES Match Length DB 3370 3370 10807 10807 2044 2044 2044 19124 6669 6669 6676 6866 8861 6866 8861 658 110469 6326 10467 6040 9347 7218 10619 11049 6801 11049 Query Result

Sequence 2, Appli Sequence 86, Appl Sequence 55, Appl Sequence 45, Appl	
US-07-867-106-2 US-10-204-708-86 US-10-204-708-55 US-10-204-708-45	US-06-213-419B-3 US-10-204-708-18 US-10-204-708-11 US-08-998-416-186 US-10-204-708-71 US-10-204-708-26 US-06-998-416-288 US-10-204-708-39
5852 11050 11015	6124 8537 615 8607 6583 19513
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GENERAL INFORMATION:
APPLICANT: Bevins, Charles L.
APPLICANT: Diamond, Gill
APPLICANT: Diamond, Gill
APPLICANT: Diamond, Gill
APPLICANT: Asioff, Michael
TITLE OF INVENTION: No. 5432270el Antimicrobial Peptides
NUMBER OF SEQUENCES: 20
CORRESPONDENCE MODGOEK Washburn Kurtz Mackiewicz & No. 5432270ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPRYERCT 5.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
FLING DATE: 1930511
CLASSIPICATION: 530
PRIOR APPLICATION DATE: 1992
ATPLING DATE: December 15, 1992
ATPLING DATE: December 15, 1992
ATPRIORY AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
ATPRENCY CACKET NUMBER: GH-0408
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: GH-0408
REGISTRATION NUMBER: 35,152
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RESULT 1
US-08-060-822A-5/c
; Sequence 5, Application US/08060822A
; Patent No. 5432270
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MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3370 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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1444..1449
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164 TCTGGCATGCTGCAATTCATGGGTCGCAAAGAGTTGGGTACCACTGAGCGACTGAAACT 105
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GENERAL INFORMATION:
APPLICANT: Bevins, Charles L.
APPLICANT: Diamond Gill
APPLICANT: Zasloff, Michael
TITLE OF INVENTION: Novel Antimicrobial Peptides
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STRERT: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIPO
ZOMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PSA/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC-10594/05257
FILING DATE: 11-MAY-1994
CLASSIFICATION NUMBER: 08/060,822
FILING DATE: 11,1993
APPLICATION NUMBER: 07/991,200
FILING'DATE: December 15, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebeca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REPERENCE/DOCKET NUMBER: 35,152
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Best Local Similarity 89.1%; Pred. No. 8.4e-07;
Matches 778; Conservative 0; Mismatches 85; Indels 10
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89.1%; Pred. No. 8.4e-07;
ive 0; Mismatches 85; Indels 1
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                                        GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Froster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Proster, Donald C.
APPLICANT: Proster, Cindy A.
APPLICANT: Proster, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Proster, Cindy A.
APPLICANT: Proster, Cindy A.
APPLICANT: Sprecher; 25
CORRESPONDENCE: 25
CORRESPONDENCE: ZymoGenetics, Inc.
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
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78.2%; Pred. No. 1.1;
tive 0; Mismatches
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1201 Eastlake Avenue East
Sequence 23, Application US/08756506 Patent No. 5905185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 206-442-6678
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 6763 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.2
Matches 279; Conservative
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STRANDEDNESS: double
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DB 1; Length 10807;
        Sequence 5, Application US/08756506
; Patent No. 5905185
; GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Temperlagham, Ian R.
APPLICANT: Temperlagham, Simon M.
APPLICANT: Preferry Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
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Similarity 78.2%; Pred. No. 0.69;
79; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                             2: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 38102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTOLING DATE:
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislar, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFANCE: 206-442-6678
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-756-506-5
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Best Local Simi:
Matches 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10807;
                                                                             GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Pallymple, Michael A
APPLICANT: Prinkard, Donna E
APPLICANT: Prinkard, Donna E
APPLICANT: Prinkard, Donna E
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
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CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELEPHONE: 206-547-8080 ext 322
TELEPHONE: 206-547-8080 ext 322
TELEPHONE: 206-548-2329
INFORMATION FOR SEQ ID NO: 7:
SEDGUENCE CHARACTERISTICS:
LENGTH: 10807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentr Policy
                                                                                                                                                                                                                                                                            E: ZymoGenetics, Inc.
4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ovine beta-lactoglobulin
RESULT 4
US-08-206-176-7
'Sequence 7, Application US/08206176
'Patent No. 5639940
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: WA
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STREET: 42
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2632 2693 GTGAACTCCTGGAGTTGGTGATGGACAGGGAGGCCTGTCCTGC-----GGCGATTCATG 2746 9548 GIGGACICCAGGAGTIGGIGAIGGACAGGAAGGCIGGCGIGCTACGGAAGCGGTITAIG 9607 9488 GGGGACGACAGGATGATGGTTGGATGGCATCACCAACACAATGGACATGGGTTTGG 9547 9312 TGAGAACTGTCTGCACACACAGAGTCCACCAGTC--ATCCTAAGGAGATCAGTCTG 9370 GTGTTCATT--GGAGGACTGATGTTGAAGCTGAAACTCCAATGCTTTGGCCACCTGATGT 2513 GGATTICITIGGAAGGAATGATGCTAAAGCTGAAACTCCAGTACTTIGGCCACCTGATCA 2633 GGGGACGACAGAGGATGAGATGGCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGG 2453 TGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTG 9428 GAAGAGCTGACTCATTTGAAAAGACCCTGATGCTGGGAAAGATTGAGGGCAGGAGGAA

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TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION:
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LOCATION:
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LOCATION:
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; NAME/KEY:
; LOCATION:
US-08-621-100-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTGATACTGGGAAAGATTGAAGG 120
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2; Gaps
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                                                                                                             GENERAL INFORMATION:
APPLICANT: BLECK, GREGORY T.
APPLICANT: BLECK, GREGORY T.
APPLICANT: BLECK, GREGORY T.
TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL
STREET: 100 E. WISCONSIN AVE., SUITE 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.1%; Score 183.2; DB 1; Length 3
Best Local Similarity 81.1%; Pred. No. 4.9;
Matches 236; Conservative 0; Mismatches 53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/071,601
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/744,765
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sarac Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F. 3262-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                          STREE: ANDRUS, SCEALES, STARKE & SAWALL STREET: 100 E. WISCONSIN AVE., SUITE 1100 STATE: WI WANDREE COUNTRY: USA ZID.
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                                                                                                                                                                                                                                                                                                                                                            ZIP: 53202-4178
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDUWTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      TELEPHONE: (608) 255-2022
TELEPHONE: (608) 255-2022
TELEPAX: (608) 255-2182
TELEPAX: 26832 ANDSTRAK
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2044 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
FEATURE:
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US-08-071-601-3
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240 TCCATGGGGTTGCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGA 290
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Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
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US-08-487-826B-13/c
                                                                                                   RESULT 9
US-09-193-562D-1/c
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Sequence 1, Application US/09930377B

FREATE NO. 6677500

APPLICANT: Wheeler, Matthew B.
APPLICANT: Bleck, Gregory T.
APPLICANT: Bleck, Gregory T.
APPLICANT: Monaco-Selgal, Marcia
TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
FILE REFERENCE: 66-00

CURRENT PILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,474

PRIOR APPLICATION NUMBER: 60/225,474

PRIOR FILING DATE: 2000-08-15

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 4532
                                                                                                                             2502 GATCAGCCCTGGGATTTCTTTGGAAGGAATGATGCTAAAGCTGAAAACTCCAGTACTTTGG
                                                                                                                                                                                     GATCAGTCCTGGGTGGTCATTGAAGGACTGATGCTGAAGTTGAAGCTCCAATACTTTGG
                                                                                                                                                                                                                                                       61 ccaccicargegaagaacigacicargigaagacccigaracigggaagarigaagg
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                                                                     Gaps
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OTHER INFORMATION: Description of Artificial Sequence:alpha-LA/IGF-I
OTHER INFORMATION: gene construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2741 TTCATGGGGTCACAAAGAGTTGGACACGACTGAGCAACTGAACTGA 2791
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   Length 2044;
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                                                                  Indels
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5.1%; Score 183.2; DB 1;
Best Local Similarity 81.1%; Pred. No. 2.3;
Matches 236; Conservative 0; Mismatches 53;
   DB 1;
5.1%; Score 183.2; D
81.1%; Pred. No. 4.9;
tive 0; Mismatches
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ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 81.1
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Unknown
FEATURE:
COTER INFORMATION: sequence encoding Lu-ECAM-1 and Lu-ECAM-1 associated
COTER INFORMATION: protein from bovine endothelial cells
US-09-193-562D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3089 ATTITGGCCACCCGATGCTAAGAGCTGACTCATTGGAAAAGATCCTAATGCTGGGGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Sequence 1, Application US/09193562D
Patent No. 630987;
GENERAL INFORMATION:
APPLICANT: Pauli, Benedicht U.
TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
TITLE OF INVENTION: Nucleotide Chloride Channel-Adhesion Molecules
FILE REFERENCE: 18617.0052
CURRENT APPLICATION NUMBER: US/09/193,562D
CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US/60/065,922
PRIOR APPLICATION NUMBER: US/60/065,922
PRIOR FILING DATE: 1997-11-17
SEQ ID NO:
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4.6%; Score 164.3; DB 1;
Best Local Similarity 69.7%; Pred. No. 5.4;
Matches 327; Conservative 0; Mismatches 117;
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GENERAL INCURENTION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: DASSESSING DNA Methylation
FILE OF ENERRORE: 5013-1012
CURRENT APPLICATION NUMBER: US/10/204,708
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10033529.7
PRIOR APPLICATION NUMBER: DE 10033529.7
PRIOR APPLICATION NUMBER: DE 10033529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
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                                             GACAATGCTTTGAGCAATAATTTAGGATATTTTGAATGGTTCATGAGTATGCTTTTGTA
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                                                                                                                                                                                                                                                                                                                                      3473 TIGCIGCIATIAAACAIGAATIAAGICTIATIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10204708
Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 47.8
Matches 322; Conservative
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APPLICANT: Wellems, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: 12 Facelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELEPHONE: (619) 235-850
TELEPHONE: (619) 235-850
TELEFEX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1914 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
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50.5%; Pred. No. 4.2
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HYPOTHETICAL:
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US-08-487-826B-13
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Matches 350;
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Sequence 10, Application US/10204708

Fatent No. 6677731

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, MINT
ITILE OF INVENTION: Dy Assessing DNA Methylation
ITILE OF INVENTION: Dy Assessing DNA Methylation
ITILE OF INVENTION: DY ASSESSING DNA METHYLATION
FILE REFERENCE: 2010-05-06
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2001-06-06
PRIOR PALICATION NUMBER: DE 10019058.8
PRIOR PALICATION NUMBER: DE 10019058.8
PRIOR PALICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10013259.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PALLING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PALLING DATE: 2000-06-01
NUMBER OF SEQ 1D NOS: 98
FROM APPLICATION NUMBER: DE 10043826.1
                                           TAATATTTACTTATTCTATTTTACTTTAATTGCACTTATTTTTTTATTGTTTTTTTATAA 3028
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ORGANISM: Artificial Sequence
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US-10-204-708-10
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APPLICANT: OLEK, Alexander

APPLICANT: PIEBENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: DAY Assessing DNA Methylation

TITLE OF INVENTION: DAY Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

FEATURE OF SEQ ID NOS: 98
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                                                                                                                                                                                   4717 ITTITAATATTTTTTATGTTGTAGATATGTTAAACGAATTGAAGTTTTTTGAAATT
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Best Local Similarity 49.1%; Pred. No. 21;
Matches 342; Conservative 0; Mismatches 336;
AGTGTTTTACCAGTTCTTTCAGGCTACTTCTTTTGATT
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Patent No. 6677731
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR PAPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 80
LENGTH: 8961
TYPE: DNA
CAGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
LOCATION: (5096)
CHERR INFORMATION: n is a or g or c or t
US-10-204-708-80
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Pred. No. 14;
0; Mismatches
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Best Local Similarity 47.9%;
Matches 345; Conservative (
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US-10-204-708-80

Sequence 80, Application US/10204708

Patent No. 6677731

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIEFENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

FILE REFERENCE: 5013.1012

CURRENT APPLICATION WUMBER: US/10/204,708

CURRENT FILING DATE: 2003-05-06

PRIOR FILING DATE: 2001-04-06
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                               Length 6070;
                                                                         Indels
                               Query Match 2.8%; Score 100.2; DB 1;
Best Local Similarity 48.3%; Pred. No. 20;
Matches 361; Conservative 0; Mismatches 378;
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Sequence 20, Application US/10204708
Patent No. 6677731.
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rerearritreaagaarriaarritritraaaarriaargerriaagaaggraaagri
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CURRENT PAPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                      Sequence 29, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 333; Conserv
3505 T 3505
                                                           6041 T 6041
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GENERAL INFORMATION:

APPLICANT: DIEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Mut
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013-1012
CURRENT APPLICATION NUMBER: US/10/204,708
PRIOR PELING DATE: 2001-05-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PELING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR PILING DATE: 2000-05-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
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                                                                                                                                                            620 GAGTATATTTTTATAATTTAGATGGTATATTTAATATATTTAGGT----TGGGTTATATG 676
                                                                                  3369 GTTTATG-ATTTATGAATTATGATGCTTTTTTTTGGGCATAAAGGTCTATGGCATATTTT
2813 TTTATATTACTCAGAAAATAGTAATTTCATATGTATTCAAAATTATTTCATAATGTTGGT
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-20
                                                                                                                                                                                                                                               TIGIGGICTATATICTTAAAATTATAAATTGGCTTTAAAAAGTATT 3473
                                                                                                                                                                                                                                                                                                                         Granartriatrichtraggrianaartricharacaaragigri 722
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2.7%; Score 96.1003; DB 1; Lengt
Best Local Similarity 47.4%; Pred. No. 20;
Matches 317; Conservative 0; Mismatches 349; Indels
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Pred. No. 2e+02;
0; Mismatches 238; Indels
                                                                                                                         NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE DOCKET NUMBER: PF/5-30306/A/CGC1976
TELEPHONE: 919-541-8587
TELEPHONE: 919-541-8689
INFORMATION FOR EQ. ID NO: 595:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 94.7002;
 US/08/998,416
                   FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1408RP
                                                                                                                                                                                                                                                                                                                                                                                                                                          2.7%;
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Best Local Similarity 50.99
Matches 248; Conservative
 APPLICATION NUMBER:
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US-10-204-708-22
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                                                                       TTAATTTTGGGATTTTAACTATTTCTTCAATGACTTGTATTTCTAATATTTACTTATTCT
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                                  APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rebischule, Philipp
APPLICANT: Rebischule, Carine
TITLE OF INVENTION: GENONIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES. 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Length 658;
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TGAAGTTTATGATTTATGAATT 3386
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.4%;
Matches 253; Conservative
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TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REPERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10013173.6
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 2.
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Pred. No. 13;
0; Mismatches 306; Indels 5; G
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.6%;
Best Local Similarity 49.1%;
Matches 300; Conservative
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Sequence 57, Application US/10204708

Sequence 57, Application US/10204708

Patent No. 6677731

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DLEM, Alexander
APPLICANT: DLEM, ALEXANDOR, Christian
APPLICANT: DLEM, ALEXANDOR, Christian
APPLICANT: DLEM, ALEXANDOR, Christian
APPLICANT: DLEM, ALEXANDOR, Christian
APPLICANT: DLEM, ALEXANDOR, Christian
APPLICANTON DAGNORS: Of Diseases Associated with DNA Replication
TITLE OF INVENTION: DY ASSESSING DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98

LERGALD DNO 57

LERGALD: AND DATE: 2000-09-01

LERGALD: AND DATE: 2000-09-01

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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 93.8003; DB 1; Lengt
Pred. No. 23;
0; Mismatches 247; Indels
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Wed Aug

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2043 TITITGITITITITITITITITIATAATITITITAAATITATIGITATITAACGGAUTIA 2102
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2.6%; Score 92.4003; DB 1; Lengt
Best Local Similarity 50.3%; Pred. No. 25;
Matches 320; Conservative 0; Mismatches 296; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 69
LENGTH: 6040
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                                                      GENERAL INFORMATION:
APPLICANT: DIEK, Alexander
APPLICANT: DIEK, Alexander
APPLICANT: DIERENBROCK, Christian
APPLICANT: BERIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: DA ASSESSING DNA Methylation
TITLE OF INVENTION: DA ASSESSING DNA METHYLATION
FILING DATE: 2003-05-06
CURRENT APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 2
LENGRIFT: 10467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 10467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
2.6%; Score 92.7003; DB 1; Lengt
Best Local Similarity 49.1%; Pred. No. 15;
Matches 323; Conservative 0; Mismatches 328; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: chemically treated genomic DNA US-10-204-708-2
                              Sequence 2, Application US/10204708
Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1503
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Sequence 69, Application US/10204708

Sequence 69, Application US/10204708

Batent No. 6677731

GENERAL INFORMATION:

APPLICANT: DIEEKLANT CHRISTIAN

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: Dy Assessing DNA Methylation

TITLE OF INVENTION: Dy Assessing DNA Methylation

TITLE OF INVENTION: Dy Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER: OF SEQ ID NOS: 98 2982 1368 3095 3096 TITCAGGCTACTICITITGATITATITIGGICCIATCTITICICAAGTITIGAATIGGCTA 3155 1549 TTTATTATATTTGATTTTTTTTTTTTTTTTTATTAAGGTTTTATGTAATTATG--- 1605 3400 TTGGGCATAAAGGTCTATGGCATATTTTTGTGGTCTATATTCTTAAATTATAATT 3457 2103 TitririataaniaGrinniaaGGrinitaaGGarininintrinintrataaintain 2160 2806 TTAGTAGTTTATTACTCAGAAATTAGTAATTTCATATGTATTCAAAATTATTTCATAA TATITIAATITITGGGATTITTAACTATITCTTCAATGACTTGTATTTCTAATATTTACTTAT TITITIAAAAAGACTITAAAATTAATTA------TCTCTTTAGTGTTTTACCAGTTC CGTAACTCATTTATCTTTATTTTGTAAATTAGCTCTTTAAATTCATTATTCTTTGATA 2866 IGTIGGITAAGATAAAATITCAAATTGATTTTTATCTTTGATTT----TTCTCTACT 1249 GATHTHTHAGTTTTTTTTTTTTAATTTAATTGTTTATTAGAGTTGAGAFATTAAT 1309 TATTGTATATTGAATTATAGTATTTGTTTTTAAGTTGGTTTTTAAGATTTTTA <u>trraititaaatatatritrargiteitatragiregititritaaatgrattrittatt</u> TITITIGITITIAAAGITITIATTAAGIAAGIAATTAAAATATATAAAATATAAAGITITIT TCTATTTTACTTTAATTGCACTTATTTTTATTGATTTTTCTAATAAAATCCAGTCCTTGT DB 1; Length 6040; ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-69

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GCTTTAAAAAGTATTTGCTGCTATTAAACATGAATTAAGTCTTATTTGGACTATAGTGGA 3518
                                                                                                                                                                                                                                          GAAGTTTTGACAATGCTTTGAGCAATAATTTAGGATATTTTGAATGGTTCATGAGTATG 3344
                                                                                                                                                                                                                                                                                 9094 AİTİTİTİRİTİRĞGETİTİTİTATGAİTİTİTAATIGĞITİTİTİTİTİTİTİTİTİTİ 9153
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tritttagitttttagigagagittigiaaggatakggatgittttagitttttagit
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                                                                3165 TITATCITIATITITIGIAAATTAGCICTITAAATTCATTATICTTTGATAACAGCTICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29,768
R: 30472/114 IMMU
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: VA
COUNTRY: USA
Z1313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08232463
Patent No. 5670367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               899149
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OIEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: by Assessing DNA Methylation
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REPERBERCE: 5013-1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
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                                                                                                                                                                                                          1719 GAĞAĞAAİTAİTİTİTİTİĞĞGGAİATİİTTTAAĞİAĞITİTİAĞTIAĞIAİTİTİ 1778
           1606 --AATTTTATTTTTTTTTTTTAATTGTTATTTTTTTTTAGGGATAGAGATTG 1663
                                                                                                                       1664 Thgritharntragriaangarrrrrrrraararrrraarar----araggiga 1718
                                                                                                                                                                   3336 ATGAGTATGCTTTTGTACTTTGGCATTTATTGAAGTTTATGATTTATGAATTATGATGCTT 3395
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                                                                                3276 ATTCTTTGTGAAGTTTTGACAATGCTTTGAGCAATAATTTAGGATATTTTGAATGGTTC
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2.6%; Score 92.3004; DB 1; Length 9347;
Best Local Similarity 48.3%; Pred. No. 16;
Matches 366; Conservative 0; Mismatches 377; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; CTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-35
                                                                                                                                                                                                                                                                                                   rijairdretriaardariiriiriarararariiriidi 1814
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Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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LENGTH: 9347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7218;
                                                                                                                                                                          ch 2.6%; Score 91.9999; DB 1; Lengt a Similarity 9.5%; Pred. No. 21; 44; Conservative 249; Mismatches 169; Indels
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated
TITLE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: Dy Assessing DNA Methylation
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/BP01/03971
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PELING DATE: 2000-06-30
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PRIOR APPLICATION DATE: 2000-06-30
PRIOR APPLICATION DATE: 2000-09-01
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Patent No. 6677731
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                          Query Match
Best Local Similarity 9.5%;
Matches 44; Conservative 2
7218 base pairs
                TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: pTZGPL-F1s

US-08-232-463-14
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US-10-204-708-3
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Patent No. 667731
Patent No. 667731
APPLICANT: OLEK, Alexander
APPLICANT: DIEPERBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REPERBRCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003.05.06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                            3128 ATAGTIGITAATITAGAGATGGTATGATTATGTTTTTGATTTGGTTATTTTAAGTAA
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                                                                                        Length 10619;
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-3
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                                                                                      DB 1;
                                                                                                                                365;
                                                                                    Score 91.5004;
Pred. No. 15;
0; Mismatches
                                                                                  Query Match
Best Local Similarity 47.4%;
Matches 332; Conservative
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US-10-204-708-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR PRIOR TOWN NUMBER: DE 10032529.7
PRIOR PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
LENGTH: 11049
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; Sequence 62, Application US/10204708 ; Patent No. 6677731

US-10-204-708-62

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## SERBEACH INFURNATION:
## APPLICANT: DLEK, Alexander
## APPLICANT: DLEK, Alexander
## APPLICANT: DLEK, Alexander
## APPLICANT: DLEFENBROCK, Christian
## APPLICANT: BERLIN, Gart
## TITLE OF INVENTION: D'ASSESSING DNA Methylation
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## TITLE OF INVENTION: D'ASSESSING DNA METHYLATION NUMBER: US/10/204,708
## PRIOR FILING DATE: 2001-04-06
## PRIOR FILING DATE: 2000-04-07
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## PRIOR FILING DATE: 2000-04-07
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sequence 33, Application US/10204708

Sequence 33, Application US/10204708

Batent No. 6677731

GENERAL INFORMATION:

APPLICANT: OLER, Alexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

TITLE OF INVENTION: by Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

SEQ ID NOS: 98
        2806 TIAGTAGTITATATTACTCAGAAAATAGTAATTTCATATGTATTCAAAATTATTTCATAA 2865
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                                                                                      3367 AAGTITATGATTATGAATTATGATGCTTTTTTGGGCATAAAGGTCTATGGCATATTT
                                                                                                                                          7692 TATTTTTTTTTAAAATTTAAGAAAATTTTAAGGTCGTTTAATTTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 'OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                      7752 TTTTAAGAATTTAAGTTAAATTTTTAATTTTAGTTGAGAA 7792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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US-10-204-708-33
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                                                                                                                                             Sequence 21, Application US/10204708.

Sequence 21, Application US/10204708.

GENERAL INFORMATION:

APPLICANT: RIEPENBROCK, Christian
APPLICANT: RIEPENBROCK, Christian
APPLICANT: RIEPENBROCK, Christian
APPLICANT: REPERING Wint
TITLE OF INVENTION: by Assessing DNA Methylation
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: $0.13.10.2
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 98
LENGTH: 11049
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6203 TITTAAGGITGIAAATITIGAAAAGAIAAAGAAAITATITAAGG 6247
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2.4%; Score 86.9003; DB 1; Lengt
Best Local Similarity 48.8%; Pred. No. 16;
Matches 313; Conservative 0; Mismatches 321; Indels
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ORGANISM: Artificial Sequence
FEATURE:
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generic 14, Application US/10204708

Pactent No. 6677731

GENERAL INFORMATION:

APPLICANT: OLEX. Alexander

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: DASSIBLE SO13.1012

CURRENT FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: PCT/EP01/03971

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR PILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

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PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                            442 AICTITITATAAGAATTATTAATAAATTATTAACTTTAATTICTTATTATTAATTT
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                                                                            DB 1; Length 636;
                                                                                                                                      9
                                                                               Score 85.4004; DB 1; Lengtl
Pred. No. 2.7e+02;
0; Mismatches 311; Indels
                                                                                  Query Match
Best Local Similarity 48.2%;
Matches 295; Conservative
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; ORGANISM: PAG1692RP
US-08-998-416-1137
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US-10-204-708-14
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APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mondland, Jurgen
APPLICANT: Mondland, Jurgen
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
STREFF
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CORRESPONDENCE ADDRESS:
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZITE: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: MAGIGS J. TIMOCHY
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-998-416-1137
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Matches 262;
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Patent No. 667731
GENERAL INFORMATION
APPLICANT: OLEK, Alexander
APPLICANT: DIEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
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                                                                                                                                                                                                                              GTTAAGATAATAAGATTTTCAAATTGATTTTTATCTTTGATTTTTTCTCTACTTATTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6113
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                                                                                                                                                  DB 1;
                                                                                                         ; OTHER INFORMATION: chemically treated genomic DNA US-10-204-708-14
                                                                                                                                                Score 84.5003; DB 1
Pred. No. 31;
0; Mismatches 300;
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 14
LENGTH: 6113
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                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                  2.4%;
                                                                                                                                                             Best Local Similarity 48.9
Matches 303; Conservative
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US-10-204-708-31
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Patent No. 5389526
GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Williams, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: chemically treated genomic DNA US-10-204-708-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83.8002;
Pred. No. 24;
0; Mismatches
| PRIOR APPLICATION NUMBER: PCT/EPO1/059/1
| PRIOR FILING DATE: 2001-04-06
| PRIOR APPLICATION NUMBER: DE 10019058.8
| PRIOR FILING DATE: 2000-04-06
| PRIOR PILING DATE: 2000-04-07
| PRIOR FILING DATE: 2000-04-07
| PRIOR FILING DATE: 2000-06-30
| PRIOR FILING DATE: 2000-06-30
| PRIOR FILING DATE: 2000-06-30
| PRIOR FILING DATE: 2000-06-01
| NUMBER OF SEQ ID NOS: 98
| SEQ ID NO 31
| LENGTH: 8093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.3%;
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WESULY 35
UG-10-204-708-86

1 Sequence 86, Application US/10204708

2 Sequence 86, Application US/10204708

2 Sequence 86, Application US/10204708

3 Sequence 86, Application US/10204708

3 Patent No. 667731

3 APPLICANT: PIEPENBROCK, Christian

4 APPLICANT: DISPERBROCK, Christian

5 APPLICANT: DISPERBROCK, Christian

5 APPLICANT: DISPERBROCK, Christian

7 TILE OF INVENTION: DASSESSING DNA MEthylation

7 TILE OF INVENTION: DASSESSING DNA MEthylation

7 TILE OF INVENTION: DASSESSING DNA METHYLATION

7 TILE OF INVENTION: DASSESSING DNA METHYLATION

7 TILE OF INVENTION: DASSESSING DNA METHYLATION

7 TILE OF INVENTION: DASSESSING DNA METHYLATION

7 TILE OF INVENTION NUMBER: DE 10019058.8

7 PRIOR PILING DATE: 2000-04-06

7 PRIOR PILING DATE: 2000-04-07

7 PRIOR PILING DATE: 2000-04-07

7 PRIOR PILING DATE: 2000-04-07

7 PRIOR PILING DATE: 2000-06-01

7 PRIOR PILING DATE: 2000-06-01

7 PRIOR PILING DATE: 2000-09-01

7 PRIOR PILING DATE: 2000-09-01

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2.3%; Score 82.4003; DB 1; Length 11050;
Best Local Similarity 46.5%; Pred. No. 18;
Matches 266; Conservative 0; Mismatches 306; Indels 0; G
                                                                                     OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris STREET: One Liberty Place 46th Floor CITY: Philadelphia STRATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 82.6003; DB 1; Length 5852;
Pred. No. 33;
0; Mismatches 369; Indels 22;
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106 FILLING DATE: 19920625 PRIOR APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: PCT/AU90/00530 FILLING DATE: 02-NOV-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTURNAL FAGATA.

NAME: Fechey, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
RELEPHONE: 215-568-3100
FELEPHONE: 215-568-3100
FELEPHONE: 215-568-3100
FELEPHONE: 215-568-3100
FELEPHONE: 215-568-3100
FELEPHONE: 215-568-3100
FELEPHONE: 215-258-3100
FELEPHONE: 215-258-3100
FELEPHONE: 215-258-3100
FELEPHONE: 215-258-3100
                                                                                                                                                                                                                   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 46.1%;
Matches 335; Conservative
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STRANDEDNESS: single
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ANTI-SENSE: NO
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NAME/KEY:
LOCATION:
FEATURE:
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, LOCATION:
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WS-10-204-708-45

WS-10-204-708-45

Sequence 45, Application US/10204708

Patent No. 6677301

APPLICANT: OLEK, Alexander

APPLICANT: PIEBENBROCK, Christian

APPLICANT: PIEBENBROCK, Christian

APPLICANT: PIEBENBROCK, Christian

APPLICANT: PIEBENBROCK, Christian

APPLICANT: PIERENBROCK, Christian

APPLICANT: PIENENBROCK, Christian

APPLICANT: PREBENBROCK, Christian

APPLICANT: PREBENBROCK, Christian

APPLICANT: PREBENBROCK, Christian

APPLICANT: PREBENBROCK, Christian

APPLICANT: PREBENBROCK, Christian

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10013529.7

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

SEQ ID NOS: 98
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7294 TitaAGGAITITAITITGITAATCGITAGGIGITITATGAITITGAGITAGTITCGIAATT
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2.3%; Score 81.3004;
Best Local Similarity 46.7%; Pred. No. 19;
Matches 316; Conservative 0; Mismatches ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FACENCE AND STATEMENT OF A PAPLICANT: OLEK, A SEXENDER APPLICANT: PIEPENBROCK, Christian APPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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RESULT 38

US-08-213-419B-3/C
US-08-213-419B-3/C
Sequence 3, Application US/08213419B
Patent No. 6333406
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Fatent No. 633406
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Fatent Fatent No. 64000
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Fatent Patent No. 64000
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5919 GTTGGAATTATAGGTATGAATT------ATCGCGTTTGGTTTTAAGGTAATTTTATT 5969
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                                                                             3337 TGAGTATGCTTTTGTACTTGGCATTTATTGAAGTTTATGATTTATGAATTATGATGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3457 TGGCTTTAAAAAGTATTT 3474
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OGRANISM: Plasmodium falciparum
FEATURE:
NAME/KEY: CDS
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NAME/KEY: CDS
LOCATION: (2598) ..(3404)
NAME/KEY: CDS
LOCATION: (3580) ..(3720)
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LOCATION: (3850)..(5835)
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OTHER INFORMATION: n is a or g or c or t
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NAME/KEY: unsure
LOCATION: (18130, 18143, 18151, 18188, 18498, 18549, 18936, 18946, 19165)
OTHER INFORMATION: n is a or g or c or t
                                                FEATURE:
NAME/KEY: unsure
LOCATION: (76, 178..179, 273, 586, 648, 651, 920, 1014, 1173, 1197, 1228)
OTHER INFORMATION: n is a or g or c or t
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LOCATION: (10005, 10075, 10150, 10159, 10165, 10356, 11123, 11166, 11360)
OTHER INFORMATION: n is a or g or c or t
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LOCATION: (13846, 14168, 16566, 17006, 17217, 17650, 17653, 17656, 17898)
OTHER INFORMATION: n is a or g or c or t
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NAME/KEY: unsure
LOCATION: (8059, 8075, 8632, 8636, 9700, 9717, 9815, 9818, 9867, 9879)
OTHER INFORMATION: n is a or g or c or t
                                                                                                                                                                                                                                                                     LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
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OTHER INFORMATION: n is a or g or c or t
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LOCATION: (4787, 4825, 4829, 4838, 4855, 5462, 5494, 5496, 5500, 5674)
OTHER INFORMATION: n is a or g or c or t
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OTHER INFORMATION: n is a or g or c or t
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LOCATION: (6244, 6288, 6776, 6873, 6891, 6980, 7028, 7656, 7876,
OTHER INFORMATION: n is a or g or c or t
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THER INFORMATION: n is a or g or c or t
        OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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NAME/KEY: unsure
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                                                                                                                                     Length 8537;
                                                                                                                                                                         7;
                                                                    ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-41
                                                                                                                                     Score 80.1003; DB 1; Lengt
Pred. No. 25;
0; Mismatches 369; Indels
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                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                     Query Match 2.2%;
Best Local Similarity 47.1%;
Matches 335; Conservative
SEQ ID NO 41
LENGTH: 8537
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Sequence 116, Application US/08998416; Patent No. 6239264; GENERAL INFORMATION: APPLICANT: Philippsen, Peter; APPLICANT: Pohlmann, Rainer APPLICANT: Steiner, Sabine APPLICANT: Wendland, Jurgen; APPLICANT: Knechtle, Philipp APPLICANT: Rebischung, Corinne

RESULT 41 US-08-998-416-186

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TAITICTAATATITAACTTATTTTAATTTAATTGCACTTATTTATTGATTTTT 3022
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Pred. No. 3.3e+02;
0; Mismatches 278; Indels 7;
GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
AND USES THEREOF
1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECISTRATION NUMBER: 36,241
REPERENGE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMINICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ 1D NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  SUFTWARE: Patentin Release #1.0, Version #1.30 APPLICATION DATA:
FILING DATE: 24-DEC-1997
CIASSIPICATION: 435
                                                                                    SEE: No. 6239264artis Corporation

1: 3054 Cornwallis Road

Research Triangle Park

No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Makigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-:
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 49.6
Matches 280; Conservative
  TITLE OF INVENTION: GE
TITLE OF INVENTION: AN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                    ADDRESSEE:
STREET: 305
CITY: Resea
STATE: No.
COUNTRY: US
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ORGANISM:
US-08-998-416-186
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	Oy 3326 IGAAIGGITGIGAGIAIGCTITIGIACTITAITAIGAGITTAIGAAIT3385  Db 6696 GATTAITITAAATGITAITITIAITITICGIAIGAGICGIAITAIGAITITITICAAI 6755  Qy 3386 IAIGAIGCTITITITIGGCCAIAAAGICTAIGGCAIAITITITICIAA 6755  Db 6756 IITIAITITICIIGAITITITITITICGIAGATAATITITITITIAIAATAITITITICIIA 3445  Qy 3446 AAAITAIAAATITICGITGITITITITITICGIAGATAATITITITIAIAATAITITITITICIIC 6815  Db 6816 AAAITAIGAGGGGAGGTTAAAAGITTITITITITITITIT	## Sequence 26, Application US/10204708  ## Patent No. 667731  ## Patent No. 667731  ## PAPLICANT: OLEK, Alexander  ## APPLICANT: OLEK, Alexander  ## APPLICANT: OLEK, Alexander  ## APPLICANT: OLEK, Alexander  ## APPLICANT: BERLIN, Kurt  ## APPLICANT: BERLIN, Kurt  ## APPLICANT: BERLIN, Kurt  ## APPLICANT: BERLIN, Kurt  ## APPLICANT: BERLIN, Kurt  ## APPLICANT: BERLIN, Kurt  ## APPLICANT: BERLIN, Kurt  ## APPLICANT: BERLIN, Kurt  ## APPLICANT: 2003-05-06  ## PRIOR APPLICANT: 2003-04-06  ## PRIOR APPLICANT: 2003-04-06  ## PRIOR APPLICANT: WUMBER: BE 10019173.8  ## PRIOR APPLICANT: 2000-04-06  ## PRIOR APPLICANT: 2000-04-07  ## PRIOR APPLICANT: 2000-04-06  ## PRIOR APPLICANT: 2000-04-07  ## PRIOR APPLICANT: 2000-04-07  ## PRIOR APPLICANT: 2000-04-07	omic DNA (Homo sapi	QUETYMETCH 2.18; Pred, No. 33;  Matches 255; Conservative 0; Mismatches 275; Indels 3; Gaps 1;  QY 2868 TEGETRAGATATAGATTICAARTGATTTTATTTTCTCTACTTATT 2927  Db 6052 TEGETRAGATTTAATAGATTATTCTCTAATATTACTTTATTTCTCTATTTA 6111  QY 2928 AATTTGGGATTTTAATTCTCTCAATGATTTTATTTGTATTACTTATTTA 6111  QY 2928 TAGTTGTTTTTTTTTTTTTTTTTAATTGTAATTTTATTTGTAATATTACTTATTTA 6111  QY 2988 TTACTTTAATTGTATTTAATTGAATTTTATTATTATTATTATTA
	RESULT 42 US-10-204-708-71 i Sequence 71, Application US/10204708 i Patent No. 667731 i GENERAL INFORMATION: i APPLICANT: PIEPRIROCK, Christian i APPLICANT: PIEPRIROCK, Christian i TITLE OF INVENTION: DASSESSING DNA Methylation i TITLE OF INVENTION: VASSESSING DNA Methylation i TITLE OF INVENTION: VASSESSING DNA Methylation i CURRENT APPLICATION NUMBER: US/10/204,708 i CURRENT FILING DATE: 2003-05-06 i PRIOR APPLICATION NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/CA110N NUMBER: PT/EPPL/EPPL/CA110N NUMBER: PT/EPPL/EPPL/CA110N NUMBER: PT/EPPL/EPPL/CA110N NUMBER: PT/EPPL/EPPL/CA110N NUMBER: PT/EPPL/EPPL/CA110N NUMBER: PT/EPPL/EPPL/EPPL/CA110N NUMBER: PT/EPPL/EPPL/EPPL/EPPL/EPPL/EPPL/EPPL/EP	PRIOR FILING DATE: 2001-04-06  PRIOR PILING DATE: 2001-04-06  PRIOR APPLICATION NUMBER: DE 10019058.8  PRIOR PILING DATE: 2000-04-06  PRIOR APPLICATION NUMBER: DE 10019173.8  PRIOR FILING DATE: 2000-04-07  PRIOR FILING DATE: 2000-06-30  PRIOR FILING DATE: 2000-06-30  PRIOR FILING DATE: 2000-09-01  NUMBER OF SEQ ID NOS: 98  SEQ ID NO 71  LENGTH: 8607  TYPE: DNA  TYPE: DNA  COGANISM: Artificial Sequence  FEATURE:  FEATURE:  COTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  US-10-204-708-71	Gaps GTATT GAATT CTTTG GATGG	

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Sequence 39, Application US/10204708

Patent No. 6677731

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: DIEK, Alexander

APPLICANT: DIERENBROCK, Christian

APPLICANT: DIERENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: Dy Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: DS/10/204,708

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: PCT/FP01/03971

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 100132529.7

PRIOR APPLICATION NUMBER: DE 10012529.7
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                                                         Score 78.3004; DB 1; Length 837;
Pred. No. 2.5e+02;
0; Mismatches 332; Indels 7;
                                                                2.2%;
                                                                                      Best Local Similarity 47.8
Matches 311; Conservative
PAG1241RP
  ) ORGANISM:
US-08-998-416-288
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                                                                                                                                                                                                                                                                                                 GITITIGACAATGCITIGAGCAATAATITAGGATATITITIGAATGGITCATGAGTATGCTT 3347
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  TCTTTTGATTTATTTGGTCCTATCTTTTCTCAAGTTTGAATTGGCTACGTAACTCATTT 3167
                                                                                                           tatititatititagitartragritricgigiratritridaalargriaggiatritra 6351
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APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rechtle, Philipp
APPLICANT: Rebisedung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
TOWNER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 288, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: modleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Philippsen, Peter
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                                                                                                                                     TYPE: DNA

'ORGANISM: Artificial Sequence

'FEATURE:

'OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-204-708-39
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 39
LENGTH: 19513
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Search completed: August 24, 2004, 13:31:55 Job time : 614 secs

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August 24, 2004, 13:34:23; Search time 279 Seconds (without alignments) 3.941 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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3572
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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096-60-SD	000-00-00-00-00-00-00-00-00-00-00-00-00	096-60-SN 096-60-SN	ALIGNMENTS	0664775 6A1	ar ar Cor Making Reco	US/10/664,775 09-17 anish Application	20 5 60/416,566 37 3.1	ney cell line	.0%; Score 3572; .0%; Pred. No. 1. 0; Mismatches	GTCAGGAAGGGGGCAGTGAGGAGAGGTACCTACCCTCGTCCAAGGTAAGGAG 	TGCGCTTTGCTGGAGCAGCCGTAAAGAGATACCCCACGCCCAAGGTAAGAGAAAC 	TGTTGTGAGAGGCATCAGAGGG                  TGTTGTGAGAGGCATCAGAGGG	aatcacactaggacc                  hatcacactaggacc	acccaagatgggca6                   acccaagatgggcag	AATGCAAACCACTTC
P 10	1202	-352-14979 -352-149 -352-7209 -352-11719	့		Recombinant Protei	on PA 2002 013			); DB 1; Length 1.4e-13; hes 0; Indels	TACCCTCGTCCAAG 	ACCCCACGCCCAAGO	arggcagacatact 	ACAGCCTTGTCTAZ 	SGTCATGGTGGAGAC 	CAGTATTCTTGCCT
equence equence equence	Sequence 11744, A Sequence 2913, Ap Sequence 2913, Ap Sequence 2913, Ap Sequence 2913, Ap Sequence 32. App Sequence 32. App	Sequence 14979, A Sequence 149, App Sequence 7209, Ap			su:	84			jth 3572; sls 0; Gaps	CCAAGGTAAGGAGCAGTAGC 60	CCGTAAAGAGATACCCCACGCCCAAGGTAAGAAACCCAAG 120	TAAGATGGTAGTGTTGTGAGGGCATCAGAGGGCAGACATACTGAAACCATACACGCA 180 	GAAAACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAG 240 	CATGCCCGTGGGGCAACCCAAGATGGGCAGGTCATGGTGGAGAGATGTGACAGAATGTG 300 	GTCCACTGGAGAAGGGAATGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAAC 360

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                     2581 GACTCACTGGAAAAGACCCTGATGCTGGGAGGGATTGGGGCGCAGGAGGAGGAGGACGA
                                                                                    CAGAGGATGAGATGGCTGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACTC
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5.10-109-551-1 Sequence 1, Application US/10109551 Publication No. US20020194635A1

RESULT 2 US-10-109

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3273 GAACITCCTGATGTTCAAGGTGGTTTTAGAAAAGGCAGAGGAACCAGAGATCAAATTGCC 33332
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                APPLICANT: DUNNE, PATRICK W.
APPLICANT: DUNNE, PATRICK W.
APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSCENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: PROUGEFORM ENCEPHALOPATHIES
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
CURRENT TAMK: 2010
CURRENT APPLICATION NUMBER: US/10/109, 551
CURRENT FILING DATE: 2002-03-28
PRIOR FILING DATE: 2002-03-18
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 78056
TYPE: DNA
ORGANISM: Bos taurus
GENERAL INFORMATION:
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                  ATGTCAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTATGCAGAG-ACATCATGAG
                                                                                                                           13065 AIGTCAAGGCIGIATATIGICACICCIGCITATITTAATITTATATGCAGAGIACATCATGAG
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1765 GAAAGGGATGGGAATACCAGACCACCTGACCTGACTTGAAAAATTTGTATGCAGGTCA
                                                     GGAAGCAACAGTTAGAACTGGACATGGAACAACAGACTGGTTCCAAGTAGGAAAAGGAGT
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Sequence 2, Application US/09884586A

Publication No. US20030046716A1

GENERAL INFORMATION:

APPLICANT: Echelard, Yann

APPLICANT: Eichner, Wolfram

APPLICANT: Sommermeyer, Klaus

TITLE OF INVENTION: GROWTH FACTOR

TITLE OF INVENTION: 10275-120001

CURRENT FILING DATE: 2001-06-19

FRIOR PEPLICATION NUMBER: 05/212,406

PRIOR PELING DATE: 2000-06-19

PRIOR FILING DATE: 2000-06-19

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FASLESQ for Windows Version 4.0

LENGTH: 23651
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27.1%; Score 966.804; DB 1; Lengt
Best Local Similarity 81.9%; Pred. No. 0.0089;
Matches 1181; Conservative 0; Mismatches 237; Indels
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(23651)
OTHER INFORMATION: n = A,T,C or G
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	CTTGCCACACAAAGCTCCATCTAGTCAAGGCT	RESULT 5 US-09-884-586A-2   Sequence 2, Application US/09884586A   Sequence 2, Application US/09884586A   Sequence 2, Application No. US20030046716A1   GENERAL INFORMATION:   APPLICANT: Bechelard, Yann   APPLICANT: Bichner, Holfram   APPLICANT: Eichner, Holfram   TITLE OF INVENTION: TRANSCRNICALLY PRODUCED PLATELET DERIVED   TITLE OF INVENTION: TRANSCRNICALLY PRODUCED PLATELET DERIVED   TITLE OF INVENTION: TRANSCRNICALLY PRODUCED PLATELET DERIVED   TITLE OF INVENTION: TRANSCRNICALLY PRODUCED PLATELET DERIVED   TITLE OF INVENTION: TRANSCRNICALLY PRODUCED PLATELET DERIVED   TITLE OF INVENTION: GROWTH FACTOR   FILE REPERENCE: 10275-12001   CURRENT APPLICATION NUMBER: 60/212,406   PRIOR PRILING DATE: 2000-06-19   NUMBER OF SEQ ID NOS: 8   NUMBER OF SEQ ID NOS: 8   SOFTWARE: FastSEQ for Windows Version 4.0
OY 2833 GTAAITTCATAIGTAITCAAAATTAITTCATAAIGTIGGTIAAGATAATAAGATTTCAA 2892  DD 12108 GTGTCATGATTAITAGGCACCTITAATTTGCATTTTCTGAAGATTGAT 12058  QY 2893 ATTGAITTTAICTTGATTTTTCCACTATTTAATTTGGATTTTAACTATTTCT 2952  DD 12057 GAIGTAGAGTATTTTACTTTAATTTAATTTAACTTTTTTAATTTCTT 2992  QY 2953 CAAIGACTGAATTTCAATATTTACTAATTTAAATTGCACTTTTTTA 3012	RESULT 4  UG-109-551-1/c  UG-10-109-551-1/c  Sequence 1. Application US/10109551  Sequence 1. Application No. US2020194633A1  Sequence 1. Application No. US2020194633A1  September 1. PRORMATION.  APPLICANT: DINNENDIAN, PATRICK W.  APPLICANT: DINNENDIAN, TRANSCRUCK W.  TITLE OF INVENTION: TRANSCRUCK W.  TITLE OF INVENTION: TRANSCRUCK W.  FILE REFERENCE: TRANSCRUCK W.  FURRENT FILE OF DATE: 2020-30-28  CURRENT APPLICATION NUMBER: 06/260,549  PRIOR APPLICATION NUMBER: 06/260,549  PRIOR PLING DATE: 2010-30-30  NUMBER OF SEQ ID NOS: 10  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1  SOFTWARE: Patentin Ver. 2.1	OY 1753 GTGGAAAATTCTGAAAGGGATGGGAATACCAGACCTGACCTGACTCTTGAAAAATTT 1812  Db 1480 GTGGGAAATTCTTAAAGAGTGGGAATACCAGACCTGACCTGCTTCTGAAAATTT 1812  OY 1813 GTATCCAGGTCAGGAACAACAGTGGAACACACACACACTGCTTCCAAGT 1872  Db 1420 GTATGCAGTTAGGAACAACAGTTAGAACTGCACACACACA

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STATEMENT INFORMATION:

APPLICANT: INFORMATION:

APPLICANT: ELERTSEN, KENNETH J.

APPLICANT: PISTER GENSKOW, MARTHA

APPLICANT: CHILDS, LYNETTE

ATION AND USE OF MOLECULAR MARKERS INDICATING

TITLE OF INVENTION: CELLULAR REPROGRAMMING

TITLE OF INVENTION NUMBER: US/09/876,143

CURRENT FILING DATE: 2001-06-06

PRIOR PELICATION NUMBER: 60/209,874

PRIOR FILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 1744

SOFTWARE: PARCENT NESSON 3.0

LENGTH 908
                                                             CGACAGAGGATGAGATGGCTGGGATGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAA 2697
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11.6%; Score 413.4; E
Best Local Similarity 85.6%; Pred. No. 18;
Matches 501; Conservative 0; Mismatches
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US-09-876-143-1493/c
Sequence 1493, Application US/09876143
; Publication No. US20040081958A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: n is a, c, g, or US-09-876-143-1493
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NAME/KEY: misc_feature
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ORGANISM: Bovine
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                                                                                                                                                                                                                                                                                                    1744 CAATAAACTGTGGAAAATTCTGAAAGGGATGGGAATACCAGACCACGTGACCTGACTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3030 GICAAACCIAIGGITITIICCAGIAGICAIAIAIGGAIGI--GAGITGAACIAIAAAGAAA
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                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                       Length 23651;
                                                                                                                                                                                                                Score 557.9; DB 1; Length
Pred. No. 0.52;
0; Mismatches 191; Indels
                                                                                                                   ; OTHER INFORMATION: n = A,T,C or G
US-09-884-586A-2
                                                                                                                                                                                                                Query Match
Best Local Similarity 78.4%;
Matches 820; Conservative
                  LENGTH: 23651
TYPE: DNA
ORGANISM: Homo sapiens
                                                                               FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(23651)
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SEQ ID NO 2
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; Sequence 844, Application US/09960352; Patent No. US2020213713941; GENERAL INFORMATION: APPLICANT: Warren, Wesley C.
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Matches 390; Conservative
                                                                                                                                                         2791 AACTGTA 2797
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US-09-960-352-13832
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Sequence 11, Application US/10299497

Publication No. US20030143601A1

Sequence 11, Application No. US20030143601A1

GENERAL INFORMATION:

APPLICANT: Hansen, Thomas R.

APPLICANT: Hansen, Thomas R.

APPLICANT: Pru, James R.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

TITLE OF INVENTION: DETECTION OF BOVINE PREGNANCY WHICH UTILIZE MEMBERS OF THE

TITLE OF INVENTION: 1-8 FAMILY OF INTERPERON INDUCIBLE GENES

TITLE OF INVENTION: 1-8 FAMILY OF INTERPERON INDUCIBLE GENES

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 60/337,090

PRIOR FILING DATE: 2002-11-16

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                     GAGGAGAGTGAAAAAGTTTGGCTTAAAGCTCAACATTCAGAAAACGAAGATCATGGCATCT 2139
                                                                                                                                                            2140 GGICCCATCACTICAIGGGAAATAGAIGGGGAAACAGIGGAAACAGIGTGAGACTITATI 2199
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                                                                                             233 GTGGAGAGTGAAAAAGTTGGCTTAAAGCTCAACATTCAGAAAACTAAGATCATGGCATCT 174
                                                                                                                                                                                                    173 GGTCCCATCACTTGATCGCNAATAAATGGG------AATTGTGGCTGNCTTTATT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 GACATTACTTTGTCGGTAAAGGTCCATATAGTCAAAGCTATGGTTTTTCCAGTAGTCATG 416
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                                                                                                                                                                                                                                                2200 TITIGGGGGCTCCAAAATCACTGCAGATGGTGACTGCAGCCATG 2244
                                                                                                                                                                                                                                                                                    TTT--GGGGGCTCCAAAATCACTGTAGATGGTGACTGCAGCCATG 82
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CRGANISM: Bos tarus
US-10-299-497-11
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LENGTH: 967
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Sequence 13812, Application US/09960352

Patent No. US2002013713941

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Warren, Wesley C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

TITLE OF INVENTION: WIGCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION

FILLE REPERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT PILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

LENGTH: 419
                                                                                                             2731 CCTGCGGCGATTCATGGGGTCACAAAAGAGTTGGACACGACTGAGCAACTGAACTG 2790
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777 agridendekagreckeagggregekakagkartekekagekergakergakerg 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: BOS taurus
; OTHER INFORMATION: Clone ID: 59-LIB3058-043-Q1-K1-G12
US-09-960-352-13832
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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-924
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                               1892 GGCTGTATATTGTCACCCGGCTTGTTTAACTTCTATGCAGAG-ACATCATGAGAAACGCT
                                                                                                                                                                                                                                                                                                                                                   1 GGCAGTATATTGTCACCCTGCTTATTTAACTTCTATGCAGAGTACATCATGAGAAACGCT
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; ORGANISM: Bos taurus
; OTHER INFERMATION: Clone ID: 22-LIB3058-039-Q1-K1-F5
US-09-960-352-5090
                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                           23;
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                                                                                                                                          ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 26-LIB34-086-Q1-E1-
US-09-960-352-6161
                                                                                                                                                                                                                                        Score 363.2; D
Pred. No. 47;
0; Mismatches
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Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local Similarity 93.4%;
Matches 410; Conservative
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Best Local Similarity 94.3'
Matches 384; Conservative
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US-09-960-352-5090
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LENGTH: 432
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usl06647

"AFFLICANT: Tao, Nengbing

"APPLICANT: Matti John C.

APPLICANT: Matti John C.

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: NUSCLE AND FAT PREPOSITION

FILE REFERENCE: 16511.006/33-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT PILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 844

LENGTH: 451
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Patent No. US2002013713941
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nendping
APPLICANT: Tao, Nendping
APPLICANT: Mathialagan, Magapan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC ACID AND FAIL BEFERENCE: 16511.006/37-21(10298)
FILE REFERENCE: 16511.006/37-21(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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Clone ID: 04-LIB34-001-Q1-E1-A7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 364.7;
Pred. No. 45;
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89.9%;
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Best Local Similarity 89.99
Matches 401; Conservative
                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Bos, taurus
                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
LOCATION: (422)
OTHER INFORMATION: U
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Db 290 TGAAATTAAAAGCACTTACTTGGAAGGAAAGTTATGACCAACTATT 349  Qy 2301 GAAAACAGAGACATTACTTGCCAACAAAGCCTATTGACCAACTATTTC 2360  Bb 350 AAATACCAGAGACATTGCATTGCAACAAAGCCCATCTAGTCAAGGCTATTGTTTTC 409  Qy 2361 AGTGGTCATGTATGATTGCATTGTCAACAAGGCTATGGTTTTTTC 409  Qy 2361 AGTGGTCATGTATGAAAAGAA 432  RESULT 13  US-09-960-352-5347  ; Sequence 5347, Application US/09960352 ; Patent No. US20020137139A1 ; GENERAL INFORMATION: APPLICANT: Tao, Nongbing. APPLICANT: Tao, Nongbing. APPLICANT: Mathalagan, Nagapan TITLE OF INVENTION: MUCCLE AND FAT DEPOSITION TITLE OF INVENTION: MUCCLE AND FAT DEPOSITION TITLE OF INVENTION: MUCCLE AND FAT DEPOSITION TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION CURRENT APPLICANT: SEQ ID NOS: 15112  SEQ ID NO 5347  LENGTH: 433	TYPE:NR	; Sequence 7158, Application US/09960352
QY         1649 AACATCCTCTGTATCATGGAAAAAGCAAGAGAGTTCCAGAAAAACATCTATTCTGCTTT 1708           Db         86 AACATCCGCTGAATCATGGAAAAGCAAGAGAGTTCCAGAAAACATCTATTTCTGCTTT 145           QY         1709 ATTGACTATGCCAAAAGCATGAGGGTCACAATAACTGTGGAAAATTCTGAAA 1768           Db         146 ATTGACTATGCCAAGAGCCTTGACTGTGGGATCACAATAACTGTGGAAAATTCTGAAA 205           QY         1769 GGAATGGGAATACCAGACCACCTGACTGACTCACTCTGAGAAATTCTGAAGAAA 1828           Db         206 AAGATGGGAATACCAGACCACCTGACTGCTCTTGAGAAATTCTGAAGGACAGGAA 265           QY         1829 GCAACAGTAGAACAGACCACTGACTGCTCTTGAGAAATCTGAAGGAATAGTT 1888           P         181	PRETENT NO. US20020131391. APPLICANT: Waster, Wesley C. APPLICANT: Waster, Wesley C. APPLICANT: Waster, Dan C. APPLICANT: Waster, Dan C. APPLICANT: Waster, Dan C. APPLICANT: Waster, Dan C. APPLICANT: Waster, Dan C. APPLICANT: Waster, Dan C. APPLICANT: Waster, Dan C. APPLICANT: Waster, Dan C. CURRENCE: 16511.006.37-211.029950.352 TITLE OF INVENTION: WUCKER 12/09/960.352 CURRENT FILLOW DATE: 2001-09-24 WUNDER OF SEQ IN NOS: 15112 CURRENT FILLOW DATE: 2001-09-24 WUNDER OF SEQ IN NOS: 15112 CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CURRENT FILLOW DATE: 2001-09-24  CUR	

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US-09-960-352-8154

Sequence 8154, Application US/09960352

Sequence 8154, Application US/09960352

Sequence 8154, Application US/09960352

Sequence 8154, Application US/09960352

Sequence 8154, Application US/09960352

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC AND PAT DEPOSITION

TITLE OF INVENTION: NUCLEIC AND PAT DEPOSITION

TITLE OF INVENTION: NUCLEIC AND PAT DEPOSITION

TITLE OF INVENTION: NUMBER: US/09/960,352

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

SEQ ID NO 8154
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                                                         Length 31412;
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                                                                                                      208; Indels
                                                         DB 1;
                                                       9,6%; Score 344.199;
69.7%; Pred. No. 3.1;
iive 0; Mismatches
                                                       Query Match
Best Local Similarity 69.77
Matches 492; Conservative
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PALENT NO. US20020137139A1

GENERAL INFORMATION: Wasten, Wealey C.
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(1029)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NOS: 15112
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; Sequence 3, Application US/10109551
; Publication No. US20020194635A1
; GENERAL INFORMATION:
; APPLICANT: DUNNE, PATRICK W.
; APPLICANT: DUNNE, PATRICK W.
; APPLICANT: PIEDRAHITA, JORGE
; TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
; FILE REFERENCE: TAMK: 2070
; CURRENT APPLICATION NUMBER: US/10/109,551
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/280,549
; PRIOR FILING DATE: 2010-03-30
; WUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3; SEQ ID NOS: 20
; LENGTH: 31412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INCEMATION: Clone ID: 31-LIB2809-013-Q1-E1-H3
US-09-960-352-7158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
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; ORGANISM: Ovis aries
US-10-109-551-3
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Best Local Simi:
Matches 385;
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Sequence 8311, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION
APPLICANT: Warlen, Weeley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC AND AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC AND AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC AND AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 8311
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                                                                                        2465 GGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTTTGG
                                                                                                                     346 GGACTGCAAAGAGTTCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTTTGG
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                  AGCACTGAAGAATTGATGCTTTTGAACTGTGTGTTGGAGAAGACTCTTGAGAGTCCCTT
                                       406 AGTCCCGAAGAATTGATGCTTTNGAACTGTGGTGTTGGAGAAGACTCTTGAGTGTCCCTT
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ORGANISM: Bos taurus

CORPER INFORMATION: Clone ID: 36-LIB188-014-Q1-E1-A12

US-09-960-352-8311
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86.7%; Pred. No. 70;
tive 0; Mismatches 55
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Best Local Similarity 86.7
Matches 357; Conservative
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Mesley C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1308
FURNATION OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCATTCTGAAGGAGAICAGCCCTGGGATTTCTTTGGAAGGAATGATGCTAAAGCTGAAA 2547
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                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 recarectaaadgagareagreergaararrearrggaaggaergargrrgaagergaag 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAAGATTAAGTGAATGAGGAGAAAGGGATGACAGAAGATGAGATGGTTGGATGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCAGTACTTTGGCCACCTGATGTGAAGAGCTGACTCATTTGAAAAGCCCATGATCCTG
                                                                                                                                                                                                                                                                                                                          61 ATGTATGGATGTGAGAATTGGACTATAAAGAATGCTGAGGAGCACCAAAGAATTGATGCTTTT
                                                                                                                                                                                                                2308 AGAGACATTACCTTGCCAACAACAAGCCCCCATCTAGTCAAGGCTATGGTTTTTCCAGTGGTC
                                                                                                                                                                                                                                                     1 AGAGACATTACCCTGCCAACAAGGTCCGTCTAGTAAAGGCTATGTTTTTTTCCAGTGGTC
                                                                                                                                                                                                                                                                                             2368 ATGTATGGATGTGAGAGTTGGACTGTGAAGAAAGCTGAGCACTGAAGAATTGATGCTTTT
                                                                                                                                                                                                                                                                                                                                                                         GAACTGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAG
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                                                                                                                                    Length 428;
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                                                                                                                                                                           58; Indels
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                                     LOCATION: (383)
OTHER INFORMATION: unsure at all n locations
CHER INFORMATION: Clone ID: 35-LIB3058-006-Q1-K1-A12
US-09-960-352-8154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure; LOCATION: (384); OTHER INFORMATION: unsure at all n locations; OTHER INFORMATION: Clone ID: 06-LIB34-016-Q1-E1-B9 US-09-960-352-1308
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                                                                                                                                      DB 1;
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                                                                                                                                  Score 335.8; D
Pred. No. 62;
0; Mismatches
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9.3%; Score 333; DB
Best Local Similarity 91.9%; Pred. No. 66;
Matches 351; Conservative 0; Mismatches
                                                                                                                                    Query Match
Best Local Similarity 86.4%;
Matches 370; Conservative
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US-09-960-352-1308/c
FEATURE:
NAME/KEY: unsure
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Sequence 14308, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
GENERAL INFORMATION:
Mesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE REPERSENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 14308
LENGTH: 409
                                                                                          APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WUSCLE AND FAI DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298) C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5499
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                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 24-LIB188-027-Q1-E1-F7
US-09-960-352-5499
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9.0%; Score 320.8; 1
Best Local Similarity 86.2%; Pred. No. 72;
Matches 355; Conservative 0; Mismatches
  Sequence 5499, Application US/09960352
Patent No. US2020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
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US-09-960-352-14308/c
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APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13834
LENGTH: 410
                                                                             2680 GACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAGGCCTGTCCTGCGGCG 2739
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                                                                                                          123 AACTIGAGTITGAATAAGCCCCAGGAGTIGGIGAIGGACAGAGAAGCAIAGAACAIACTIGCA 64
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                                                                                                                                                                          2740 ATTCATGGGGTCACAAAGAGTTGGACACGACTGAGCTGAACTGAACTGA 2791
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OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 59-LIB3058-044-Q1-K1-G4
US-09-960-352-13834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.0%; Score 321.6; DB 1; Best Local Similarity 88.9%; Pred. No. 73; Matches 368; Conservative 0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                         US-09-960-352-13834
; Sequence 13834, Application US/09960352
; Patent No. US20020137139A1
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US-09-960-352-5499/c
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APPLICANT: Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Byat., John C.
APPLICANT: Byat., John C.
APPLICANT: Byat., John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE PEPERRENCE: 16511.005,37-21(10298) C.
CURRENT APPLICANTON NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3391
LENGTH: 422
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CITTAITITITGGGGGCTCCAAAATCACTGCAGATGGTGACTGCAGCCATGAAATTAAA
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; OTHER INFORMATION: Clone ID: 15-LIB3058-036-Q1-K1-D11
US-09-960-352-3391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
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Pred. No. 81;
0; Mismatches
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Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local Similarity 86.0
Matches 363; Conservative
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
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OCGANISM: Bos taurus
OCANISM: Clone ID: 41-LIB3058-043-Q1-KI-C10
US-09-960-352-9545
                                                                 all n locations
61-LIB3058-039-Q1-K1-H2
                                                                                                                                                                                                                                         42;
                                                                                                                                                                                 DB 1;
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Pred. No. 74;
0; Mismatches
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Best Local Similarity 87.4%; Pre
Matches 375; Conservative 0;
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Clone ID:
                                                                                                                                                                                 Query Match
Best Local Similarity 89.3
Matches 366; Conservative
                                                                 OTHER INFORMATION:
COTHER INFORMATION:
US-09-960-352-14308
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US-09-960-352-9545
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APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLBIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21 (10298) C
CURRENT APPLICATION NUMBER: U5/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
ESCO ID NO 11945
LENGTH: 447
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Parent No. US20020137139A1

GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Mathialagan, Nagapan

APPLICANT: Mathialagan, Nagapan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: NUMBER: US/05/37-21 (10298) C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILLING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                       Length 447;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 51-LIB3058-047-Q1-K1-E4
US-09-960-352-11945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ; ORGANISM: BOS taurus CHERINFORMATION: Clone ID: 18-LIB3058-024-Q1-K1-E9 US-09-960-352-4133
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Pred. No. 85;
0; Mismatches
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 84.1%;
Matches 360; Conservative C
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US-09-960-352-4133/c
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LENGTH: 410
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Warren, Weeley C.
APPLICANT: Warren, Weeley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT APPLICANTON NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 336
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                                          AGGTGAAAGAGAGAGAGAAAAAAGTTGGCTTAAAAGCTCAACATTCAGAAAAGGATCA
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Pred. No. 1e+02;
0; Mismatches 23; Indels
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COTHER INFORMATION: unsure at all n locations
COTHER INFORMATION: Clone ID: 48-LIB3058-021-Q1-K1-D8
US-09-960-352-11214
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; Sequence 11945, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Weeley C.
; APPLICANT: Tao, Nengbing
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Best Local Similarity 93.2
Matches 313; Conservative
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ORGANISM: Bos taurus
FEATURE:
NAME/KEY: unsure
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US-09-960-352-11214
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Sequence 13376, Application US/09960352
Sequence 13376, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLE AND FAT DEPOSITION
TITLE OF INVENTION: NUCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13376
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                                                  TGCTTTTGAACTGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATC 2480
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                                                                       118 TGCTTTTGATCTGTGGTGTTTGGAGAAGACTCTTGAGAGTCCCTTGGATTGCAAGAGATC
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; OGGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 59-LIB34-027-Q1-E1-G4
18-09-960-352-13876
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Pred. No. 1e+02;
0; Mismatches 45,
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Best Local Similarity 87.6%;
Matches 345; Conservative
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Patent No. U920020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley
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US-09-960-352-13876
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US-09-960-352-9592
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GENERAL INFORMATION:
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: MATHION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER: OF SEQ ID NOS: 15112
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                                                                                                                                                                        GGTGAATGGTTCTATGAAGACCTACAAGACCTTCTAGAAACAACACCCCCAAAATATGTC
                                                                                                                     AATTGGAAAGGGTCAAACAGGAGATGGCAAGAATGAACATCAACATTTTAGGGATCACTG
                                                                                                                                                   AACTAAAATGGACTGGAATGGGTGAATTTAACTCAGATGACCATT-ATATCTACTACTGC
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                         Length 410;
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                                                       50; Indels
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; OTHER INFORMATION: Clone ID: 17-LIB34-010-Q1-E2-E1
US-09-960-352-3913
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Pred. No. 1.1e+02;
0; Mismatches 26
                         DB 1;
                         Score 296; DB
Pred. No. 92;
0; Mismatches
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US-09-960-352-3913/c
; Sequence 3913, Application US/09960352
· Patent No. US20020137139A1
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Best Local Similarity 91.6%;
Matches 327; Conservative
                       8.3%;
al Similarity 86.9%;
358; Conservative
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                         Query Match
Best Local S:
Matches 358
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GCAGGTCAAGAAGAAAC----AGAACTGGACATGGAAAATGGACTGGTTCAAAATTGGG 234
          Gaps
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) OTHER INFORMATION: Clone ID: 57-LIB3057-008-Q1-K1-G2
US-09-960-352-13323
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83.0%; Pred. No. 16+02;
tive 0; Mismatches 66;
          Mismatches
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Patent No. US20020137139A1
GENERAL INFORMATION:
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          Conservative
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Best Local Similarity 83.0
Matches 356; Conservative
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US-09-960-352-13323
          337;
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          Matches
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C
APPLICANT: Byatt, John C
APPLICANT: Byatt, John C
APPLICANT: Machialagan, Nagappan
APPLICANT: Machialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21 (10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
SEQ ID NOS: 15112
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Sequence 13585, Application US/09960352

Patent No. US2002013713941

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialgan, Wasley C.
APPLICANT: Mathialgan, Wasley C.
APPLICANT: Mathialgan, Muscher Acid And OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US/09/960,352

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 13585

LENGTH: 407
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Pred. No. 1e+02;
0; Mismatches 58; Indels 8
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; OTHER INFORMATION: Clone ID: 58-LIB3058-010-Q1-K1-G6
US-09-960-352-13585
                                                                                                                                                                                                              ; TYPE: DNA
; OGGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 41-LIB34-030-Q1-E1-C2
US-09-960-352-9592
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No. 1e+02;
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Best Local Similarity 83.5%;
Matches 334; Conservative 0
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Best Local Similarity
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APPLICANT: Warren, Wesley C.
APPLICANT: Byatt. John C.
APPLICANT: Byatt. John C.
APPLICANT: Byatt. John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NOS: 15112
SEQ ID NO 13323
LENGTH: 423 2436 ij 2616 2556 2676 ATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAGGCCTGTCCTGCG 2736 1756 1696 1816 169 178 108 ATGGACATGAGCTTGAGCAAACTCCGGGAGTTGGTGATGTACAGGGCAGCCTGGTATGCT 49 168 GARAGCATRAGGAGAACGGGACGACAGAGGATGTGATGGTTGAATGGCATCACCGACTCG 288 AATGAAATCAGTCCTAAATATTCATTGGAAGGACTGATGCTGAAGCTGAAACTCCAGTAC 407 rereasastresastar-aasaaastreascacsaaaaatreatsertraaacreres 2437 TGTTGGAGAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTG AAGGAGATCAGCCCTGGGATTTTCTTTTGGAAGGAATGATGCTAAAGCTGAAACTCCAGTAC 228 TTTGGCCACCTGATGTGAAGAACTGACTCATTTGAAAGAACCTGATGCTGGGAAAGATT 2617 GGGGGCAGGAGGAGAAAGGGGACGACAGAGGATGAGATGGCTGGATGGCATCACTGACTCG 1637 GACCAAATTGCCAACATCCTCTGTATCATGGAAAAAGCAAGAGAGTTCCAGAAAAACATC 1697 INTITICISCITINITICACINICAAAAGCCITIGACIGIGGGGGICACAATAAACIGIGG 1757 AAAATTCTGAAAGGGATGGGAATACCAGACCACCTGACCTGACTCTTGAAAATTTGTAT 119 AAAATTCTGAAAGGGATGGGAATACCAGACCACCTGATCTGCCTCTGAGAATCTGTAT 1817 GCAGGTCAGGAAGCAACAGTTAGAACTGGACATGGAACAACAGACTGGTTCCAAGTAGGA 61 TACATCTACTTCATGAACTACCTTATAGCCTTTGACTGTGGGATCACAAAC--TGG

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Query Match
Best Local Similarity 88.7%;
Matches 330; Conservative
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byat, John C.
APPLICANT: Machialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION UNMBER: US/09/960,352
CURRENT APPLICATION 1006/37-21(10298)C
CURRENT APPLICATION 1006/37-21(10298)C
CURRENT APPLICATION 1006/37-21(10298)C
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                                                                                                                    ATCATGAGAAACGCTGGAAGAAGCACAAGCTGGAATCAAGATTGCCGGGAGAAAT 1995
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                                               235 AAAGGITTAIGICAAGGCIGCATAITGICACCCIGCTTAITTAACITAIAIGGAGAGIAC 294
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                                                                                                                                                                                                                                                                                                      Score 279.1; DB 1; Length 365; Pred. No. 1.2e+02; 0; Mismatches 14; Indels 7
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ORGANISM: Bos taurus
CRANISM: Bos taurus
US-09-960-352-13570
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Best Local Similarity 94.2%;
Matches 341; Conservative
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US-09-960-352-13570
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/ Sequence 6765, Application US/002013713941

/ Sequence 6765, Application US/09960352

/ Sequence 6765, Application US/09960352

/ APPLICANT: Warren, Wesley C.

/ APPLICANT: Mathialagan, Nagapan

/ APPLICANT: Mathialagan, Nagapan

/ APPLICANT: Mathialagan, Nagapan

/ TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

/ TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

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Sequence 10238, Application US/09960352
; Patent No. US20020137139A1
; GRERRAL INFORMATION
; APPLICANT: Warren, Weeley C.
; APPLICANT: Byatt, John C.
; APPLICANT: Byatt, John C.
; APPLICANT: Byatt, John C.
; TITLE OF INVENTION: NUCLEIC ACID AND CTHER MOLECULES ASSC.
; TITLE OF INVENTION: NUCLEIC ACID AND CHER MOLECULES ASSC.
; TITLE OF INVENTION: NUCLEIC ACID AND CHER MOLECULES ASSC.
; TITLE OF INVENTION: NUCLEIC ACID AND CHER MOLECULES ASSC.
; CURRENT FILING DATE: 2001-09-24
; CURRENT FILING DATE: 2001-09-24
; SEQ ID NO 10238
; LENGTH: 448
; TYPE: DNA
; ORGANISM: BOS taurus
; OTHER INFORMATION: Clone ID: 44-LIB3058-004-Q1-K1-C8
US-09-960-352-10238
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Pred. No. 1.1e+02;
0; Mismatches 33
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us10664775-2.rnpb

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Sequence 11256, Application US/09960352
Retent No. US20020131139A1
APPLICANT: Warren, Weeley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Machialagan, Nagappan
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21 (10299)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                   1875 GAAAAGGAGTATGTCAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTATGCAGAG-
                                                                                  153 AGAAAAGAGTACTTCAAGGCAGTGTATTGTCACCCTGCTTATGTAATATGCAGAGC
                                                                                                                                                                                                                                                                                                               273 ATATCAGTAACCTCAGATATGCAGAGACACCATCCTTATG-----ATGAAGAGGAAC
                                                                                                                                             1934 ACATCATGAGAAACGCTGGGAGGAGGAGCACAAGCTGGAATCAAGATTGCCGGGAGAA
                                                                                                                                                                                   213 ACATCATGTGAAATGCCAGGTTGCATGAAGCACAAGTTGGAGTCAAGATTTCAGGGAGAA
                                                                                                                                                                                                                                                             ATAGCAATAACCTCAGATATGCAGATGATACCACCCTTATGGCAGAAAGTGAAGAGGAAC
                                                                                                                                                                                                                                                                                                                                                                      TAAAAAGCCTCTTGATGAAGGTGAAAGAGGAGAGTGAAAAAGTTGGCTTAAAGCTCAACA
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; OTHER INFORMATION: Clone ID: 48-LIB3058-056-Q1-K1-D12
US-09-960-352-11236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.6%; Score 270.2; DB 1; Best Local Similarity 84.5%; Pred. No. 1.2e+02; Matches 326; Conservative 0; Mismatches 58;
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Patent No. US20020137139A1
GENERAL INFORMATION
APPLICANT: Warren, Weeley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MOSLE AND PAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
SEQ ID NOS: 15112
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                                                                                                                                             48; Indels
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; OTHER INFORMATION: Clone ID: 29-LIB3058-049-Q1-K1-H1
US-09-960-352-6765
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; OTHER INFORMATION: Clone ID: 40-LIB3058-011-Q1-K1-B8
US-09-960-352-9318
                                                                               Score 273.7; DB 1;
Pred. No. 1.1e+02;
0; Mismatches 48;
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Pred. No. 1.1e+02;
0; Mismatches 67;
                                                                                  7.7%;
81.2%;
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Best Local Similarity 81.8%;
Matches 336; Conservative (
                                                                               Query Match
Best Local Similarity 81.23
Matches 349; Conservative
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Sequence 7893 Application US/09960352

Facent No. US20020131139A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagapan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCIE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICANTON NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 7893
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                                                                                                                                                                                                                                                                                                                              Query Match 7.5%; Score 269.3; DB 1; Length 347; Best Local Similarity 90.1%; Pred. No. 1.38+02; Matches 299; Conservative 0; Mismatches 32; Indels 1.
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; CTHER INFORMATION: Clone ID: 34-LIB3057-006-Q1-K1-A6
US-09-960-352-7893
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ilarity 85.7%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 50;
                                                                                                                                                                                                 TYPE: DNA
CGANTSM: Bos taurus
COTHER INFORMATION: Clone ID: 50-LIB34-023-Q1-E1-E6
US-09-960-352-11744
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TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION PILE REFERENCE: 1651.006/37-21(10298)C CURRENT APPLICATION NUMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 15112 LENGTH: 347
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Best Local Similarity
Matches 330; Conserv
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NAME/KEY: unsure
LOCATION: (311)
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                                                                                                                                                                                                                                               APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: WUCCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: WUSCLE AND PAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND PAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND PAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND PAT DEPOSITION
TITLE OF EXPERIENCE: 16511.06/37-21(10298)C
CURRENT APPLICATION WINBER: U5/09/9560,352
VURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 CCACCTTACCTGACAC---AGAAATCTGTGCAGGACAAGAAACAACAACAGTAGTACTGG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 TTTTATAT----GGATCACAACAACTGTGAAAATCTTAAAGAGGTGGGAATATCAGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGBABABAGCAAAGAAATTTBABABABABATCTBCTTCTGTGTCATTGACTBCACTBABGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1666 GGAAAAAGCAAGAGAGTTCCAGAAAAACATCTATTTCTGCTTTTATTGACTATGCAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTGACTGTGGGGGTCACAATAAACTGTGGAAAATTCTGAAAAGGGATGGGAATACCAGA
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nogappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.6%; Score 270.2; DB 1; Length 449; 82.1%; Pred. No. 1.1e+02; Live 0; Mismatches 58; Indels 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA CAGANISM: BOS taurus CHER INCORATION: Clone ID: 34-LIB3058-004-Q1-K1-A6 US-09-960-352-7912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2072 AGGTGAAAGAGGAGAGTGAAAAAGTT 2097
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           TTAGATCTGATCAACAGAGTGCTGAA
                                                                                                                                                                      ; Sequence 7912, Application US/09960352; Patent No. US20020137139A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 82.1
Matches 366; Conservative
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US-09-960-352-11744/c
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APPLICANT: Infigen Inc.
APPLICANT: EILERTSEN, KENNETH J.
APPLICANT: EILERTSEN, KENNETH J.
APPLICANT: EILERTSEN, KENNETH J.
APPLICANT: FETSTER-CENSKOW, MARTHA
APPLICANT: FORSYTHE, TODD
APPLICANT: FORSYTHE, TODD
APPLICANT: EIGHOP, MICHAEL D.
ITILE OF INVENTION: IDENTIFICATION AND USE OF MOLECULAR MARKERS INDICATING
ITILE OF INVENTION: CELLULAR REPROGRAMMING
ITILE OF INVENTION: CELLULAR REPROGRAMMING
ITILE OF INVENTION: UNMBER: US/09/876,143
CURRENT APPLICATION NUMBER: 60/209,874
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 1744
SOFTWARE: Patentin version 3.0

SEQ ID NO 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1859 GACTGGTTCCAAGTAGGAAAAGGAGTATGTCAAGGCTGTATATTGTCACCCGGCTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 GCGTGGTTCCAAATAGGAAAAGGAGTACGTCAAGGCTGTATATTGTCNCCCTGTTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 ATCTTATATGCAGAGTACATCATGAGAACCGCTGGGACTGGAAGAAGCACAAGCTGGAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 AGAAAGTGAAGGGAACTAAAAAGCCTCTTGATGAAAGTGAAAAGAGGAGAGGAAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 crcingagaarcererarecaegreaegacecaacaeraagaceregacareaaecaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AAGATTGCCAGGAGAAATATCAATAACCTCATATATGCAGATGATCNCCTCCCTTATGGC
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Pred. No. 1.4e+02;
0; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTTAAAGCTCAACATTCAGAAAACGAAG 2127
                                                       134 AGGCTGTGGTTTTTCCAGTGGTCATATAAG 105
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APPLICANT: Warren, Wesley C. APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Nagappan
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О
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Publication No. US20040081958A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
| LOCATION: (1)..(347)
| OTHER INFORMATION: n is a, c, g, US-09-876-143-32
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Best Local Similarity 91.2'
Matches 302; Conservative
     2345 AGGCTATGGT1
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US-09-960-352-14979/c
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ORGANISM: Bovine
FEATURE:
                                                                                                                                                                JS-09-876-143-32/c
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| Patent No. US20020137139A1
| GENERAL INFORMATION:
| APPLICANT: Marren, Wesley C. | APPLICANT: Marren, Wesley C. | APPLICANT: Marren, Wesley C. | APPLICANT: Mathialagan, Nagappan |
| TITLE OF INVENTION: WICCLE CALD AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND |
| TITLE OF INVENTION: WISCLE AND FAT DEPOSITION |
| TITLE OF INVENTION: WISCLE AND FAT DEPOSITION |
| TITLE OF INVENTION: WISCLE AND FAT DEPOSITION |
| TITLE OF INVENTION: WISCLE AND FAT DEPOSITION |
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| TITLE OF INVENTION: WISCLE AND FAT DEPOSITION |
| TITLE OF INVENTION: WISCLE AND FAT DEPOSITION |
| TITLE OF INVENTION: WISCLE AND FAT DEPOSITION |
| TITLE OF INVENTION: LONG: 15112 |
| TYPE: DNA |
| TYPE: DNA |
| TYPE: DNA |
| ORGANISMATION: CLONE ID: 13-LIB3058-024-Q1-K1-D1 |
| US-09-960-352-2913
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                                                                                                                                                        2120 AAACGAAGATCATGGCATCTGGTCCCATCACTTGGGAAATAGGAGGGAAACAGTGG
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                                                                                                                                                                                                                                                                                                                203 AAACAGIGICATACTITATGGITT--TGGGCTCCAAAATCACTGCAGATGGTGACTGCAG 146
TAACTICAGATATGCAGATGACACCACCTTTATGTCAGAGAGTGAACAGCAACTACAGAG 324
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                                                                                                                                                                                                                                                                                                                                                                                                   145 CCATGAAAGTGACAGACACTTACTCCTTGGAAAGAAAGTATATGTCCAACGTAGATAGCAT
                                                                                              323 CCTCGGTATGATNGTGATACAGTAGAGTGAGCAAGTTGGCTTAAAGCTCGAACATTCAGA
                                                                                                                                                                                                                                                            2180 AAACAGIGICAGACTITATITITIGGGGGGGTCCAAAATCACIGCAGAIGGIGACTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCAGTGGTCATGTATGGATGTGAG 2382
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Matches 303; Conservative
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RESULT 44
US-09-960-352-7209
US-09-960-352-7209
US-09-960-352-7209
Sequence 7209, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION
APPLICANT: Warten, Wealey C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Hat, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACITATION AND
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACITATION AND
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACITATION AND
TITLE OF INVENTION: NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
SEQ.ID NOS: 15112
SEQ.ID NOS: 15112
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                                                                                                                                                                                                      2152
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                                                         GAATCAAGATTGCCGGGAGAAATAGCAATAACCTCAGATATGCAGATGATACCACCCTTA
                                                                            279 GAGTCAAGATTGCCAGGAGACATATCAACAATCTCAGATATGTAGATAATACCACCTTAA
                                                                                                                                                                                                                                    AAGCTGGCATAAAACTCAAAATTCACAAACTGAGATCCTGGCAACTGATCTCATCACTT
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                                                                                                                                                                                                                                                                                                                                                                                CAAAAICACTGCAGACAGTGACTGCAGCCATGAAATTAAAAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 31-LIB3058-021-01-K1-H11
US-09-960-352-7209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 254.8; DB 1;
Pred. No. 1.3e+02;
0; Mismatches 57;
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Best Local Similarity 83.6%;
Matches 300; Conservative (
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Patent No. US2002013713941

GENERAL INFORMATION:
APPLICANT: Warien, Wesley C.
APPLICANT: Byat, John C.
APPLICANT: Byat, John C.
APPLICANT: Byat, John C.
APPLICANT: Byat, John C.
APPLICANT: Byat, John C.
APPLICANT: Byat, John C.
APPLICANT: Byat, John C.
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 149
 TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REPRENCE: 15511.06/37-21(10298)C
CURRENT APPLICATION NUMBER: U5/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 14979
LENGTH: 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AACATCCGCTGGATCATGGAAAAAACAAGAGAGTTCCAGAAAACATCTATTTCTGCTTT
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                                                                                                                                                                                                                                                    423;
                                                                                                                                                                                                                                                Score 258.1; DB 1; Length
Pred. No. 1.3e+02;
0; Mismatches 24; Indels
                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INPORMATION: Clone ID: 64-LIB3058-007-Q1-K1-H8
US-09-960-352-14979
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ilarity 91.9%;
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Best Local Similarity
Matches 283; Conserv
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US-09-960-352-149/c
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Best Local S
Matches 330
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Sequence 11719, Application US/09960352

Batent No. US20020137139A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tao, Nengbing

APPLICANT: Byatk, John C.

APPLICANT: Byatk, John C.

APPLICANT: Machialagan, Nagappan

IITLE OF INVENTION: MUSCLE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10299)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

LENGTH: 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.9%; Score 246.3; DB 1; Length 430; Best Local Similarity 76.3%; Pred. No. 1.4e+02; Matches 326; Conservative 0; Mismatches 92; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Bos taurus
CITHER INFORMATION: CLONE ID: 50-LIB3058-058-Q1-KI-E6
US-09-960-352-11719
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RESULT 45
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:

August 24, 2004, 13:40:03; Search time 73 Seconds (without alignments) 3.947 Million cell updates/sec

US-10-664-775-2 3572

1 gtcaggaaggggggggggtga.....gcaacaacagcagaaagctt 3572 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

45 segs, 40327 residues Searched:

90 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

rst2.seq:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	SION: CC58344	:CC4797	SION: CC47936	CCESSION: CC50817	CCESSION: CC54497	CCESSION: CC57707	CCESSION: CC5146	CCESSION: CC58688	CCESSION: CC52094	CCESSION: CC52079	CCESSION: CC54843	CCESSION: CC59470	CCESSION: BZ88258	CCESSION: CC48011	CCESSION: CC47523	1059363	86	10536	:C47649	C27965	σ	C24366	C24724	C48029	105891	C54122	C54610	SSION: CC51145	CCESSION: CC49510	CCESSION: CC53985	CCESSION: CC5285	CCESSION: CC50874	SION: CC51203
SUMMAKIES	CC583446	79	793	381	49	2	œ	88	5	5	34	7	325	30	752	336	38				CC500971			803	89	412	461	114	953	398	CC528566	9	120
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23.2%; Score 829.8; DB 1; Length 909;

Query Match

ACCESSION: CC581072 ACCESSION: CC536979 ACCESSION: CC591633 ACCESSION: CC586052 ACCESSION: CC586052 ACCESSION: CC5840709 ACCESSION: CC533944 ACCESSION: CC581655 ACCESSION: CC581625 ACCESSION: CC581625 ACCESSION: CC591655 ACCESSION: CC591655	NTS DNA linear GSS 18-JUN-2003 caurus genomic clone CH240_379F21,	<pre>traniata; Vertebrata; Euteleostomi; tyla; Ruminantia; Pecora; Bovoidea; tber,S., Smailus,D., Prabhu,AL.,</pre>	TSAI, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B. P. and Tellam, R. Bovine BAC Back Sequences from Library CHORI-240, PLATES 294 to 398 JAL Unpublished (2003) Cher GSSS: CH240, 379F21.TARBAC13P2 Contact: Rob Holt	Sequencing The British Columbia Cancer Agency Genome Science Centre 5600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6 Tel: 604-877-6085  Tax: 604-877-6085  Email: rholt@bcgsc.ca Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IEBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.  Plate: 379 row: F column: 21	A"  ord"  Cl.3; Site 1: Mbol; Site 2: Mbol;  no 59375; CHORI-240 Bovine BAC  ed by Pieter de Jong"
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CH240 306H6.T7 CHORI-240 Bos taurus genomic clone CH240\_306H6,
GC479701.1 GI:31757509
GSS.
Bos taurus (cow)

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

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The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave. Vancouver, British Columbia, Canada V5Z 4E6 Fax: 604-877-6085
Fax: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
British Columbia Genome Sciences Centre, Canada.
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1 (Bases 1 to 926)
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1 Fasi,M., Cloutier,A., Lee,D., Barber,S., Smailus,D., Prabhu,A.-L., Tsai,M., Cloutier,A., Lee,D., Brown-John,M., Olson,T., Mayo,M., Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Ghan,A., Chiu,R., Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S., Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W., Balrymple,B.P. and Tellam,R.

L Unpublished (2003)
Contact: Rob Holt
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/cell type="Blood"
/clone_lib="CHOR1-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mbo
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mbo
Hereford bull Li Domino 99375; CHOR1-240 Bovine BAC
library (Male) produced by Pleter de Jong"
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94.4%; Pred. No. 0.11;
ive 0; Mismatches 50;
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/mol type="genomic DNA"
/strain="breed: Hereford"
/db_xref="teaxon:9913"
/clone="KGT240_306H6"
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1 (bases 1 to 949)

2 Holt, R., Stoctt, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Mathewson, C., Wye, N., Marcherick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Schein, J., Warra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B.P. and Tellam, R.

1 Dalrymple, B.P. and Tellam, R.

1 Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

1 Unpublished (2003)

2 Contact: Rob Holt

2 Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     949 bp DNA linear GSS 16-JUN-2003
CH240 306K22.T7 CHORI-240 Bos taurus genomic clone CH240_306K22,
Genomic survey sequence.
CC479360
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600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ
Tel: 604-877-6085
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Email: rholt@bcgsc.ca
Clones are derived from
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(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the Briteish Columbia Genome Sciences Centre, Canada. Seq primer: T7 Class: BAC ends.
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/note="Vector: pTARBACL.3; Site_1: MboI; Site_2:
Hereford bull in Domino 99375; CHORI-240 Bovine B
library (Male) produced by Pieter de Jong"
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| /organism="Bos taurus"
| /mol_type="genomic DNA"
| strain="breed: Hereford"
| /db_xref="taxon:9913"
| /clone="CH240_306K22"
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                                                                                                                                588 AGGCAAATTGGAAGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      648 CAGCGAACTAAAATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATATTTACTA
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                                                                                             Gaps
                                                                                        7;
                                                   Length 927;
        de Jong
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        library (Male) produced by Pieter
                                                   DB 1;
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                                              Score 821.9; DF
Pred. No. 0.11;
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Best Local S:
Matches 876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Blitish Columbia Canada.
Seg primer: 17
Class: BAC ends.
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                                                                                                                                                  GAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGA 2503
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778
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
Hereford_bull_Li_Domino_99375; CHORI-240_Bovine_BAC
                                                                                          719 TTTGGACTGTGAAGAAGGCTGAGCACCGAAGAATTGATGCTTTTGAACTGTGGTGTTGGA
                                                                                                                                                                            779 GAAGACTCTTGAGAGTCCTTTGGACTGTAAGGAGAGTCCAACCAGTCCATTCTGAAGGAGA
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                                                                GTTGGACTGTGAAGAAAGCTGAGCACTGAAGAATTGATGCTTTTGAACTGTGGTGTTGGA
                                                                                                                                                                                                                                                                          TCAGCCCTGGGATTTCTTTGGAAGGAATGATGCTANAGCTGAAACTCCAGTACTTTGGCC
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6
Fax: 604-877-6085
                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_350K18"
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KEYWORDS
SOURCE
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JOURNAL
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FEATURES

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	TACTTGGATGCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTT	1016 AAITTGGCCTTGGAATACGGAATGAAGGGCAAAGACTAATAGAGTTTTGCCAAGAAA 1075 731 AAITTGGCCTTGAAATATGGAATGAAGCAGGCAAAGACTAATAGAGTTTTGCCAAGAAA 790 1076 ATGCACTGGACTGAAATATGGAATGAAGCAGGCAAAGACTAATAGAGTTTTGCCAAGAAA 790 1076 ATGCACTGGTCATAGCAAACCCCTCTTCCAACAACACAAGAGAAGACTCTACACATGGA 1135 791 ATGCACTGGTCATAACAAACCCTCTTCCAACAACACAAGAGAGACTCTAACATGGA 850 1136 CATCACCAGATGGTCAAAACACCCTTTCCAACAACAAAGAGAGGACTCTATACATGGA 850 1137 CATCACCAGATGGTCAACACCGAAATCAGATTATATTCTT 1179 851 CATCACCAGATGGTCAACACCGAAATCAGATTATATTCTT 894 CCC577078 919 bp DNA linear GSS 18-JUN-2003 N CH240 455012. TARBAC13P2 CHOR1-240 Bos taurus genomic clone CCC577078 161-11920393	GSS.  GSS.  GSS.  Bos taurus (cow)  Bos taurus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Bovidae; Bovinae; Bos.  1 (bases 1 to 919)  1 (bases 1 to 919)  1 (cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,  Eutterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A.,  Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A.,  Schein, J., Marra, M., de Jong, P., Keele, J.W. and Kappes, S.M.  Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478  Unpublished (2003)  Other GSSs: CAL400, 455012.T7  Contact: Rob Holt  Sequencing  The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6  Fax: 604-877-6085  Email: rholt@bcgsc.ca
	6 6 6 6 6 6 6	Oy 1  Oy 1  Db  Oy 1  Oy 1  Db  CC577078/C LCCUS  DEFINITION ACCESSION	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS JOURNAL COMMENT
0003 1; 5a;	7. 7. 8	t pe	1; 355 70 415 130 190 535 250
LOCUS  CC544978  CH240 427A14.TARBAC13P2 CHOR1-240 Bos taurus genomic clone  ACCESSION  CC544978.1  CC544978.1  CC544978.1  G1:31863262  SOURCE  Bos taurus (cow)  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1  CC544978.1	Mathewson, C., Was, N., Masson, A., Brown-John, W., Jones, S., Schein, J., Marra, M., de Jong, P., Keele, J. W. and Kappes, S., Bovine Bad End Sequences from Library CHORI-240, PLATES 399 to 476 Unpublished (2003)  COMMENT CONTACT: Rob Holt CONTACT: Rob Holt Sequencing The British Columbia Cancer Rob Holt Sequencing The British Columbia Cancer Rob Holt Sequencing The British Columbia, Canada V5Z 4E6 Tal: 604-877-6276  Email: rholt@bcgsc.ca Clones are derlived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.crg)	Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada. Plate: 427 row: A column: 14 Seq primer: SP6 Class: BAC ends.  Location/Qualifiers  1. 894   corganism="Bos taurus"     mol type="genomic DNA"     strain="breed: Hereford"     clone="CHIACON"     clone="CHIACON"     clone="CHIACON"     clone="CHIACON"     clone="CHIACON"     clone="CHIACON"     clone="CHIACON"     clone="CHIACON"     clone="CHIACON"     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIACON     clone="CHIA	22.9%; Score 818.2; DB 1; Length 894;  y 96.0%; Pred. No. 0.12;  rvative 0; Mismatches 33; Indels 2; Gaps  CTGGAGAAGGGATGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCA  CTGGAGAAGGGATT-GCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCA  ATGAAAAGGCAAATGATAGGAACTGAAAGAGAACTCCCCAGGTCAGTAG  ATGAAAAGGCAAATGATAGGATACTGAAAGAGAACTCCCCAGGTCAGTAG  TATGCTACTGGAGATACTGAAATAACTCCAGAAAGAATGAAGAATGAAGAATGAAGAATGAAGAATGAAGAA

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Location/Qualifiers
1. 882
/organism="Bos taurus"
/mol type="Genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                        1358 TGAGAAATAGATTTAAGGGCCTA 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9913"
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CC514626.1 GI:31832914
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ORGANISM
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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CC514626
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Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada. British Columbia Genome Sciences Centre, Canada. Seg primer: SPG Seg primer: SPG Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGAGITITIGCCAAGAAATGCACTGGTCATAGCAAACACCCTCTTCCAACAACACAAGA 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGGGTCCGATATGCAGTACTTGGATGCAATCTCAAAAATGACAGAATGATGATCTCTGTTC 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 TCAAAAAAGATGTCCTTTTCATTATAGGGGACTGGAAATGCAAAAGTAGGAAGTCAAGAAA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 TAGAGTICTGCCAAGAGAATGCACTGGTCATAGCAAACACACCCTCTTCCAACAACAAGA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAGAATGAAGAGATGGAAGCCAAAAGAATACCCAGCTGTGGATGTGACTGGTG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATGAATCAAGGCAAATTGGAAGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACA 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561 GITTCCAAGGCAAACCATTCAATATCACAGTAATCCAAGTCTATGCCCCCAACCAGTAATG 502
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                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Blood"
/clone_lib="CHORI-240"
/clone_lib="CHORI-240"
/note="Vector: pTARBACI.3; Site_l: MboI; Site_2: MboI;
Hereford bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 740 TTCTAGGAATCAGCAAACTAAAATGGACTGCAATGGACTGAATTTAACTCAGATGACCATT
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                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              sex="Male"
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Matches 871; Conservative
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Sequencing
The British Columbia Cancer Agency Genome Science Centre
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave. Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
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1 (Bases 1 to 882)

Holt.R., Stott.J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,

Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,

Butterfield,Y., Kirkpetrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,

Mathewson,C., Wye,N., Masson,A., Brown.John,M., Jones,S.,

Schein,J., Marray,M., de Jong,P., McWilliam,S., Barris,W.,

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Other GSSs: CR440

Contact: Rob Holt

Contact: Rob Holt
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Bos taurus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                               144
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/clone_lib="CHORI-240"
/note="Vector: pIARBAC1.3; Site_1: Mbo1; Site_2: Mbo1;
                                                               1238 GIGGCICAGAICAIGAACICCITAITGCCAAAITCAGACITAAAITGAAGAAAGIAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 GIGGCTCAGATCATGAACTCCTTATTGCCAAATTCAGACTTAAATTGAAGAAAGTAGGA
                                                                                                                                                                                                              TITGCAGCCAAAGATGGAGAAGCTCTATACAGTCAGCAAAAACAAGACCAGGAGCTTACT
                                                                                                                                                                                                                                                                                                               201 TTTGCAGCCAAAGATGGAGAAGCTCTATAAAGTCAGC--AAACAAGACCAGGAGCTGATT
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GI:31939990

us10664775-2.rst

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Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave. Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6085
Fax: 604-877-6086
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Seg primer. 17:
                                                  SM Bos tearus (cow)

Bos tearus (cow)

Bos tearus

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;

Boxdae, Bovinae; Bos.

Bovidae, Bovinae; Bos.

1 (bases 1 to 86;)

Tsai, M. Cloudier, A., Lee, D., Glrn, N., Olson, T., Mayo, M.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Glson, T., Mayo, M.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Glson, R.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Glson, R.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Glson, R.,

Butterfield, Y., Masson, A., Brown, John, M., Jones, S.,

Schahn, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,

Dalrymple, B.P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Lu Unpublished (2003)

Contact: Rob Holt
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                                                                                                                                                                                                                                                                                     TGGAAGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGGAATCAGCGAAC
                                                                                                Gaps
  Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
                                                                                            ö
                                                      22.6%; Score 806.8; DB 1; Length 882; larity 94.7%; Pred. No. 0.14; Conservative 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTAAGACCTAAATCCAATCCCTTATGATTATACAGTGGAAG 1357
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/organism="Bos taurus" /mol\_type="genomic DNA" /strin="breed: Hereford" /db\_xref="teaxon:9913" /clone="CH240\_384H21"

Location/Qualifiers 1. .866

569 629 807 747 689 687 749 627 809 567 510 GACTGGTGATATAAGCAAGGTCCGATGCTGTAAAGAGCAATATTGCATAGGAACCTGGAA GACTGGTGATAGAAGCAAGGTCCGATGCTGTAAAGAGCAATATTGCATAGGAACCTGAAA TGTCAGGTCCATGAATCAAGGCAAATTGGAAGTGGTCAAACAAGAGATGGCAAGAGTGAA rereagerecargaareaagecaaacregaagregreaaacaagagaregecaagagreaa TGACCATTATATGTGCTGCGGGCAGGAATCCCTCAGAAGAAATGGAGTAGCCATCAT GGTCAACAAAAGAGTCCGAAAATGCAGTACTTGGATGCAGTCTCAAAAACGACAGAATGAT TGTCAACATTCTAGGAATCAGCGAACTAAAATGGACTGGAATGGGTGAATTTAACTCAGA Gaps ij Length 866; Indels 33; DB 1; 22.4%; Score 801.7; DE 96.1%; Pred. No. 0.15; ive 0; Mismatches Conservative Similarity Query Match Best Local Simi Matches 832; 989 750 626 용 Š 셤

CCS86882 866 bp DNA linear GSS 18-JUN-2003 CH240 384H21.T7 CHORI-240 Bos taurus genomic clone CH240 384H21, genomic survey sequence.

RESULT 8 CC586882/c LOCUS

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TGTCCTTCTCATTATAGGGGACTGGAATGCAAAAGTAGGAAGCAAAGAAACACCTGGAGT 1007
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/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_368M20"
/sex="Male"
                                                                                                                                     Location/Qualifiers
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Best Local Similarity 94.6
Matches 839; Conservative
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1 (bases 1 to 887)

S Holl,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L., Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M., Butterfield,Y., Kirkpatrick,R., Liu,J., Clan,R., Chan,A., Chiu,R., Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S., Schenin,J., Marra,M., de Jong,P., McWilliam,S., Barris,W., Dalrymple,B.P. and Tellam,S., Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398 Other GSSS: CR240,368M20.T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CH240_368M20.TARBAC13P2 CHORI-240 Bos taurus genomic clone CH240_368M20, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                1110 ACACAAGAGAAGACTCTACACATGGACATCACCAGATGGTCAACACCGAAATCAGATTGA 1169
                                                                                                                                                                                      CAAAGAAACACCTGGAGTAACAGGCAAATTTGGCCTTGGAATACGGAATGAAGCAGGGCA 1049
                                                                                                                                                                                                                                                   AAGACTAATAGAGTTTTGCCAAGAAAATGCACTGGTCATAGCAAACACCCTCTTCCAACA 1109
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                              507
                                                                                                                                                        446 ACTAACACCCAAAAAGATGTCCTTTTCATTATA-GGGACTGGAATGCAAAATAGGAAG 388
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                     CTCTGTTCGTTTCCAAGGCAAACCATTCAATATCACAGTAATTCAAGTCTATGCCCCAAC
                                                                                   CAGTAACACTGAAGAAGCTGAAGTTGAACGGTTCTATGAAGACCTACAGGACCTTTTAGA
                                                                                                                                                                                                                    387 TCAAGAATACCTGGAGTAACAGGCAAATTTGGCCTTGGAATACAGAATGAAGCAGGGCA
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                                                             CAGTAATGCTGAAGAAGCTGAAGTTGAACGTCCTATGAAGACCTACAAGACCTTTTAGA
                                                                                                                         ACTAACACCCCAAAAAAGATGTCCTTCTCATTATAGGGGACTGGAATGCAAAAGTAGGAAG
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
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(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering.information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada. Blate: 368 row: M column: 20 Seg primer: SP6 Class: BAC ends. 9 347 407 120 467 180 527 240 587 300 647 360 707 420 480 540 887 600 TGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAACTAACACCCAAAAAAGA 947 767 827 9 /cell\_type="Blood" /clone\_lib="CHORI-240" /note="Vector: pTARBACL.3; Site\_1: MboI; Site\_2: MboI; Hereford bull il Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong" 241 GGTCCGATGCTGTAAAGAGCAATATTGCATAGGAACCTGGAATGTCATGTCCGTGAATCA 361 CAGCGAACTAAAATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATCTACTA CAPACCATTCAATATCACAGTAATCCAAGTCTATGCCCCAACCAGTAACATTGAAGAAGC 289 TGACAGAATGTGGTCCACTGGAGAAGGGAAT-GCAAACCACTTCAGTATTCTTGCCTTGA 61 GAACCCCATGAACAGTATGAAAAGGCCAAAATGATAGGATACTGAAAGAGAAACTCCTCAG 121 GTCAGTAGGGGCCCAATATGCTACTGGAGATCAGTGGAGAAATAACTCCCGGAAAGAAGAAGA AGGCAAATTGGAAGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGGAAT CAGCGAACTAAAATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATCTACTA AAATGCAGTACTTGGATGCAATCTCAAAACGACAGAATGATCTCTGTTCGTTTCCAAGG 1 reacagaargreercaacregagaaggraargecaaaccacrrcagrarrerrecerrea 348 GAACCCCATGAACAGTATGAAAAGGCAAAATGATAGGATACTGAAAAGAGGAACTCCCCAG AGAGATGAGACCAAAGCAAAAAGAATACCCAGCTGTGGATGTGACTGGTGATATAAGCAA GGTCCGATGCTGTAAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATGAATCA CTGCGGGCAGGAATCCCTCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAAGAGTCCG CTCTGGGCAGGAATCCCTCAGAAGAAATGGAGTAGCCATCTTGGTCAACAAAAGAGTCTG CAAACCATTCAATATCACAGTAATCCAAGTCTATGCCCCCAACCAGTAATGCTGAAGAAGC Gaps ä Length 887; Indels 22.4%; Score 800.3; DB 1; 94.6%; Pred. No. 0.14; ive 0; Mismatches 47;

Matches         886;         Conservative         0;         Mismatches         55;         Indels         7;         Gaps         5;           Qy         1811         TTGTATGCAGGTCAGGAACAGTAGAACTGGACACAGACTCGATCCAACAGACTCGATCTCTACCAA         1870           Db         951         TTGTATGCAGGTCAGGAACACACAGACTTAGAACTCGAACTCGAACTCTATATAGCA         894           Qy         1871         GAGGAAAAGGAGTAACACACAGACTATATATTCTCACCCTGCTTTTTNTAACTTCTATATGCA         834           Db         893         AGAGGAAAAGGAGTAACATCAAGGCTGAACACACACACAC	773 AGAATATCAATAACCTCAGATATGCAGATGCACCCCTTATGGCAGAAAGTGAAGAG 2050 GAACTAAAAAGCCCCTTGATGAAGAGGAGAGAGAGAGAGA	DD   S93 GAACAGTGGAAACAGTGTCAGACTTTATTTTCTGGGCTCCAAAATCACTACAGATG 536	Qy         2468         CTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTGGGATTTCTTTGGAAG         2527           Db         295         CTGCAAGGAGTCCAACCAGTCCAATCTGAAGGAGTCAGCCCTGGGATTTCTTTTGGAAG         236           Qy         2528         GAATGATGCTAAAGCTCGAAACTCCAGTACTTGGCCACCTGATCAGAAGAGTTGATTCTTTTGGAAG         2587           Db         235         GAATGATGCTAAAGCTGAAACTCCAGTACTTTGGCCACCTGATGAGAGAGTGACTCAT         176           Qy         2588         TGGAAAAGACCCTGATGCTGGAGGATTGGGGGAGGAGGAGGAGGAGTGACTCAT         176           Db         175         TGGAAAAGACCCTGATGCTGGAGGGATTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGA	RESULT 11 CC548437 LOCUS CC548437 LOCUS DEFINITION CH240 432010.T7 CHORI-240 Bos taurus genomic clone CH240_432010, genomic survey sequence. ACCESSION CC548437
	RESULT 10 CC520792/c LOCUS DEFINITION CH403 386C2.T7 CHORI-240 Bos taurus genomic clone CH240_368C2, ACCESSION CC520792. CC520792.1 GI:31839080 KEXWORDS Bos taurus (cow) CRGANISM Ruminantia; Bovoidea;	REFERENCE 1 (bases 1 to 951) AUTHORS 1 to 951) AUTHORS HOLL, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, AL., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Markoh, C., Wayo, M., Masson, A., Brown, John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B.P. and Tellam, R., McWilliam, S., Barris, W., Dours, S., Contact: Rob Holt Sequencing The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6 Fax: 604-877-6085	Email: rholt@bcgsc.ca Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSTRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada. British Columbia Genome Sciences Centre, Canada. Class: BAC ends.  Class: BAC ends.  Location/Qualifiers  1. 951  / organism="breed: Hereford" / for the peamonic DNA" / strain="breed: Hereford" / for the peamonic DNA" / clone="GR240_368C2" / clone="GR240_368C2" / clone="GR240_368C2" / clone="GR240_368C2" / clone="GR240_368C2" / clone="GR240_368C2" / clone="GR240_368C2"	/notes="Vector: praffsAct.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; GHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"  Query Match 22.4%; Score 800.1; DB 1; Length 951; Best Local Similarity 93.5%; Pred. No. 0.13;

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### DNA linear GSS 18-JUN-2003 CH240_396F13.T7 CHORI-240 Bos taurus genomic clone CH240_396F13, CC594700 CS94700 GS94700.1 GI:31955684 GSS.
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Ext. 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library cavallability, please contact Pieter de Jong (pdejong@mail.cho.org).
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302 CAAGAGTGAATGTCGACATTCTAGGAATCAGCGAACTGAAATGGACTGGAATGGGTGAAT 361
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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1 (bases 1 to 938)
Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chai, A.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chai, A.,
Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,
Dalrymple, B.P. and Tellam, R.
Boyine BAC End Sequences from Library CHORI-240, PLATES 294 to 35
Contact: Rob Holt
Contact: Rob Holt
                                                                                                     362 TTAACTCAGATGACCATTATATCTACTACTGTGGGCAGGAATCCCTCAGAAGAAATGGAG
                                                                                                                                                                                                        422 TAGCCATCATGGTTAACAAGAGAGTCCGAAATGCAGTACTTGGATGCAATCTCAAAAACG
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Bos taurus (cow)
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing Columbia Cancer Agency Genome Science Centre Sequencing The British Columbia, Canada V52 4E6 (700 W. 10th Ave. Vancouver, British Columbia, Canada V52 4E6 Tel: 604-877-6085 Fax: 604-877-6085 Fax: 604-877-6276 Email: rholt@bcgsc.ca Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACEAPR Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livescock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
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                                                                                                                                                                        1 (bases 1 to 836)
11 (bases 1 to 836)
12 (bases 1 to 836)
13 (bases 2 totto, 'Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Schein,J., Marra,M., de Jong,P., Keele,J.W. and Kappes,S.W.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Other GSSS: CH203)
Contact: Rob Holt
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                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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/noce="Vector: pTARRACL.3; Site 1: MboI; Site 2: MboI;
Hereford bull_L1 Domino 99375; CHORI-240 Boviñe BAC
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/strain="breed: Hereford"
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/clone="CH240_432010"
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1. .836
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       CC548437.1 GI:314
GSS.
Bos taurus (cow)
Bos taurus
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/db_xref="taxon:9913"
/clone="CH240_195M2"
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Best Local Simi:
Matches 877;
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VERSION
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BZ882580
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                                                                                                                                                                                                                                                                                                                                                                                                                                       878 AA-CCCATGAACAGTATGAAAAGGCAAAATGATAGGATAATGAAAGGGGAACTCCNCAGG 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAACCATTCAATATCAGAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGCT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAACTAACACCCAAAAAAGAT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAĞTTAAACAGTTCTATGAAGACCTACAAGACCTTTTAGAACTAAACACCCCCAAAAGAT 280
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                                                                                                                                                                                                                                                                                                                                                290 GACAGAATGTGGTCCACTGGAGAAGGGAA-TGCAAACCACTTCAGTATTCTTGCCTTGAG 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGATGGAGCCAAAGCAAAAGAATACCCAGCTGTGGATGTGACTGGTGATATAAGCAAG 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /coll_type="Blood"
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Hereford bull il Domino 99375; CHORI-240 Bovine BAC.
library (Male) produced by Pieter de Jong"
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                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                  DB 1; Length 938;
                                                                                                                                                                                                                                                                                 22.3%; Score 798.2; DB 1; Length 93.1%; Pred. No. 0.14; ive 0; Mismatches 59; Indels
British Columbia Genome Sciences Centre, Canada.
Plate: 396 row: F column: 13
Seg primer: T?
Class: BAC ends.
                                                                                                     /mol type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH440_396F13"
/sex="Male"
                                                                                             organism="Bos taurus"
                                                        Location/Qualifiers
1. .938
                                                                                                                                                                                                                                                                                 Query Match 22.3
Best Local Similarity 93.1
Matches 876; Conservative
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Bos taurus (cow)

Eukaryotea,

Bos taurus

Eukaryotea,

Bos taurus

Boridae;

Bukaryotea,

Bovidae;

 Riggs,F., de Jong,P.,

Crawford,A.M.

Contact:

Bovidae;

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Consortium (IBBMC) by AgResarch Lidx, New Zealand and The

Institute of Genomic Research (IIGR), USA.

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CH240 195M2.TVB CHORI-240 Bos taurus genomic clone CH240_195M2,
genomic survey sequence.
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                                                                                                                                                                         1069 CAAGAAATGCACTGGTCATAGCAAACACCCTCTTCCAACAACACAAGAGAGACTCTAC 1128
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Hereford bull li Domino 99375; CHORL-240 Bovine B
library (Male) produced by Pieter de Jong"
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                                                                                                                                                                                                                                                                                                                                                       1188 AAGATGGAGAAGCTCTATACAGTCAGCAAAAACAAGACCAG 1228
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/clone_lib="CGIORI-240"
/note="Vector: pTARBACL.3; Site_1: Mbo1; Site_2: Mbo1;
Hereford bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                 AATCTCAAAAATGACAGAACAATATCTGTTCGTTTCCAAGGCAAACCATTCAATACCA
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                                                                                                                                                                                    AGAAGAAATGGAGTAGCCATCATGGTCAACAAAAGAGTCCGAAATGCAGTACTTGGAT
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                                                                                                                                                 Gaps
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0
                                                                                                               Length 899;
                                                                                                                                               48; Indels
                                                                                                           22.3%; Score 797.2; DB 1; 94.5%; Pred. No. 0.15; iive 0; Mismatches 48;
                                                                                                                                                 Conservative
                                                                                                                                nilarity
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CC480115
CR40.37074.T7 CHORI-240 Bos taurus genomic clone CH240\_30704,
CR40.3015
CC480115.
CC480115.1 GI:31758328
GSS.
Bos taurus (cow)
Bos taurus (cow)
Bos taurus (cow)
Bos taurus, (cow)
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

VERSION KEYWORDS SOURCE ORGANISM ACCESSION

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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6
Fal: 604-877-61085
Fax: 604-877-61085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pierer de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
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CH240_300L11.T7 CHORI-240 Bos taurus genomic clone CH240_300L11,
genomic survey sequence.
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                                                                                                                        TACAGTCAGCAAAAACAAGACCAGGAGCTTACTGTGGCTCAGATCATGAACTCCTTATTG 1264
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                                         AIGGICAACACCGAAAICAGAIIGAIIAIAIITCIIIGCAGCCAAAGAIGGAGAAAGCICIA 1204
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TCATAACAAACACCCTCTTCCAACAACACAAGAGAAGACTATATACATGGACATCACAAA 480
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Bazi, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., Ge Jong, P., McWilliam, S., Barris, W., Dalrymple, B.P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 399 Other GSSS: CR203

Other GSSS: CR203

Contact: Rob Holt
                                                                                                                                                                                                                                      TGATAGACAGAGTGCCTGATGAACTATGGAATGAGGTTCATGACATTGTACAGGAGACAG
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                                                                      ATGGTCAACACCCGAAATCAGATTGAGATTATATATTCTTTGCAGCCAAAGATGGAGAAGCTCTA
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VERSION
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AUTHORS
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JOURNAL
COMMENT
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CC475230
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2225
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                                                                                                                                                                                                     /sex="Male" //cell type="Blood" /cell type="Blood" /cell type="Blood" /cell type="Blood" /cole="Vector: pTARBAC1.3; Site 1: Mbol; Site 2: Mbol; /hoote="Vector: pTARBAC1.3; Site 1: Mbol; Site 2: Mbol; Hereford bull il Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pleter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2284 AACCTAGATAGCATATTGAAAAGCAGAGACATTACCTTGCCAACAAAGCCCCATCTAGTC
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                                                                          1. 958
/organism="Bos taurus"
/orl_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_300L11"
금
                                                           Location/Qualifiers
  Plate: 300 row:
Seg primer: T7
Class: BAC ends.
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1 (bases 1 to 944)

1 (bases 1 to 944)

1 Tsai,M., Clouti,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Ghan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

L Unpublished (2003)
Other GSSS: CR240 395K17.TARBAC13P2
                                                                                                                                                                                                                                            CH240_395K17.T7 CHORI-240 Bos taurus genomic clone CH240_395K17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Seq primer: 77
 2583
                                                                 TCACTGGAAAAGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGGAGGAGGACGACAG 2643
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GAAGGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGAC
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Far: 604-877-6085
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22.3%; Score 796.001; DB 1; Length 944;
Best Local Similarity 92.0%; Pred. No. 0.14;
Matches 871; Conservative 0; Mismatches 70; Indels 6;
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/mol type="genomic DNA"
/strain="breed: Hereford"
/db xref="texon:9913"
/clone="CH240_395K17"
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Location/Qualifiers
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CC593631.1 GI:31953524
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CH240_343D3.T7 CHORI-240 Bos taurus genomic clone CH240_343D3,
genomic survey sequence.
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1 GAATACCAGGCCACCTGACCTCTTGAGAAACCTATATGCAGGTCAGGAAGCAACAG
                                                                                                                                                                                                                                                                                                                                                                         241 CAGATGACACCCCTTATGGCAGAAAGTGAAGGGAACTAAAGAGCCTCTTGATGAAGA
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                                                                                                       121 GTATGTTGTCACCCTGCTTATTTAACTTATAGCAGAGTACATCATGAGAAACACTGCGC
                                                                                                                                                                                                                                                                    181 TGGAAGAAGCACAAGCTGGAATCAAGATTGCTCGGAGAAATATCAATAACCTCAGCTATG
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                                                                  1836 TTAGAACTGGACATGGAACAACAGCTGGTTCCAAGTAGGAAAAGGAGTATGTCAAGGCT
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CC503865.1 GI:31822147
GSS.
Bos taurus (cow)
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904 bp DNA linear GSS 17-JUN-2003
CH240 415B11.TARBAC13P2 CHORI-240 Bos taurus genomic clone
CCH240 415B11, genomic survey sequence.
CC536522
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Bos taurus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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Contact: Rob Holt
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             GACTTTATTTTTGGGGGGCTCCAAAATCACTGCAGATGGTGACTGCAGCCATGAAATTA
                                                                                                                                                                                                                                                                                                                   486 gagacatractricercaacaaaagricercracteaaggecrafgerritricergrageca
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                                                 368 GACTITATITIT--CIGGACICCAAAICACIGCAGAIGGIGACIGCGGCCAIAAAAIIA
                                                                                                                                   AAAGACACTTACTCCTTGGAAGAAAGTTA--ACCAACCTAGATAGCATATTGAAAAGCA
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The British Columbia Cancer Agency Genome Science Centre
The British Columbia, Canada V52 4E6
Tel: 604-877-6085
Fax: 604-877-6276
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Seq primer: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2131 ATGGCATCTGGTCCCATCACTTCATGGGAAATAGATGGGGAAACAGTGGGAAACAGTGTCA 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367
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                                                                                                            1 (Dates 1 to 914)
1 (Dates 1 to 914)
1 (Dates 1 to 914)
1 Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
1 Tsai, M., Cloutier, A. Lee, D., Girn, N., Olson, T., Mayo, M.,
1 Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
8 Mathewson, C., Mye, N., Masson, A., Brown-John, M., Jones, S.,
8 Schein, J., Marram, de Jong, P., McWilliam, S., Barris, W.,
Dalrymple, B.P. and Tellam, R.
Bevine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSS: CH20, 343D3.TARBACI3P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTGTATATTGTCACCCTGCTTATTTAACTTATATGCAGAGTACATCATGAGAAACGCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The British Columbia Cancer Agency Genome Science Centre 600 W 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6 rel: 604-877-6626 Emel: 604-877-6276 Email: rholt@bcgsc.ca Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Plater de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources.
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Bos taurus
Sukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
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Herefood bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
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/mol type="genomic DNA"
/drain="breed: Hereford"
/db xref="taxon 5913"
/clone="CH240_343D3"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Unpublished (2003)
Other_GSSs: CH240_30208.TARBAC13P2
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/organism="Bos taurus"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (cow)
Bos taurus
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availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada. Plate: 415 row: B column: 11 Seg primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526
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                                                                                                                                                                                                                                                        /cell_type="Blood"
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Hereford bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                 289 TGACAGAATGTGGTCCACTGGAGAA--GGGAATGCAAACCACTTCAGTATTCTTGCCTTG
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Pred. No. 0.15;
0; Mismatches 42;
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                                                                                                                                                                     organism="Bos taurus"
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ilarity 94.7%;
Conservative 0
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Email: whole@beggec.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 302 row: O column: 8
Seg prime: T7
Class: BAC ends.
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659 AIGICCTITICATIAIAGGGACIGGAGIGCAAAAGIAGGAAGICAAGAAACACCTGGAG
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Sequencing Control Science Centre Sequencing The British Columbia, Canada V5Z 4E6 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6 7E1: 604-877-6276 500 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6 7E1: 604-877-6276 500 M. 10th Gbcgsc.ca Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada. Plate: 374 cow: G column: 1 Seq primer: T7 Class: BAC ends.
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/strain="breed: Hereford"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Bos taurus"
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CC579657
CH240 374G1.T7 CHORI-240 Bos taurus genomic clone CH240\_374G1, genomic survey sequence.
CC579657.1 GI:31925542

RESULT 20 CC579657/c LOCUS DEFINITION

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Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering information.htm). This work was undertaken a part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada. Plate: 339 row: C column: 15 Seq primer: SP6 Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male" | Cell type="Blood" | Cell type="Blood" | Cell type="Blood" | Clone lib="CHORI-240" | Note="Vector: pTARBACI.3; Site 1: MboI; Site_2: | Hereford bull Li Domino 99375; CHORI-240 Bovine B library (Male) produced by Pieter de Jong"
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22.0%; Score 784.6; DE
Best Local Similarity 93.0%; Pred. No. 0.16;
Matches 863; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_339C15"
                                                                                                                                                                                                                                  Location/Qualifiers
1. .925
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Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
                                                                                                                                                                                                      ATTGATTATATTCTTTGCAGCCAAAGATGGAGAAGCTCTATACAGTCAGCAAAACAAGA 1224
                                                                                                                                                                                                                                                                                                                     CCAGGAGCTTACTGTGGCTCAGATCATGAACTCCTTATTGCCAAATTCAGACTTAAATTG 1284
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British Columbia, Canada V5Z
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The British Columbia Cancer
600 W. 10th Ave, Vancouver,
Tel: 604-877-6085
Fax: 604-877-6276
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Other GSSs: CH240 339C15.T7
Contact: Rob Holt
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Bovidae; Bovinae; Bos.

I (bases 1 to 934)

S Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Mathewson, C., Wye, N., Margatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Schein, J., Marra, M., de Jong, P., Keele, J.W. and Kappes, S.M.

Bovine BAC BRG Sequences from Library CHORI-240, PLATES 399 to 478

L Unpublished (2003)

Contact: Rob Holt
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/clone_lib="CHORI-240"
/note="Vector: pTARBACL.3; Site_l: Mbol; Site_2: Mbol;
Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                        GATTICITIGGAGGGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGCCACCTCATGA
                            GGATITCITTGGAAGGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGCCACCTGATCA
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CR240_425B21"
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Query Match

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                                                                                                                                                                                              AG-ACATCATGAGAAACGCTGGGCTGGAAGAAGCACAAGCTGGAATCAAGATTGCCGGGA
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QY         2095         GTTGGCTTAAAGCTCAACATTCAGAAAACGAAGATCATGGCATCTGGTCCCATCACTTCA         2154           Db         300         GTTGGCTTAAAGCTCAACATTCAGAAAACGAAGATCTGGTCCCACCACTCTCA         359           QY         2155         TGGGAAATAGATGGGGAAACAGTGGAAACAGTCTCAGACTTTATTTTTTGGGGGCTCCA         2214           Db         360         TGGGAAATAGATGGGGAAACAGTGGAAACAGTGCAGACTTTATTTTTCTGGGGGCTCCA         417           QY         2215         AAATCACTGCAGATGGCGACATGAAATTAAAAGACTTATTTTTCTGGGAAGAA         2274           Db         418         AAATCACTACAGATGGTGACTGCAGCATGAAATTAAAAGACCTTACTTCCTTGGAAGAA         477           QY         2275         AAGTTAACCAACCTAGATAGCATTATGAAAATTAAAAGACACTTGCCAACAAAAGC         2332           Dh         478         AATHALLAAACACTACAAAACAATGCAATATTGAAAATTAAAAACCTTGCCAACAAAAGC         2332           Dh         AAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2333 2393 2393 598 2453 658 2513 718	693 693 693 CC	taurus genomic clone CH240_3  Craniata, Vertebrata, Eutel actyla, Ruminantia; Pecora;  arber,S., Smailus,D., Prabhu Girn,N., Olson,T., Mayo,M., v., Liu,J., Guin,R., Chan,A., P., McWilliam,S., Barris,W., Library CHORI-240, PLATES 2  C13P2  gency Genome Science Centre ritish Columbia, Canada V5Z
ACCESSION CC547247  VERSION CC547247.1 GI:31865531  KEYWORDS GSS.  SOURCE BOS tearurs (cow)  ORGANISM Bos tearurs (cow)  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  Bovidae; Bovinae; Bos.  1 (bases 1 to 907)  AUTHORS Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,AL.,  Rati,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mathewson,C., Wye,N., Masson,A., Liu,J., Guin,R., Chan,A., Chiu,R.,  Mathewson,C., Wye,N., Masson,A., Enchandon,M., Jones,S.,  Schein,J., Marra,M., de Jong,P., Keele,JW. and Kappes,S.,  Schein,J., Marra,M., de Jong,P., Keele,JW. and Kappes,S.,  TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478	Unpublished (2003) Other 26SS: CH240_430B11.T7 Contact: Rob Holt_ Contact: Rob Holt_ Sequencing The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada v5Z 4E6 Tel: 604-877-6085 Tel: 604-877-6085 Good W. 10th Ave, Vancouver, British Columbia, Canada v5Z 4E6 Tel: 604-877-6085 Tel: 604-877-6085 Good W. 10th Ave, Vancouver, British Columbia, Canada v5Z 4E6 Enail: rholtobogs.c.a Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and tip Pritish Columbia Genome Sciences Centre, Canada. Seq primer: SP6	Class: BAC ends.  Location/Qualifiers  source  1907    Organism="Bos taurus"	Query Match         21.9%; Score 783.8; DB 1; Length 907;           Best Local Similarity         94.1%; Pred. No. 0.16;         48; Indels 6; Gaps 4;           Amatches 855; Conservative         0; Mismatches 48; Indels 6; Gaps 4;           QY         1796 TGACTCTTGAAAATTTGTATGCAGGTCAGGAAGCAACAGTTAGAACTGGACATGAACA         1855           Db         1 TGCTCTTGAAAATTGTATGCAGGTCAGGAAGCAACAGCATAGAACTGGACATGAACA         60           QY         1856 ACAGACTGGTTCCAAAAGGAGAAAGGAGTACGTCAAGATTGTCACCCGGATTA         120           QY         1916 TTTAACTTCTATGCAGAAAAGGAGAACGCAAGGCTGATATTTGTCACCCTGTTTA         120           QY         1916 TTTAACTTCTATGCAGAGAAAGGAAAAGGAAAACGCAGAGATACCACAGATATGCAAAACACAAGCTGGA         179           QY         1916 TTTAACTTATATGCAGAAAAGGAAAACGCAGAAAAAAAAA

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Fax: 604-877-6276

Baail: tholt@bogsc.ca

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (ISBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              836 AGGTCCGATGCTGTAAAAAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATG-TTC 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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Hereford bull in Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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Matches 839; Conservative 0; Mismatches 57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
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Class: BAC ends.
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(http://www.chori.org/bacpac/codesing_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
Seq primer: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GESTAL SABARTTY CHORI-240 bp DNA linear GSS 18-JUN-2003 CH240_388A3.TY CHORI-240 Bos taurus genomic clone CH240_388A3, CC589137
                                                                                                                                                         1187 AAAGATGGAGAAGCTCTATACAGTCAGCAAAAACAAGACCAGGAGCTTACTGTGGCTTCAG 1246
                                                    1247 ATCATGAACTCCTTATTGCCAAATTCAGACTTAAATTGAAGAAAGTAGGGAAAACCACTA 1306
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave. Vancouver, British Columbia, Canada V52 4E6
Tel: 604-877-6085
Exe: 604-877-6085
Email: rholt@bogsc.ca
Clones are derived from the bovine BAC library CHORI-240
availability, please contact Peiter de Jong (Decjong@mail.cho.org).
Clones may be purchased from BACBAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

1 (Dases 1 to 949)
Holt.R., Stott.J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L., Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M., Mathewson,C., Wye,N., Masson,A., Erom.-John,M., Jones,S., Schein,J., Marray,M., de Jong,P., McWilliam,S., Barris,W., Dalrymple,B.P. and Tellam,R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
                                                                                         237 ACACAIGGACATCACCAGAIGGICAAIAACCAAAATCAGAITGAITAIATATTTTTTGCAGCC 178
                                                                                                                                                                                                   177 AAAGATGGAGAAGCTCTATACAGT---CAACAACAAGAGCCAGGAGCTGACTGTGGCTCAG 121
60 AACGATTCAGGCATGACCTAAATCAAATCCCTTATGATTATACAGTGAAGAAGAAAAAAA
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/note="Vector: pTARBACI.3; Site 1: Mbol; Site 2: Mbo
Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="teaxon:9913"
/clone="CH240_388A3"
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Other GSSs: CH240 388A3.TARBAC13P2
Contact: Rob Holt
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   Query Match 21.8%; Score 779.601;
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GSS 17-JUN-2003

DNA

890 bp

CC541222

RESULT 26 CC541222/c LOCUS

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Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
7E1: 604-877-6285
Fax: 604-877-6285
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBWC) by CSIRO Livestock Industries, Australia and the
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Bos taurus genomic clone CH240_42205
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larity 93.4%; Pred. No. 0.17;
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_42205"
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CH240_42205.T7 CHORI-240
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Bos taurus (cow)
Bos taurus
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/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_429C1"
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/cell_type="Blood"
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1 (bases 1 to 881)

Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Waye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., Keele, J. W. and Kappes, S.W. Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478 Other GSSs: CH240 429C1.TARBAC13P2
                                       TCTAGGAATCAGCGAACTAAAATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTA 698
                                                                                                                                        AAGAGTCCGAAATGCAGTACTTGGATGCAGTCTCAAAAACGACAGAATGATCTCTGTTTG 818
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                           590 rcraddaarcadcaaacrdaaarddacrddaarddgarcraaarrcagardaccarra 531
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650 CATGAATCAAGGCAAATTGGAAGTGGTCAAACAGGACATGGCAAGAGTGAATGTCGACAT 591
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z
Tel: 604-877-6085
Fax: 604-877-62
Email: rhollebogsc.ca
Clones are derived from the bovine BAC library CHORI-240
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(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
Plate: 429 row: C column: 1
Class: BAC ends.
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Fax: 604-877-6085
Easi: 604-877-6086
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Piters de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
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CH240 355A2.T7 CHORI-240 Bos taurus genomic clone CH240_355A2,
genomic survey sequence.
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14 (bases 1 to 945)

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18 (barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Schein, J., Marson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B.P. and Tellam, R. Bovine BAC End Squences from Library CHORI-240, PLATES 294 to 398
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Other GSSs: CH240 355A2.TARBAC13P2
Contact: Rob Holt
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_355A2"
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(http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
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Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Matsen, G., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., Keele, J. W. and Kappes, S. M. Unpublished (2003)

Other GSSS: CH203 420A14.TARBAC13P2
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CH240 420A14.T7 CHORI-240 Bcs taurus genomic clone CH240_420A14,
genomic survey sequence.
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                                301 AAACTGAAATGGACTGGAATGGGTGAATTTAACTCAGATGACCAGTATCTACTACTGT
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Email: rholt@bcgsc.ca Clones are derived from the bovine BAC library CHORI-240 Clones are derived from the bovine 240 htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBNC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
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                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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Hereford bull Lil Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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21.7%; Score 775.4; DB 1; Length 8
Best Local Similarity 95.7%; Pred. No. 0.19;
Matches 797; Conservative 0; Mismatches 36; Indels
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        GI:31808185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Rob Holt
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                                                                                                                     ORGANISM
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1947 CGCTGGGCTGGAAGAAGCACAAGCTGGAATCAAGATTGCCGGGAGAAATAGCAATAACCT 2006
                      2447 GACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCA
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94.0%; Pred. No. 0.18;
ive 0; Mismatches 47;
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1. .896
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                                                                                                                                                                                                                                                                                                                                                                                                              778
                                                                                                                                                                                                                           301 GCTGGAATCAAGATTGCCTGGAGAAATATCAATAACCTCAGATATGCAGATGACACCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2269 GAAGAAAAGTTA--ACCAACCTAGATAGCATATTGAAAAGCAGAGACATTACCTTGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               719 GGACTGTGAAGACGCTGAGCACCGAAGAATTGATGCTTTTGAACTGTGATGTTGGAGAA
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British Columbia Genome Sciences Centre, Canada.
Plate: 420 row: A column: 14
Seq primer: 17
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                     Score 774.7; DE Pred. No. 0.18; 0; Mismatches
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1. 887
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94.0%;
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Best Local Similarity 94.0°
Matches 836; Conservative
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Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering\_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBWC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 404 row: A column: 15
Seq primer: SP6
Class: BAC ends. 896 bp DNA linear GSS 17-JUN-2003 CH240-404A15.TARBAC13P2 CHORL-240 Bos taurus genomic clone CF240, 404A15, genomic survey sequence. CC528566 CC528566.1 GI:31846854 4 1888 TCAAGGCTGTATATTGTCACCCGGCTTGTTTAACTTCTATGCAGAG-ACATCATGAGAAA 1946 1 (bases 1 to 896)

Holt R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,

Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,

Schein, J., Marra, M., Masson, A., Brown-John, M., Jones, S.,

Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478

Other GSSs: CH40-4044415.T7 838 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos. 779 GACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATGA 896 TCAAGGCTGTATAATGTCACCCTGTTTATTTAACTTATATGCAGAGTACATCATGAGAAA Gaps /cell\_type="Blood"
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Hereford bull l1 Domino 99375; CHORI-240 Bovine Elibrary (Male) produced by Pieter de Jong" Sequencing The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z Tel: 604-877-6085 7; Length 896;

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2067 GATGAAGGTGAAAGAGAGAGAGAGAGAAAAGTTGGCTTAAAAGTCAAAACTTCAGAAAAGGA 2126
                                                                                   2007 CAGATATGCAGATGATACCACCCTTATGGCAGAAAGTGAAGAGGAACTAAAAAGCCTCTT 2066
                                                                                                                                                                                                                                                                                                                        GATCATGGCATCTGGTCCCATCACTTCATGGGAAATAGATGGGGAAAACAGTGGAAAACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2247 ATTAAAAGACACTTACTCCTTGGAAGAAAAGTTA--ACCAACCTAGATAGCATATGAAA 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2425 TITGAACTGTGGTGTTGGAGAAGACTCTTGAGAGTCCCTTGGACTGCAAGGAGATCCAAC 2484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2485 ÇAĞTÇÇATTÇTGAAĞGAĞATÇAĞCCÇTĞĞĞATTTCTTTĞGAAĞĞAATĞATĞATĞCTAAAĞCTĞ 2544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2545 AAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGACTCACTGGAAAAGACCCTGATG 2604
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836 CGCTGGACTGGAAGAAACACAAGCTGGAATCAAGATTGCCAGGAGAAAT--CAATCACCT 779
                                                                                                                                           778 CAGATATGCAGATGACACCACCTTATGGCAGAAGTGAAGAGGAGTCAAAAGCTTTT 719
                                                                                                                                                                                                                                              718 GATGAAAGTGAAAGTGGAGAGTGAAAAGTTGGCTTAAAGCTCAACATTCAGAAAACGAA 659
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                                                                                                                                                                                                                                                                                                                                                                                658 GATCATGGCATCTGGTCCCATCACTTCACGGGAAATAGATGGGGAAATAGTGGAAACATT 599
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(http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the Plates 351 rows: A column: 11
                                                                                                                                                                                                     The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6 600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6 Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pleter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
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Mathewson, C., Wye, N., Marsson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McMilliam, S., Barris, W., Dalsymple, B.P. and Tellam, R. Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398 Unpublished (2003)
Other GSSs: CH40-351A11.T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGCTGTGGATGTGACTGGTGATAGAAGCAAGGTCCGATGCTGTAAAGAGAGAATATTGCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            678 ATTTAACTCAGATGACCATTATATCTACTACTGCGGGCAGGAATCCCTCAGAAGAATGG 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 AGTAGCCATCATGGTCAACAAAGAGTTCGTAATGCAGTACTTGGATGCAATCTCAAAAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell type="Blood"
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/note="Vector: pTARBACL.3; Site_1: Mbol; Site_2: Mbol;
Hereford bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Piéter de Jong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
/mol type="genomic DNA"
/strain="breed: Hereford"
/db_xref="teaxon:9913"
/clone="CH240_351A11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex≈"Male"
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GGATITICITIGGAAGGAATGAIGCTAAAGCIGAAACITCCAGIACITIGGCCACCIGAICA 2572
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/clone_lib="CHORI-240"
/note="Vector: pTARACL.3; Site_l: Mbc/
Hereford_bull_ibomino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                            Length 898,
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Pred. No. 0.18;
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'clone="CH240_356E9
                                                                                                                                                          Query Match 21.7%;
Best Local Similarity 94.0%;
Matches 846; Conservative
                   /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (cow)

Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

1 (Bases I to 899)

RS Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,

Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,

Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,

Mathewson,C., We,N., Masson,A., Brown-John,M., Jones,S.,

Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,

Balrymple,B.E. and Tellam,R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Unpublished (2003)

Contact: Rob Holt

Sequencing

The British Columbia Cancer Agency Genome Science Centre

600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6

Tel: 604-877-6276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           898 bp DNA linear GSS 17-JUN-2003
CH240_356E9.T7 CHORI-240 Bos taurus genomic clone CH240_356E9,
CC512039
CC512039.1 GI:31830327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: buta-to-rosto

Chones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Chones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering information.htm). This work

was undartaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by CSIRO Livestock Industries. Australia and the

British Columbia Genome Sciences Centre, Canada.

Plate: 356 row: E column: 9

Seq primer: T7
                                                                                    978 AAAAGTAGGAAGCAAAGAAACACCTGGAGTAACAGGCAAATTTGGCCTTGGAATACGGAA 1037
                                                                                                                                                                  1038 TGAAGCAGGCAAAGACTAATAGAGTTTTGCCAAGAAAATGCACTGGTCATAGCAAAGAC 1097
                                                                                                                                                                                                                                                 CCTCTTCCAACAACAACAAGAGAAGACTCTACACATGGACATCACCAGATGGTCAACACGG 1157
                                                                                                                                                                                                                                                                                                                             AAATCAGATTGATTATATTCTTTGCAGCCAAAGATGGAGAAGCTCTATACAGTCAGCAAA 1217
                                                      540
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              977
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                             541 AAAAGTAGGAAGTCAAGAAACACCTGGAGTAACAGGCAAATTTGGCCTTGGAATACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                             1218 AACAAGACCAGGAGCTTACTGTGGCTCAGGATCATGAACTCCTTATTG 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
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CC512039
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata, Craniata, Ruminantia; Pecora; Bovoidea;
Mammalia, Eutheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

1. (base; 1 to 915)
12. Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A.,
Mathewson, C., Mye, N., Masson, A., Brown-John, M., Jones, S.,
Schein, J., Marra, M., de Jong, P., Keele, J.W., and Kappes, S.M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Uppublished (2003)
Other GSSs: CH240-416G6.TARBACI3P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           915 bp DNA linear GSS 17-JUN-2003
Bos taurus genomic clone CH240_416G6,
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                                                                                                                                                                                                                                                                                                                                                                                               AAGTTA--ACCAACCTAGATAGCATATTGAAAAGCAGAGACATTACCTTGCCAACAAAGC 2332
                                                                                                                                                                                                                                                                                                         2215 AAATCACTGCAGATGGTGACTGCAGCCATGAAATTAAAAGACACTTACTCCTTGGAAGAA 2274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 TGGGAAATAGATGGGGAAAACAGTGGAAACAGTGTCAGACTTTATTTTT--CTGGGCTCCA 418
181 ATCAAGATTGCCAGGAGAAATATCAATAACCTCAGATATGCAGATGACACAACCTTATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2333 CCCATCTAGTCAAGGCTATGGTTTTCCAGTGGTCATGTATGGATGTGAGATTGGACTG
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                                                                                 241 GCAGAAAGTGAAGAAGCACCTCTTGATGAAGGTGAAAGGGGAGAGAGTGAAAA
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                                            GCAGAAAGTGAAGAGGAACTAAAAAGCCTCTTGATGAAGGTGAAAGAGGAGGAGAGTGAAAAA
                                                                                                                                   GITGGCITAAAGCICAACATICAGAAAACGAAGAICATGGCAICIGGICCCAICACTICA
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6
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CC536979/c
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The British Columbia Cancer Agency Genome Science Centre
600 w 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Seq primer: 77
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                                                                                                                                                                                                                                                                             1 (bases 1 to 881)
Holt, R., Stott, J., Barber, S., Smailus, D., Prabhu, A.-L., Holt, R., Stott, J., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Giin, R., Chan, A., Chiu, R., Mathewson, C., Wey, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B.P. and Tellam, R. Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398 Unpublished (2003)
Other GSSs: CH240_376A7.TARBACI3P2
                                                     881 bp DNA linear GSS 18-JUN-2003
Bos taurus genomic clone CH240_376A7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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|mol_type="genomic DNA"
|strain="breed: Hereford"
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/clone="CH240_376A7"
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                                                          CC581072
CH240_376A7.T7 CHORI-240
genomic survey sequence.
                                                                                                                                          CC581072.1 GI:31928363
GSS.
                                                                                                                                                                                             taurus (cow)
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Best Local Similarity
Matches 832; Conserv
                                                                                                                                                                                             Bos taurus
Bos taurus
                                                                                                                                CC581072
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CC581072
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314 CATICGGGTAIGACCTAAATCAAATCCCTTAIGATTATACAGTGGAAGTGACAAATAGAT
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1. .846
/organism="Bos taurus"
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CC505149/c
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JOURNAL
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AUTHORS
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KEYWORDS
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                      Email: Tholtobogsc. ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejongemail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
British Columbia Genome Sciences Centre, Canada.
Seq primer: T7
Class: BAC ends.
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llarity 93.8%; Pred. No. 0.18;
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Best Local Similarity
Matches 834; Conserv
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Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Liveetock Industries. Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 345 row: P column: 10
Seg primer: T7
Class: BAC ends.
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Hott. R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Tsai, M., Cloutier, J. Lee, D., Girn, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A.,
Schein, J., Marson, A., Brown-John, M., Jones, S.,
Schein, J., Marram, de Jong, P., McWilliam, S., Barris, W.,
Dalrymple, B.P. and Tellam, R.
Bevine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSs: CH40-345P10.TARBAC13P2
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SSS.
Bos taurus (cow)
Bos taurus Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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1370 ITAAGGGCCTAGATCTGATAGACAGAGTACCTAATGAACTATGGACAGAGGTTCATGACA
                                                                                               254 TTAAGGGACTAGATCTGATAGATAGAGTGCCTGATGAACTATGGACGAGGTTTGTGACA
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Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6
Tel: 604-877-608
Fax: 604-877-6276
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Sequencing
The British Columbia Cancer Agency Genome Science Centre
The British Columbia Cancer, British Columbia, Canada V52 4E6
Tel: 604-877-6276
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovines/Ong). For BAC library
availablity, please contact Piecer de Jong (pdejong@mail.cho.org).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
Plate: 392 row: I column: 11
Seg primer: T7
Class: BAC ends.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidea; Bovidea; Bovidea; Bovidea; Bovidea; Boses 1 to 947)
Holt.R., Stott.J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L., Taai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M., Butterfield,Y., Kirkogatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R., Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S., Schein,J., Marral,M., de Jong,P., McWilliam,S., Barris,W., Dalrymple,B.P. and Tellam,R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
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Herefrod bull lib Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/mol type="genomic DNA"
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Other GSSs: CH240_392111.TARBAC13F2
Contact: Rob Holt
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Matches 869; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1074 AAATGCACTGGTCATAGCAAACACCCTCTTCCAACAACAAAAGAGAAGACTCTACACATG 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTCATTATAGGGGACTGGAATGCAAAAGTAGGAAGCAAAGAAACACCTGGAGTAACAGG 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rcaacegrrcrargaagaccracaagaccrrrragaacraaccccaaaaaagargrccr 247
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                                                                                                                                          355 ATGAACAGTATG-AAAAGGCAAAATGATAGGATACTGAAAGAGGAACTCCCCAGGTCAGT
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                                                                                               Gaps
                                                                                                 ä
                                                          Length 846;
               library (Male) produced by Pieter de Jong'
                                                                                                 Indels
                                                          DB 1;
                                                                                                 34;
                                                      Score 770.7; D
Pred. No. 0.2;
0; Mismatches
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                                                        21.6%;
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Bos taurus
                                                                                 Similarity
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SOURCE
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CC591633/c
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availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada. Plate: 383 row: G column: 13 Seg primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                           TGACAGAATGTGGTCCACTGGAGAAGGGAAT-GCAAACCACTTCAGTATTCTTGCCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACCCCATGAACAGTATGAAAAGGCAAAATGATAGGATACTGAAAGAGGAACTCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGACAGAAAAGTGGTCCACTGGAGAAGGGAATGGCAAACCACTTCAGTATTCTTGCCTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GGTCTGAFGCTGTAAAGAGCAATATTGCATAGGAACCTGAAATGTCAAGCCCATGAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCCTTCTCATTATAGGGACTGGAATGCAAAAGTAGGAAGCAAAGAAACACCTGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588 AGGCAAATTGGAAGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCGAACTAAAATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATCTACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAACCATTCAATATCACAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTGAAGAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 858;
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                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                       21.5%; Score 768.8; D
94.9%; Pred. No. 0.2;
iive 0; Mismatches
                                                                                                                                                                Location/Qualifiers
1. 858
1. 858
7. organism="Bos taurus"
Mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_383G13"
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.9
Matches 815; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289
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Buxaryota, Butheria; Cetartiodactyla, Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

1 (Dases 1 to 858)
1 (Dases 1 to 858)
1 Holt, Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Glain,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Contact: Rob Holt
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                                                                                             533 TTAAAAGATGCTTACTCCTTGGAAGGAAAGTTATGACCAACCTAGACAGCGTATTCAAAA 474
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                   TCAGACTTTATTTTTGGGGGGCTCCAAAATCACTGCAGATGGTGACTGCAGCCATGAAA
                                                                      TTAAAAGACACTTACTCCTTGGAAGAAAGTTA--ACCAACCTAGATAGCATATTGAAAA
                                                                                                                                                                  TCATGTATGGATGTGAGAGTTGGACTGTGAAGAAAGCTGAGCACTGAAGAATTGATGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6
7E1: 604-877-6085
Fax: 604-877-6236
Faxil: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CH240 383G13.TARBAC13P2 CHORI-240 DNA linear GSS 18-CH240 383G13.TARBAC13P2 CHORI-240 Bos taurus genomic clone CH340 383G13, genomic survey sequence. CC586052 CC586052.1 GI:31938331 GSS.
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KEYWORDS
SOURCE
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CC586052
LOCUS
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587

300 647 360 707 420 767 480 827 1007

540

887 600 947 099

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344 TTGAGAACCCCATGAACAGTATGAAAAGGC-AAAATGATAGGATACTGAAAGGCGAACTC	463 ANTGARGAGGGCCAAACCAAAGGATACCCAGCTGTGGATGTGGTGGTGATATA  757 AATGAAGGGATGGAGCCAAAGCAAAACAATATCCAGCTGTGGATGTGACATAGA  523 AGCAAGGTCCGATGCTGTAAAGAGCAATATGCATAGGAATGTGACTGGTGATAGA  523 AGCAAGGTCCGATGCTGTAAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATG	Db   697 AGCAAGGTCCGATGCTGTAAAGAGCAATATTGCATAGGAACCTGGAATGTCAGGTCCATG 638	Qy         763 GTCCGAAATGCAGTACTTGGATGCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTT	Qy         943 AAAGATGTCCTTCTCATTATAGGGGACTGGAATGCAAAGAAGCAAAGAAACACCT         1002           Db         277 AAAGATGTCCTTTTCATTATAGGGGACTGCAAAGATGCAAAAGTAGGAAGTCAAGAAACACCT         218           Qy         1003 GGAGTAACAGGCAAATTTGGCCTTGGAATACGGAATGAAGCAGGCAAAGACTAATAGAG         1062           Db         217 GGAGTAACAGGCAAATTTGGCCTTTGGAATACGGAATGAAGGGGCAAAGGCTAATAGAG         118           Qy         1063 TTTTGCCAAGAAATGCCTCTTTGAATACGGAATGAGGGGGAAGGGCTAATAGAG         112           Db         157 TTTTGCCAAGAAATCCTGGCTCATAGCAAACACCCTCTTCCAACAACACACAC	Oy 1182 CAGCCAAAGATGGAGAAGCTCTATACAGTCAGCAAAACAAG 1223
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Sequencing
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Email: rholt@bcgsc.ca
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(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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                                                    TTGCATGCAATCTCAAAAAACGACAGAATGATCTCTGTTCGTTTCCAAGGCAAACCATTCA
                                                                                                                                                              361 ATATCACAGTAATCCAAGTCTATGCCCCAACCAGTAACACTGAAGAAGCTGAAGT
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                                                                                                                                                                                                              899 GGTCCTATGAAGACCTACAAGACCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCA
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Seg primer: T7
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Clones are derived from the bovine BAC library CHORI-240
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was undertaen as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
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Class: BAC ends.
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1 (balt, R. Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R.,
Rathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
Schein, J., Marra, M., de Jong, P., Keele, J. W. and Kappes, S. M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Other GSSS: CH203)
Contact: Rob Holt
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Fax: 604-877-6276
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Sequencing
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Email: rholt@bcgsc.ca
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was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
Plate: 376 columbia Genome Sciences Centre, Canada.
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                                                                                                                                                                                          COSSIGN 822 bp DNA linear GSS 18-JUN-2003 CH240 376F14.T7 CHORI-240 Bos taurus genomic clone CH240_376F14, CRSR 4.5-E
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                                               1040 AAGCAGGCAAAGACTAATAGAGTT 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             805 AAGACAGGCGGTCATGCTGGAGAAAATCTGACAGAAAATGTGGTCCACTGGAAAAAAGGGAAATG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 TTAACTCAGATGACCATTATATCTACTACTGTGGTAAGAATCCCTCAGAAGAAATGGAG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 ACAGAATGGTCTCTGTTCCAAGGCAAACCATTCAATATCACAGTAATCCAAGTCT 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 CACTAGGACCACAGCCTTGTCTAACTCAATGAAA-CTAAGCCATGCCCGTGGGGCAACCC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 AAGATGGGCAGGTCATGGTGGAGAGTCTGACAGAATGTGGTCCACTGGAGAAGGGAATG 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 TAGCCATCATGGTCAACAAAAGAGTCCAAAATGCAGTACTTGGATGCAATCTCAAAAAGG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          800 ACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCAATATCACAGTAATCCAAGTCT 859
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                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                             Query Match 21.5%; Score 768.4; DB 1; Length 865; Best Local Similarity 94.5%; Pred. No. 0.2; Matches 817; Conservative 0; Mismatches 46; Indels 2
                                                                                         /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_412K21"
                                                                       /organism="Bos taurus"
                     Location/Qualifiers
Class: BAC ends.
                       FEATURES
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The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave. Vancouver, British Columbia, Canada VSZ 4E6 7e1: 604-877-6085

Fax: 604-877-6276

Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/codering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
Plate: 396 row: L column: 24
Seg primer: 8P6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_396124"
/sex="Male"
/sex="Male"
/clone="Iba"CH30A13; Site 1: MboI; Site 2: MboI;
/note="Vector: PIARBAC1.3; Site 1: MboI; Hereford bull in Domino 99375; CHOR1-240 Bovine BAC library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       980 AAGTAGGAAGCAAAGAAACACCTGGAGTAACAGGCAAATTTGGCCTTGGAATACGGAATG 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.5%; Score 767; DB 1; Length 861; 94.5%; Pred. No. 0.2; ive 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 94.5
Matches 815; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

1. (bases 1 to 861)
1. Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Tsai,M.; Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Mathewson,C., Wye,N., Kaikepatrick,R., Liu,J., Guin,R., Chan,A.,
Mathewson,C., Wye,N., Masson,A., Eliu,J., Guin,R., Jones,S.,
Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
Bavine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Ultpublished (2003)
Other_GSSs: CH240_396L24.T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          861 bp DNA linear GSS 18-JUN-2003
CH240_396L24.TARBAC13P2_CHORI-240 Bos taurus genomic clone
CH240_396L24, genomic survey sequence.
CC595021
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                                                                             AGGCAAATTGGAAGTGGTCAAACAAGAGATGGCAAGAGTGAATGTCAACATTCTAGGAAT 647
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                                                                                                                         AGGCAAATTGGAAGTGAAGAAGAGATGGCAAGAGTGAATGTCGACATTCTAGGAAT 583
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                                                                                                                                                                       CAGCGAACTAAAATGGACTGGAATGGGTGAATTTAACTCAGATGACCATTATATCTACTA
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Hereford bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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E voltiae; Bovinae; Bos.

E (bases 1 to 870)

S Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Mason, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, P.P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398 Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rholt@bogsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CGIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Seq primer: SPS row: L column: 21
Seq primer: SPC column: 21
                                                                                  AAGCAGGGCAAAGACTAATAGAGTTTTTGCCAAGAAAATGCACTGGTCATAGCAAACACCC 1099
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600 AAGCAGGGCAAAGGCTAATAGAGTTTTTGCCAAGAGAATGCACTGGTCATAGCAAAACACC 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC512505 870 bp DNA linear GSS 17-CH240_356121.TARBAC13P2 CH041-240 Bos taurus genomic clone CH240_356121, genomic survey sequence.
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Strain="breed: Hereford"

/db_xref="taxon:9913"

/clone="CH240_356L21"

/sex="Male"
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Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Seq primer: Se
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7
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                      Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown John, M., Jones, S., Schein, J., Marra, M., de Jong, P., Keele, J. W. and Kappes, S. M. Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 470 Unpublished (2003)
Other GSSS: CH240, 420F7.T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6
Tel: 604-877-6085
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Holt, R., Stott, J.,
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                                                                                                                                                                                         taurus (cow)
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Best Local Similarity
Matches 815; Conserv
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KEYWORDS
SOURCE
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241 GGAACCTGGAATGTTAGGTCCATGAATCAAGGCAAATTGGAAGTGGTCAAACAAGAGATG 300
                                                                                      678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACCTTTTAGAACTAACACCCAAAAAGAIGICCTTCTCATTATAGGGGACTGGAATGCA 978
                                                                                                                                   GCAAGAGTGAATGTCGACATTCTAGGAATCAGCGAACTGAAATGGACTGGAATGGGTGAA
                                                                                619 GCAAGAGTGAATGTCAACATTCTAGGAATCAGCGAACTAAAATGGACTGGAATGGGTGAA
                                                                                                                                                                                                     TTTAACTCAGATGACCATTATATCTACTACTGCGGCCAGGAATCCCTCAGAAGAAATGGA
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0y 1590 TGATTATTATGCACTGTGGGGAGTTTCTTTCCGGTCCAALCTATTGGTGTTTTTTTTTT	RESULT 35 US-10-32-281-495   Sequence 495, Application US/10322281   Sequence 495, Application US/10322281   Sequence 495, Application US/2040126762A1   Sequence 495, Application US/2040126762A1   Publication No. US20040126762A1   APPLICANT: Max C. Malandro   TILLE OF INVENTION: Novel Compositions and Methods in Cancer TILLE OF INVENTION: Novel Compositions and Methods in Cancer TILLE OF INVENTION: US/2010000   CURRENT PELING DATE: 2002-12-17   NUMBER OF SEQ ID NOS: 866   SEQ ID NO 495   SEQ ID NO 495   TYPE: DAA ORGANISM: Mus musculus   FEATURE: No. 1864     TYPE: DAA ORGANISM: Novel Cancer Seq ID NOS: 866   DE 17. (16594)     COCATION: (1)(176594)   DE 24.5%; Score 558.6; DE 1; Length 176594;     LOCATION: (1)(176594)   DE 24.5%; Score 558.6; DE 1; Length 176594;     CURRENT INVENTATION: n = A,T,C or G
\$36.0 AGTITTGGGTTTTG-GTGAAATAGTCTGTAAATACT-CTAGGTCCACTTGGTTTATGA \$87.5 \$16.0 AGTITTGGTTTTG-GTGAAATAGTCTGTAAATACT-CTAGGTCCACTTGGTTTATGGTTCATAG \$36.37 \$16.0 AGTICTTTGGTTTGAATTGAATTGAATTGAATTGAATTGA	1052 CATTGATGTTGAGAATTATCAATGAGCAGTGTTGTGGATTCTTGTTATCTTGTGTATTTTTTTT